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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEЛА CELLS OR OTHER HUMAN CERVICAL EPITHELIAL CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells is described. Also described are single exon nucleic acid probes expressed in the HeLa cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HELA CELLS OR
OTHER HUMAN CERVICAL EPITHELIAL CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the 10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of 15 UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
20 REFERENCE THEREOF

The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in 25 triplicate, containing a file named pto_HELA.txt, created 24 January 2001, having 18,781,468 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In 35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human HeLa cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had 10 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane 20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes 30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of 35 mRNA – are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this 5 approach, often the only biological information that is known *a priori* with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of 10 the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot 15 be presumed; often the only *a priori* biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing 20 approaches – and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species – there is an increasing need for methods that rapidly and effectively permit the functions of nucleic 25 sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and 30 apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 35 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al., *Ismb* 5:294-302 (1997); and GENSCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known,
5 however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.

Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may
15 need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the
20 expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in
25 Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes 5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of 10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally 15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Summary of the Invention

20 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present 25 invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel 30 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in 35 sequence to, probes on the genome-derived single exon

microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 18,392 or a complimentary sequence, or a portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 5
5 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is 10 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

15 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane 20 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, 25 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is 30 provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of 35 amplifiable probes corresponding to the probes, or one or

more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

5 In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon 10 probes that include specifically-hybridizable fragments of SEQ ID Nos. 9,291 - 18,392, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,290.

15 Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule comprising a nucleotide 20 sequence as set out in any of SEQ ID NOS.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

25 In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.

30 In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID 35 NOS.: 18,393 - 26,941 or a complementary sequence or a

fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or 10 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. 15 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art. 30

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a 35 single exon nucleic acid probe in accordance with either

the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
5 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to
10 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

15 contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells;
20 and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:
25

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

30 wherein said detectably labeled nucleic acids are derived from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon,
35 said probe is included within a single exon microarray in

accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,
5 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in
10 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types
15 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 18,392 wherein said sequence encodes a peptide.

20 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 9,291 - 18,392, or a complementary sequence or coding portion thereof.

25 In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 9,290.

30 In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 18,393 - 26,941.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 18,393 - 26,941, or fragment thereof.

35 In another aspect, the invention provides means

for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for 5 electronic search, query, and analysis of such annotated sequence.

Detailed Description of the Invention

10

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each 15 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called 20 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books 25 Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary 30 planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

35 As used herein with respect to a nucleic acid

microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons

encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a 5 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF 10 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another 15 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit 20 specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display 25 of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual 30 object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

Brief Description of the Drawings

The present invention is further illustrated with
5 reference to the following non-limiting figures and
examples in which:

FIG. 1 illustrates a process for predicting
functional regions from genomic sequence, confirming the
functional activity of such regions experimentally, and
10 associating and displaying the data so obtained in
meaningful and useful relationship to the original sequence
data;

FIG. 2 further elaborates that portion of the
process schematized in FIG. 1 for predicting functional
15 regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical
annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of
20 ORF length and PCR products as obtained, with ORF length
shown in black and PCR product length shown in dotted
lines;

FIG. 6 is a histogram showing the distribution,
among exons predicted according to the methods described,
25 of expression as measured using simultaneous two color
hybridization to a genome-derived single exon microarray.
The graph shows the number of sequence-verified products
that were either not expressed ("0"), expressed in one or
more but not all tested tissues ("1" - "9"), or expressed
30 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
expression of verified sequences that showed expression
with signal intensity greater than 3 in at least one
tissue, with: FIG. 7A showing the expression as measured by
35 microarray hybridization in each of the 10 measured

tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for 5 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the 10 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than 1e-30 (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than 1e-30 (1×10^{-30}) ("known");

15 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

20

Methods and Apparatus for Predicting, Confirming,
Annotating, and Displaying Functional Regions From Genomic
Sequence Data

25 FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained 30 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence 35 is usually obtained from subgenomic fragments, the sequence

data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C. briggsii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by 5 the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into 10 mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into 15 process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will 20 be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental 25 confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the 30 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often 35 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the 5 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within 10 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

15 The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

20 FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and 25 facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or 30 interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of 35 functional sequence within genomic sequence according to

process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 5 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis 10 approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, 15 corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

20 The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic 25 sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in 30 addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 35 only those sequences present within contigs sufficiently

long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40 kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic,

temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as

processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, 5 or that would interfere with, the subsequent analysis.

Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.

Such removal can readily be performed by identification and 10 subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual 15 sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, 20 including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known 25 restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be 30 removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired 35 sequence can be excised from the returned genomic sequence,

leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X

chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function 5 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as 10 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for 15 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) 20 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene 25 finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; 30 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, 35 consensus among methods will in general increase

reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such 5 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored 10 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further 15 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 20 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three 25 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used 30 approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison 35 can be performed not only on genomic nucleic acid sequence,

but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the 5 multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 10 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to 15 identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon 20 consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene 25 expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible 30 secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving 35 hybridization stringency can be applied to identify that

subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such 5 sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 10 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in 15 process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the 20 sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression 25 of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon 30 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the 35 polymerase chain reaction (PCR). Although PCR is

conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with 5 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

10 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer 15 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify 20 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

25 Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it 30 has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

35 The putative ORFs selected in process 300 are

thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently; a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology

: A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 5 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

10 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, 15 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes 20 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single 25 exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see 30 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, 35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, 5 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

10 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination 15 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or 20 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

25 As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can 30 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create 35 a nucleic acid microarray can consist entirely of natural

nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.

- 5 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using
10 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on
15 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.

- 20 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads
25 provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high
30 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will
35 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one 5 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

10 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created 15 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived – either directly or 20 indirectly – from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" 25 libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure 30 expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective 35 genes within the tissues, and by the ability of the message

successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be 5 determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the 10 present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA 15 library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

20 In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present 25 invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse 30 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, 35 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric 5 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-10 derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present 15 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the 20 specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically 25 include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector 30 sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes 35 disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning

artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 35 75, 80, 85, 95 or 99% of probes deposited in the genome-

derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA.

Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to 5 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

10 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present 15 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved 20 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention 25 typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their 30 complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower 35 percentage differences in melting temperature across the

range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* – that is, only about 4 - 5% – have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about

one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

5 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization
10 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the
15 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can
20 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see
25 Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of
30 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As
35 further described in Example 2, *infra*, Cy3 and Cy5 dyes

prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

5 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are
10 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain
15 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for
20 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived
25 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate
30 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits
35 addressable withdrawal of reagent from fluidly-

noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' 10 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

15 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

20 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered 25 set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing 30 information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate 35 that incorporates recordable media, such as is described in

international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

5 The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

10 Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

15 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

20 For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to 35 inform analyses subsequently undertaken in process 200,

process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data 5 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or 10 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or 15 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence 20 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic 25 works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given 30 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left 35 border of display 80 to its right border. By convention

herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

5 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides
10 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other
15 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.
20 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or
25 fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity
30 or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection
35 tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method

and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-

selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the 5 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional 10 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an 15 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

20 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 25 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the 30 probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of 35 expression databases with the sequences predicted in

process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting 5 thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

10 Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be 15 predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified 20 in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and 25 displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity 30 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links 35 directly to the sequences identified by the query of

expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further

information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data 5 from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the 10 physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence 15 that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to 20 rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

25

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from 30 genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of 35 the present invention rapidly yield large numbers of

single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

5 It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon 10 microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of these ORFs in 15 HeLa cells.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in HeLa cells is currently available for use in measuring the level of its ORF's 20 expression in HeLa cells.

Expression in HeLa cells provides a first level screen for demonstrating the expression of exons predicted from genomic sequence.

HeLa cells are derived from human cervical cells. 25 Accordingly, it would be appreciated by one of skill in the art that each single exon probe having demonstrable expression in HeLa cells is available for measuring the level of its ORF expression in other human cervical epithelial cells thus making such detection of expression 30 useful in grading and/or staging of diseases of cervix, notably cervical carcinoma.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. 35 and Maniatis et al. - each probe reports the level of

expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the HeLa cells has been demonstrated are useful for both 5 measurement in the HeLa cells or other human cervical epithelial cells and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

10 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the 15 ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was 20 measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or 25 tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the 30 present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

Gene expression analysis using microarrays – 35 conventionally using microarrays having probes derived from

expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple

Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf *et al.*, "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 5 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi *et al.*, "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of 10 pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

15 For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part.

20 Analogously, where gene expression analysis is used to assess side effects of pharmacological agents – whether in lead compound discovery or in subsequent screening of lead compound derivatives – the inability of the agent to alter a gene's expression level is evidence that the drug does 25 not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene 30 expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in 35 Gerhold *et al.*, *Trends Biochem. Sci.* 24(5):168-173 (1999)

and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in HeLa
5 cells.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

10 Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules
15 so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,
20 morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the
25 amplified product is thereafter to be used in the hybridization reactions that probe gene expression.

Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to
30 PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are to be provided in a form suitable for amplification, the
35 range of nucleic acid analogues and/or internucleotide

linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form suitable for amplification, the quantity need not be 5 sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be 10 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first 15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe 20 composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the 25 present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the 30 genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however - that is, for use in a hybridization reaction in which the probe is not first 35 bound to a support substrate (although the target may

indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that 5 dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human 10 genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention 15 can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,291 - 18,392, respectively, for probe SEQ ID NOS. 1 - 9,290. The minimum amount of ORF required to be included in the probe of the present invention in order to 20 provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,291 - 18,392 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, 25 *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a 30 humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization 35 at 65°C in 6X SSC. Lower stringency conditions, suitable

for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room
5 temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single
10 exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more
15 than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more
20 than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well
25 understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in
30 both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and
35 below, and double-stranded probes one strand of which has

sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that 5 the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can 10 usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, 15 *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for 20 ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be 25 provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural 30 individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

35 If, as earlier mentioned, the ORF-specific

5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human HeLa 10 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

15 The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid 20 amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays 25 useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a 30 plurality of probes known to be expressed in human HeLa cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,290.

35 When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from
10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the
15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as
20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,290 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,291 - 18,392, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,290 can be
25 used, or that portion thereof in SEQ ID NOS. 9,291 - 18,392 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially
30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo
35 Alto, CA; Protein Fusion & Purification (pMAL™) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7), Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,291 - 18,392. Such amino acid sequences are set out in SEQ ID NOS: 18,393 - 26,941. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted
in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method 5 approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support 10 substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF 15 was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was 20 commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to 25 add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon 30 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR® 35 green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp,
25 constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent 5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was 10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using 15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of 20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) 25 produced an exact match (BLAST Expect ("E") values less than $1 e^{-100}$) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from $1 e^{-5}$ to $1 e^{-99}$). The remaining 45% of 30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt 35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5 Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant 5 signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single 10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of 15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the 20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using 25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e- 30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. ...In brain, 200 uniquely expressed genes were 35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more
5 "novel" genes among those that were up-regulated in only
one tissue, as compared with those that were down-regulated
in only one tissue. In fact, it was found that ORFs whose
expression was measurable in only a single of the tested
10 tissues were represented in sequencing databases at a rate
of only 11%, whereas 36% of the ORFs whose expression was
measurable in 9 of the tissues were present in public
databases. As for those ORFs expressed in all ten tissues,
fully 45% were present in existing expressed sequence
databases. These results are not unexpected, since genes
15 expressed in a greater number of tissues have a higher
likelihood of being, and thus of having been, discovered by
EST approaches.

Comparison of Signal from Known and Unknown Genes

20 The normalized signal of the genes found to have
high homology to genes present in the GenBank human EST
database were compared to the normalized signal of those
genes not found in the GenBank human EST database. The
data are shown in FIG. 8.

25 FIG. 8 shows the normalized Cy3 signal intensity
for all sequence-verified products with a BLAST Expect
("E") value of greater than 1e-30 (designated "unknown")
upon query of existing EST, NR and SwissProt databases, and
shows in blue the normalized Cy3 signal intensity for all
30 sequence-verified products with a BLAST Expect value of
less than 1e-30 ("known"). Note that biological background
noise has an averaged normalized Cy3 signal intensity of
0.2.

As expected, the most highly expressed of the
35 ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large
5 number of even the high expressers were "unknown". Since
the genomic approach used to identify genes and to confirm
their expression does not bias exons toward either the 3'
or 5' end of a gene, many of these high expression genes
will not have been detected in an end-sequenced cDNA
10 library.

The significant point is that presence of the
gene in an EST database is not a prerequisite for
incorporation into a genome-derived microarray, and
further, that arraying such "unknown" exons can help to
15 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
described above to identify genes from raw genomic
20 sequence, expression of two of the probes was assayed using
reverse transcriptase polymerase chain reaction (RT PCR)
and northern blot analysis.

Two microarray probes were selected on the basis
of exon size, prior sequencing success, and tissue-specific
25 gene expression patterns as measured by the microarray
experiments. The primers originally used to amplify the
two respective ORFs from genomic DNA were used in RT PCR
against a panel of tissue-specific cDNAs (Rapid-Scan gene
expression panel 24 human cDNAs) (OriGene Technologies,
30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray
hybridization to be present in cardiac tissue, and sequence
AL031734_1 was shown by microarray experiment to be present
in placental tissue (data not shown). RT-PCR on these two
35 sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and
5 indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in
10 expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

15 To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed
20 high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences
25 showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain

Microarray Sequence Name	Normal Signal	Expressed on Ratio	Homology present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca²⁺ binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191
(1999)). Two microarray sequences, AP000047-1 and
15 AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of
these genes, showing the power of designing microarrays in
this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,
AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 10 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again 5 demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray 10 experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15 For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding 20 programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual 25 display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

30 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S
ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in HeLa cell line.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,290 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,290 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,290. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,291 - 18,392, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the 5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

20 The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

25 Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

30 The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human HeLa cells and thus presents the subset of probes that was recognized to be 5 useful for measuring expression of their cognate genes in human HeLa cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,291 - 18,392 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to 10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as 20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the 25 SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of 30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is 35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: . The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about 1e-05 and 1e-100), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of 1e-05 (i.e., 1×10^{-5}) and 1e-100 (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of 1e-30 was used as the boundary when only two classes were to be defined for analysis (unknown, >1e-30; known <1e-30) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about 1e-100 - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely 5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present 10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached 15 sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 9,290) and probe exon (SEQ ID NOS.: 9,291 - 18,392, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which 20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST 25 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and 30 BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX 35 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human HeLa cells

Table 4 (382 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human HeLa cell line.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human HeLa cells or other human cervical epithelial cells comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,290 or a complementary sequence, or a portion of such a sequence.
10
2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,291 - 18,392.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid

probes as claimed in any of claims 1 to 6, wherein the average length of the single exon nucleic acid probes is between 200 and 500 bp.

5 8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

10 9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

15 10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

20 11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

25 12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human
30 gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 9,290 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a
35 nucleic acid molecule expressed in the human HeLa cells or

other human cervical epithelial cells.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ 5 ID NOS.: 9,291 - 18,392 or a complementary sequence or a fragment thereof.

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human HeLa cells 10 or other human cervical epithelial cells which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 18,393 - 26,941, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high 15 stringency to a nucleic acid expressed in the human HeLa cells or other human cervical epithelial cells.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid 20 probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb 25 in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

30 19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

35 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and

bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one of claims 13 - 20, wherein said probe lacks homopolymeric 5 stretches of A or T.

22. A method of measuring gene expression in a sample derived from human HeLa cells or other human cervical epithelial cells, comprising:

10 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human HeLa cells or other human cervical epithelial cells; and then
15 measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

20 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived 25 from mRNA from the HeLa cells or other human cervical epithelial cells of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 30 12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

35 identifying a plurality of exons from genomic

sequence according to the method of claim 23; and
then

measuring the expression of each of said exons in a
plurality of tissues and/or cell types using
5 hybridization to single exon microarrays having a
probe with said exon,

wherein a common pattern of expression of said exons in
said plurality of tissues and/or cell types indicates that
the exons should be assigned to a single gene.

10

25. A nucleic acid sequence as set out in any of SEQ ID
NOS: 1 - 18,392 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
15 SEQ ID Nos: 1 - 18,392.

27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 18,393 - 26,941.

20

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
456	9709	18846	5.87				
898	10134	19296	11.93				
1032	10278		2.08				
1309	10525	19885	19.17				
1593	10806	19882	2.78				
1613	10526	20001	12.21				
1700	10912	20098	1.72				
1721	10933	20116	1.1				
1727	10939	20122	9.25				
1856	11063	20254	1.76				
1947	11151	20353	2.13				
2131	11330	20348	1.94				
2244	11439	20663	2.03				
3119	12384	21517	3.28				
3428	12651	21781	1				
3489	12713	21849	8.63				
3535	12758		0.67				
3637	12658	21977	0.97				
3923	13139		1.02				
4179	13383	22484	1.57				
4248	13451	22342	7.61				
4286	13469	22581	0.84				
4286	13469	22582	0.84				
4330	13531		1.28				
4388	13587	22889	0.79				
4854	14043	23137	1.05				
4888	14087		0.89				
5070	14250	23333	5.18				
5404	14632		5.28				
5488	14714		6.43				
5525	14632		4.42				
5548	14770	24137	3.03				
5659	18062	24282	1.69				
5659	14608	24301	1.91				

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6484	15681	25150	2.19				
6830	16123	25580	5.79				
7275	16494		2.73				
7422	18078	26126	1.85				
7586	16789		3.09				
7689	17115	26847	2.51				
7887	18432	25919	2.03				
7887	18432	25920	2.03				
8034	17170		2.59				
8748	17691		1.72				
8085	17892	23899	1.79				
9279	16041		1.22				
5689	14909	24202	15.7	9.9E+00	A1239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
6468	15663	25134	2.2	9.8E+00	U52716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
2874	12112	21240	3.14	9.4E+00	AB0443785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
6788	15881	25417	3.22	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5326	14558	23828	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5326	14558	23830	2.48	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5676	14698	24298	5.52	8.9E+00	BE071806.1	EST_HUMAN	6016510238R1 NIH_MGC_B1 Homo sapiens cDNA clone IMAGE:3834582 3'
5824	15041	24444	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CptIbx3 premature mRNA, partial cds
5824	15041	24445	2.15	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CptIbx3 premature mRNA, partial cds
446	9700	18836	1.88	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6886	15602	25068	2.76	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see 2a)
7728	18928		2.49	8.0E+00	P14820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
6229	15410		1.77	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
5572	14798	24170	4.33	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:42855506 5'
6703	15898	25359	2.97	7.4E+00	PO4929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
6703	15698	25360	2.97	7.4E+00	PO4829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2834	12172	21305	3.8	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
2834	12172	21306	3.8	7.2E+00	L12051.1	NT	Lycopersicon esculentum Mill. GTPase (SAR2) mRNA, complete cds
6880	16138		11.08	7.1E+00	AL161895.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
7824	17137	28698	4.06	7.1E+00	PO5850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-RPHB INTERGENIC REGION

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7088	16245	25720		3.26	7.0E+00	P48810	SWISSPROT ARGININE KINASE (AK)
7802	16995	28509		1.94	7.0E+00	Q22489	SWISSPROT WD-40 REPEAT PROTEIN MS13
6553	15749	25210		5.33	6.9E+00	P35679	SWISSPROT 60S RIBOSOMAL PROTEIN L4 (L2)
7137	16314	25785		4.45	6.8E+00	Q03570	SWISSPROT HYPOTHETICAL 167.0 kDa PROTEIN C38C10.5 IN CHROMOSOME III
7097	16274	25752		2.93	6.6E+00	Q9ZE07	SWISSPROT URIDYLATE KINASE (UK) (URIDYLIC MONOPHOSPHATE KINASE) (UMP KINASE)
7097	16274	25753		2.83	6.6E+00	Q9ZE07	SWISSPROT URIDYLATE KINASE (UK) (URIDYLIC MONOPHOSPHATE KINASE) (UMP KINASE)
7588	16887			2.54	6.6E+00	Q10309	SWISSPROT PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
6824	18018	25483		6.58	6.5E+00	P03374	SWISSPROT ENV POLYPROTEIN (CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP56)
5885	15102	24513		6.98	5.9E+00	AF155142.1	NT
3497	12721			0.84	5.8E+00	7661557	NT
8011	16448	25936		2.42	5.6E+00	Q55276	Homo sapiens DESC1 protein (DESC1), mRNA
7580	16576			1.76	5.5E+00	AF175425.1	SWISSPROT LYCOPENE BETA CYTCLASE
8010	16445	25935		3.03	5.5E+00	P11980	NT
82222	17352			1.85	5.5E+00	AL164571.2	SWISSPROT PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
4795	13984	23089		1.28	6.3E+00	[L]43126.1	NT
6492	15689			3.71	5.3E+00	P54098	Arabidopsis thaliana DNA fragment No. 67
8147	17279	26824		1.68	5.3E+00	Q27805	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
7749	16946			2.12	6.2E+00	Q10138	SWISSPROT PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
7119	16368	25846		4.81	5.0E+00	AF162445.2	SWISSPROT HYPOTHETICAL 61.1 kD PROTEIN C35E2.03C IN CHROMOSOME I
7838	17030	26546		12.07	5.0E+00	P23890.1	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
4038	13249			12.68	4.8E+00	AF185555.1	NT
65358	15831			4.93	4.8E+00	AW750067.1	Eukarya australis histone H3 (H3) gene, partial cds
284	9568	18700		2.43	4.7E+00	BF240552.1	PN0-BT0547-31010-002-504 BT0547 Homo sapiens cDNA
285	9568	18700		2	4.7E+00	BF240552.1	EST_HUMAN 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3241	12475	21606		1.02	4.7E+00	AL163280.2	EST_HUMAN 601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
8131	17285	26809		1.9	4.5E+00	AE001044.1	Archaeoglobus fulgidus section 63 of 172 of the complete genome
8235	17384	26902		1.67	4.5E+00	BF668841.1	EST_HUMAN 6022423238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3005	12241	21371		0.96	4.4E+00	BF530893.1	EST_HUMAN 602072585F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3005	12241	21372		0.96	4.4E+00	BF530893.1	Plasmidium falci parum R29R-var1 gene, exon 1
6268	15448	24887		2.48	4.3E+00	Y13402.1	NT
7438	16847	26140		8.75	4.3E+00	AF240786.1	Human sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	14974			3.45	4.2E+00 P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP)(DEHYDROPEPTIDASE-I)(RENAL DIPEPTIDASE) (RDP)
5988	15270	24697		1.82	4.2E+00 P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
5988	15270	24698		1.82	4.2E+00 P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6757	15952	25410		8.13	4.2E+00 AI808013.1	EST_HUMAN	w67803.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
6363	15543	24998		7.72	4.1E+00 Q23810	SWISSPROT	YY1 PROTEIN PRECURSOR
6409	15590	25050		3.79	4.1E+00 P28984	SWISSPROT	GENE 58 PROTEIN
6439	15690	25051		3.79	4.1E+00 P28984	SWISSPROT	GENE 58 PROTEIN
6430	15627	25092		4.55	4.1E+00 U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
7482	18670			2.98	4.1E+00 P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
7543	16748			15.02	4.1E+00 BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:38006051 5'
3520	12744			0.69	4.0E+00 P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
8009	18444	25934		1.69	4.0E+00 P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
							GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8082	17217	26751		4.02	4.0E+00 P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
8082	17217	28752		4.02	4.0E+00 P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3477	12701	21837		4.32	3.9E+00 X184518.1	NT	N_leucium chitinase gene 50 (or class I chitinase C
4312	13513			0.83	3.9E+00 AF055468.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5515	14740	24105		2.78	3.9E+00 BE814337.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5515	14740	24108		2.78	3.9E+00 BE814337.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6029	15237	24680		4.25	3.9E+00 P18299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
6238	16419	24869		3.77	3.9E+00 M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
6566	15762	25225		2.27	3.9E+00 X958865.1	NT	X.laevis mRNA for M4 muscarinic receptor
7929	16405	25889		3.21	3.9E+00 Y18000.1	NT	Human sapiens NF2 gene
2593	11779			1.77	3.8E+00 AE001682.1	NT	Helicobacter pylori, strain J89 section 123 of 132 of the complete genome
3898	13209	22314		12.82	3.7E+00 AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7869	17148	26883		2.5	3.7E+00 BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
7969	17148	26884		2.5	3.7E+00 BF669279.1	EST_HUMAN	602120551F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4277748 5'
8390	17471			1.73	3.7E+00 AB013746.3	NT	Gallus gallus mRNA for hypoxe-inducible factor-1 alpha, complete cds

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
600	9847	18985		3.4E-00	AV781055.1	EST_HUMAN	AV781055 MDS Homo sapiens cDNA clone MDSBUE10'5'
4812	14001		0.96	3.6E-00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
6687	15862	25321	4.88	3.6E-00	AE04447.1	NT	Pseudomonas aeruginosa PA01, section 8 of the complete genome
6687	15862	25322	4.88	3.6E-00	AE04447.1	NT	Pseudomonas aeruginosa PA01, section 8 of the complete genome
7430	16840		4.12	3.6E-00	M98795.1	NT	Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds, and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and the repressor protein (glpR) genes, complete cds
3214	12448	21580	1.13	3.6E-00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1501	10714	18886	2.55	3.4E-00	AF254577.1	NT	Brassica napus RP85 mRNA, complete cds
6237	15418	24898	2.38	3.4E-00	PD4052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7155	16332	25815	3.88	3.4E-00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8083	17198	28738	2.13	3.4E-00	L77570.1	NT	Human DiGeorge syndrome critical region, centromeric end
507	9759	18886	1.73	3.2E-00	X86422.1	NT	D_rerio ZP-50 POU gene
4004	9759	18886	0.85	3.2E-00	X86422.1	NT	D_rerio ZP-50 POU gene
4739	13930	23034	1.09	3.2E-00	4502404 NT	NT	Human sepians carcinembryonic antigen-related cell adhesion molecule 1 (bilinary glycoprotein) (CEACAM1), mRNA
5491	14717	24074	2.88	3.2E-00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5491	14717	24075	2.88	3.2E-00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5780	15007	24410	1.78	3.2E-00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5780	15007	24411	1.78	3.2E-00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6406	15688	25044	2.53	3.2E-00	Y13855.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6405	15586	25045	2.53	3.2E-00	Y13855.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
6773	15988		9.1	3.2E-00	P13061	SWISSPROT	PERIPASMIC [NFE] HYDROGENASE SMALL SUBUNIT (NFE HYDROGENASE SMALL CHAIN)
7122	16289	26781	3.21	3.2E-00	AB016081.2	NT	Oryzias latipes OIGCF gene for glutamyl cyclase C, complete cds
7650	16850	26348	1.75	3.2E-00	AJ235270.1	NT	Rickettsia prowazekii strain Madrid E, complete genome, segment 1/4
8350	17444		1.83	3.2E-00	L39836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5602	14826	24202	2.1	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
6658	15851	25308	4.85	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
6658	15851	25310	4.85	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE-I 5'DEIODINASE) (DIO1) (TYPE 1 DI) (5DI)
6842	16047		3.67	3.1E+00	Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMNDAR2C)
7178	16355	25833	7.65	3.1E+00	P49365	SWISSPROT	DEOXYHYDROSYNTHASE (DHS)

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7899	16434			2.92	3.1E+00 P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)] retinoic acid nuclear receptor isoform beta 2 [mice], embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
8018	17155			3.7	3.1E+00 S568860.1	NT	
8144	15328			12.2	3.0E+00 P18408	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH161)
7241	16461	25650		1.7	3.0E+00 Q16181	SWISSPROT	CDC10 PROTEIN HOMOLOG
7579	16784	26277		6.87	3.0E+00 P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYLATE CYCLASE F) (GC-F)
7579	16784	26278		6.87	3.0E+00 P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYLATE CYCLASE F) (GC-F)
1979	11183	20391		2.21	2.9E+00 AE002225.2	NT	Chlamydia pneumoniae Ar339, section 53 of 94 of the complete genome
6046	15214	24634		1.71	2.8E+00 Z38879.1	NT	F. prugnei gdesPA gene for P-protein of the glycine cleavage system
6110	15352	24789		4.54	2.9E+00 O14514	SWISSPROT	BRAINS-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6110	15352	24790		4.54	2.9E+00 O14514	SWISSPROT	BRAINS-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6278	15459	24800		5.32	2.9E+00 P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1456	10569	19842		4.19	2.8E+00 AF1/B6398.1	NT	Buxus perfoliata murensis K (malk) gene, partial cds; chloroplast gene for chloroplast product
1610	10823			2.03	2.8E+00 AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
6210	15391	24835		4.9	2.8E+00 8393724	NT	Mus musculus endomucin (LOC53423), mRNA
236	8515	18843		13.15	2.7E+00 6678306	NT	Mus musculus per-hexameric repeat gene 3 (Phox3), mRNA
236	9515	18844		13.15	2.7E+00 6678308	NT	Mus musculus per-hexameric repeat gene 3 (Phox3), mRNA
5487	14693	24048		1.84	2.7E+00 L14005.1	NT	Homo sapiens apoa polymorphism Kinglie IV gene, exons 1 and 2
4677	13871	22970		5.06	2.6E+00 AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5465	14691	24043		2.01	2.6E+00 9755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5485	14691	24044		2.01	2.6E+00 6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
6682	14806			2.38	2.6E+00 Y17062.1	NT	Mycobacterium fortuitum furA II gene
8376	15558			5.52	2.6E+00 AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 18 through 27, and complete cds
6980	16168	25630		2.9	2.6E+00 AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7597	16860	26282		1.74	2.6E+00 AF143675.1	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
8012	18264			2.67	2.6E+00 11418220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1460	10673	19845		2.85	2.5E+00 AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NC:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1460	10673	19846	2.85	2.5E+00 A 271844.1	NT		Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5578	14802	24174	2.14	2.5E+00 P 3485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
5578	14802	24175	2.14	2.5E+00 P 3485	SWISSPROT	TEICOIC ACID BIOSYNTHESIS PROTEIN F	
8347	17442		2.33	2.5E+00 AF 289685.1	NT	Mus musculus Elavl4 gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds	
2976	12212	21350	1.58	2.4E+00 M 24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end	
4928	14116	23212	7.8	2.4E+00 4533352	NT	Homo sapiens double C2-like domain, alpha (DCC2A) mRNA	
5660	14983	24271	4.18	2.4E+00 P 02843	SWISSPROT	VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)	
6532	15728		2.7	2.4E+00 AE 001498.1	NT	Helicobacter pylori strain J99 section 47 of 132 of the complete genome	
6728	15923	25362	12.95	2.4E+00 P 24081	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHIN-B)	
7149	16326		6.73	2.4E+00 P 08099	SWISSPROT	XYLULOSE KINASE (XYLUOKINASE)	
7175	16352	25829	2.32	2.4E+00 BE 326702.1	EST_HUMAN	hr63f06_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187.3	
7175	16352	25830	2.32	2.4E+00 BE 326702.1	EST_HUMAN	hr63f06_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187.3	
7645	16845	26343	1.91	2.4E+00 Y 14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees; gfpPKD operon and downstream	
7898	17114	26846	2.65	2.4E+00 AF 1588652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds	
1260	10475	19837	10.92	2.3E+00 Z 46724.1	NT	G. domesticus artificial single chain antibody gene (L3)	
4101	13308		1.51	2.3E+00 JA 01081.1	NT	Bos taurus partial cypb gene for cyclochrome b	
5284	14437	23511	2.28	2.3E+00 U 12024.1	NT	Astyanax mediterraneus green opsin gene (g101) gene, complete cds	
6277	15457	24898	2.33	2.3E+00 6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA	
6330	18368		3.14	2.3E+00 P 07199	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)	
7380	16598	26083	1.72	2.3E+00 Q 07076	SWISSPROT	ANNEXIN VII (SYNEXIN)	
8247	17316	26910	2.87	2.3E+00 BF 541987.1	EST_HUMAN	602069121F1 NIH MGCG_58 Homo sapiens cDNA clone IMAGE:40881173.5'	
8247	17316	26911	2.87	2.3E+00 BF 541987.1	EST_HUMAN	602069121F1 NIH MGCG_58 Homo sapiens cDNA clone IMAGE:40881173.5'	
8579	17584	24002	4.79	2.3E+00 BE 895237.1	EST_HUMAN	601436773F1 NIH MGCG_72 Homo sapiens cDNA clone IMAGE:3918843.5'	
3993	13207	22313	0.95	2.2E+00 AF 020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds	
4302	13503	22598	3.87	2.2E+00 D 67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)	
4302	13503	22600	3.87	2.2E+00 D 67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)	
5360	14590	23667	10.24	2.2E+00 Q 88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATED WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) >	

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Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar ('Top') Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN BINDING REPEATS) (LR11) (> 2.2E+00)	
5380	14590	23698	10.24	2.2E+00	088307	SWISSPROT	SWISSPROT	SWISSPROT
5695	14915	24309	9.16	2.2E+00	BE290333.1	EST_HUMAN	60094340171 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'	EST_HUMAN
6815	15032	24433	4.17	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2	SWISSPROT
5932	15148	24558	2.96	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)	SWISSPROT
6067	14514		3.74	2.2E+00	AA584574.1	EST_HUMAN	n95502.s1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'	EST_HUMAN
6338	15518	24986	16.61	2.2E+00	AA449012.1	EST_HUMAN	z05g10.71 Scores total_fetus_Nb2HF8_3w Homo sapiens cDNA clone IMAGE:785634 5'	EST_HUMAN
6884	16054		18.68	2.2E+00	BE741678.1	EST_HUMAN	601594733F NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5	EST_HUMAN
6946	18075		2.79	2.2E+00	Q04706	SWISSPROT	TRANSPOSON TY1 PROTEIN A	SWISSPROT
7090	16287	25743	2.51	2.2E+00	A1280373.1	EST_HUMAN	qm69b03.x1 Scores_placenta_B6wks_2NbHP8cgW Homo sapiens cDNA clone IMAGE:1893965 3'	EST_HUMAN
7090	16287	25744	2.51	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Scores_placenta_B6wks_2NbHP8cgW Homo sapiens cDNA clone IMAGE:1893965 3'	EST_HUMAN
7109	16288	25767	2.44	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:170433 GLUTATHIONE PEROXIDASE (HUMAN);	EST_HUMAN
7200	16317	25698	3.22	2.2E+00	AF183418.1	NT	601855891F NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'	EST_HUMAN
7977	18412	25698	4.63	2.2E+00	PO78911	SWISSPROT	Hom sapiens ovarian granulosa cell 13.0 kDa protein HGR74 hordeum mRNA, complete cds	EST_HUMAN
8138	17271	28816	4.81	2.2E+00	P10407	SWISSPROT	UROMYCIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)	EST_HUMAN
576	11971	18945	8.07	2.1E+00	AF152612.2	NT	EARLY ET-128 KD PROTEIN	EST_HUMAN
2979	12215	21351	1.86	2.1E+00	AF208532.1	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region	EST_HUMAN
3565	12788		1.24	2.1E+00	AW448386.1	EST_HUMAN	Homo sapiens fatty acid omega-hydroxylase CYP4A11 (CYP4A11) gene, complete cds	EST_HUMAN
6000	15292	24715	3.28	2.1E+00	O70159	SWISSPROT	UI-H-B13-4R-0-8-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'	EST_HUMAN
6103	15197	24615	5.28	2.1E+00	N28575.1	EST_HUMAN	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUINA)	EST_HUMAN
1204	10423	18578	1.81	2.0E+00	AF180527.1	NT	y08a10.s1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270818 3' similar to gb:M56864	EST_HUMAN
1204	10423	18578	1.81	2.0E+00	AF180527.1	NT	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);	EST_HUMAN
1343	10557	19723	0.84	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds	EST_HUMAN
1554	10788		2.32	2.0E+00	P25582	SWISSPROT	Oncotologus uncirculus Na ⁺ -K ⁺ -ATPase beta 1 subunit mRNA, complete cds	EST_HUMAN
2117	11318	20533	6.95	2.0E+00	Z78279.1	NT	PUTATIVE RNA METHYL TRANSFERASE SPB1	EST_HUMAN
2117	11318	20534	6.85	2.0E+00	Z78279.1	NT	R, nonnegicous mRNA for collagen alpha1 type I	EST_HUMAN
1078	13288	22386	1.88	2.0E+00	AW564409.1	EST_HUMAN	R, nonnegicous mRNA for collagen alpha1 type I	EST_HUMAN
							h13c05.x1 NCI_CGAP_G11 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677	
							GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE. LIVER (HUMAN);	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4078	13288	22387	1.88	2.0E+00	AW664496.1	EST_HUMAN	h13c5.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
6472	15689	25138	6.44	2.0E+00	AB0088678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6472	15689	25139	8.44	2.0E+00	AB0088678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6472	15689	25140	8.44	2.0E+00	AB0088678.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6752	15947	25405	5.02	2.0E+00	FJ1500.1	EST_HUMAN	HPD22703 HM3 Homo sapiens cDNA clone s4000117B08
8624	182222	23694	8.36	2.0E+00	5834843	NT	Gallus gallus mitochondrial genome
5489	14715	24071	4.76	1.9E+00	8754389	NT	Mus musculus insulin 1,4,5-triphosphate receptor 1 (Itp1), mRNA
5489	14715	24072	4.76	1.9E+00	8754389	NT	Mus musculus insulin 1,4,5-triphosphate receptor 1 (Itp1), mRNA
5579	15193			2.35	1.9E+00	CB83627	SWISSPROT CTD-BINDING SR-LIKE PROTEIN RA4
6817	15813	25271	2.91	1.9E+00	P02467	SWISSPROT COLLAGEN ALPHA 2(I) CHAIN PRECURSOR	
6817	15813	25272	2.91	1.9E+00	P02467	SWISSPROT COLLAGEN ALPHA 2(I) CHAIN PRECURSOR	
6872	15887			2.61	1.9E+00	EF380206.1	EST_HUMAN CM3-M10114-010800-3234-12 NT0114 Homo sapiens cDNA
3058	12294	21419	2.04	1.8E+00	P21004	SWISSPROT PROTEIN B8 PRECURSOR	
3084	12320	21441	2.25	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctrA) and ATP synthase epsilon subunit (ctrE) genes, complete cds
3084	12320	21442	2.25	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctrA) and ATP synthase epsilon subunit (ctrE) genes, complete cds
5599	14823			1.79	1.8E+00	P18502	SWISSPROT HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5709	14928	24323	1.93	1.8E+00	BF311989.1	EST_HUMAN	601897854f1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6733	15928	25387	3.27	1.8E+00	C43281	SWISSPROT EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)	
7163	16340			2.67	1.8E+00	AF111849.1	NT
8709	18195			5.06	1.8E+00	AF314254.1	NT
8792	17718			3.48	1.8E+00	9508404	NT
9100	18095	23803	1.32	1.8E+00	BF212412.1	EST_HUMAN	Rattus norvegicus Actin-related protein complex 1b (Atpc1b), mRNA
9285	18043			1.45	1.8E+00	BF316805.1	EST_HUMAN
1116	10340	18490	2.08	1.7E+00	Q80114	SWISSPROT LEVANSUCRASE (BETA-D-FRUCTOFURANOSEYL TRANSFERASE (SUCROSE 6-FRUCTOSYL TRANSFERASE)	
2238	11431	20656	2.49	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2340	11533	20756	2.43	1.7E+00	AI41067.1	EST_HUMAN	ozz43hsu.x1 Scarce_NihMP_u_S1 Homo sapiens cDNA clone IMAGE:16781373
5665	14887	24277	3.48	1.7E+00	Q9TRR8	SWISSPROT COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF1)	
6817	18074	25476	3.96	1.7E+00	C60479	SWISSPROT HOMEBOX PROTEIN DLX-3	
6817	18074	25477	3.86	1.7E+00	C60479	SWISSPROT HOMEBOX PROTEIN DLX-3	

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8124	17258	26800	2.25	1.7E+00	W/22424.1	EST_HUMAN	87B7 Human retina cDNA Tsp509I-cleaved sublibrary Homo sapiens cDNA not directional
8660	17637	23975	1.61	1.7E+00	A/078443.1	EST_HUMAN	tub2d07_X1_NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1 t1 MSR1 repetitive element;
9176	17869	23857	2.33	1.7E+00	A/1188573.1	EST_HUMAN	qf5001_X1_Soares_litter_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1 t1 L1 repetitive element;
2002	11205	20416	14.44	1.6E+00	AF/198839.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2010	11213	20422	3.58	1.6E+00	AF/077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2016	11218	20427	1.35	1.6E+00	Y/11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
2248	11443		1.07	1.6E+00	X/98373.1	NT	B nephus gene encoding endo-polygalacturonase
2915	12153	21298	1.34	1.6E+00	W/58426.1	EST_HUMAN	za22501.11 Soares fetal heart NBH119W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
4009	13221		8.38	1.6E+00	BF/570077.1	EST_HUMAN	60218608571 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4310591 3'
4345	13547	22838	1.87	1.6E+00	AF/155827.1	NT	Homo sapiens proliferation-associated Snf2-like protein (SMARCA6) mRNA, complete cds
4345	13547	22839	1.87	1.6E+00	AF/155827.1	NT	Homo sapiens proliferation-associated Snf2-like protein (SMARCA6) mRNA, complete cds
5027	14212	23295	0.63	1.6E+00	AF/075384.1	NT	Urothelius chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5027	14212	23296	0.63	1.6E+00	AF/075384.1	NT	Urothelius chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5113	14283	23380	1.96	1.6E+00	Y/11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5113	14283	23381	1.96	1.6E+00	Y/11344.1	NT	Mus musculus ST6GalNAcIII gene, exon 2
5583	14807	24180	2.43	1.6E+00	L/04808.1	NT	Brachydantio revo MHC class II DA-beta-2'T01 gene, 3' end
6182	16384	24804	2.64	1.6E+00	BE/697267.1	EST_HUMAN	RC0-C0415-200700-032-c10 C/0416 Homo sapiens cDNA
6590	15788	25245	3.83	1.6E+00	A/J287131.1	NT	Mus musculus SII, MAP-17, CYP_B, SCL & CYP_b genes
7420	14846	24227	6.93	1.6E+00	AF/005681.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
8197	17329	26971	3.2	1.6E+00	AF/10431.1	NT	Homo sapiens unknown mRNA
9221	18000		1.43	1.6E+00	AV/764043.1	EST_HUMAN	AV764043 MDS Homo sapiens cDNA clone MDSDAH08 5'
34	8330	18435	5.46	1.5E+00	U/53449.1	NT	Rattus norvegicus jun dimerization protein 2 (Jdp-2) mRNA, complete cds
237	8516	18645	2.45	1.5E+00	AE/002201.2	NT	Chlamydomonas pneumoniae AR39, section 32 of 84 of the complete genome
627	9872		1.95	1.5E+00	8752981	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metaradin) (Adam15), mRNA
1882	11089	20280	3.71	1.5E+00	AF/275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptp) gene, exons 10 and 11 and partial cds
2373	11568	20787	2.06	1.5E+00	AJ/131402.1	NT	Poletai virus A RNA complete genome, isolate U
2481	11871	20889	1.63	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

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 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3103	11568	20787	1.67	1.5E+00 AJ131402.1	NT	Potato virus A RNA complete genome, isolate U	
3353	12581	21721	0.82	1.5E+00 AE001945.1	NT	Deinococcus radiodurans R1 section 82 of the complete chromosome 1	
5829	15046	24450	2.78	1.5E+00 R17879.1	EST_HUMAN	Deinococcus radiodurans R1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:316893 5'	
6148	15332	24768	18.58	1.5E+00 P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BA72-DALS INTERGENIC REGION PRECURSOR	
6148	15332	24769	18.58	1.5E+00 P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BA72-DALS INTERGENIC REGION PRECURSOR	
7026	16203	25680	11.13	1.5E+00 BF378754.1	EST_HUMAN	RGO-TN0078-150900-034-905 TNQ078 Homo sapiens cDNA	
7132	16309	25780	3.83	1.5E+00 AA017689.1	EST_HUMAN	263Ba06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'	
7132	16309	25781	3.83	1.5E+00 AA017689.1	EST_HUMAN	263Ba06.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'	
7937	17077	26605	4.18	1.5E+00 AL134187.1	EST_HUMAN	DKFZp547P243 'st' 547 (synonym: hbfr1) Homo sapiens cDNA clone DKFZp547P243 3'	
8074	17209		6.7	1.5E+00 X07380.1	NT	Maize mitochondrial tRNA-Ser gene and tRNA-Pre pseudogene	
8494	17537		1.33	1.5E+00 6753287	NT	Mus musculus caspase 8 associated protein 2 (Caspasp2), mRNA	
8653	18290	23887	1.24	1.5E+00 D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds	
8885	17780		3.71	1.5E+00 AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5	
8988	17852		1.25	1.5E+00 6978492	NT	Rattus norvegicus 5'-Lipoxygenase (Alox5), mRNA	
31	8327	18431	1.22	1.4E+00 7661685	NT	Homo sapiens DKFZp386M0122 protein (DKFZp386M0122), mRNA	
31	8327	18432	1.22	1.4E+00 7661685	NT	Homo sapiens DKFZp386M0122 protein (DKFZp386M0122), mRNA	
1711	10923	20108	1.28	1.4E+00 H16859.1	EST_HUMAN	5yf7g03.1 Soares adult brain N263hB55Y Homo sapiens cDNA clone IMAGE:172540 5'	
2242	11437		1.38	1.4E+00 AF053357.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds	
2302	11498		9.69	1.4E+00 U67822.1	NT	Ovis aries prion protein gene, complete cds	
2829	11812	21030	1.38	1.4E+00 X74463.1	NT	Human papillomavirus type 7 genomic DNA	
2729	11968	21122	2.38	1.4E+00 AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds	
2729	11908	21123	2.38	1.4E+00 AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds	
4243	13446	22536	1.72	1.4E+00 AW900455.1	EST_HUMAN	CMO-NIN1005-140300-296-H06 NN1005 Homo sapiens cDNA	
4243	13446	22537	1.72	1.4E+00 AW900455.1	EST_HUMAN	CMO-NIN1005-140300-296-H06 NN1005 Homo sapiens cDNA	
4557	12273	21401	1.2	1.4E+00 AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome	
4557	12273	21402	1.2	1.4E+00 AE002324.2	NT	Chlamydia muridarum, section 55 of 85 of the complete genome	
4584	13778		1.41	1.4E+00 BF681547.1	EST_HUMAN	80215668/F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'	
5455	14881		5.68	1.4E+00 AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds	
5780	14988	24400	2.74	1.4E+00 Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA	
5784	18387		4.59	1.4E+00 AB020712.1	NT	Homo sapiens mRNA for KIAA0805 protein, complete cds	
5832	15049	24454	2.62	1.4E+00 Q92777	SWISSPROT	SYNAFSIN II	
5832	15049	24455	2.62	1.4E+00 Q92777	SWISSPROT	SYNAFSIN II	

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 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	15384	24826	2.21	1.4E+00	AJ133269.1	NT	Homo sapiens caveolin-1/-2 locus, Contig1, D75522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6715	15910		8.09	1.4E+00	AJ2711735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6827	16021	25487	5.92	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-30128e-012-f05_B70313 Homo sapiens cDNA clone IMAGE:6655112 5 similar to contains element z36e09.11 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:6655112 5 similar to contains element MER22 repetitive element
7637	16937	26333	2.22	1.4E+00	AA195528.1	EST_HUMAN	Hom sapiens APECED mRNA for AIRE-1, complete cds
7778	16973	28486	6.19	1.4E+00	AB006682.1	NT	6016551B4R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
7943	17083	26811	3.78	1.4E+00	BE862107.2	EST_HUMAN	6016551B4R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
7943	17083	26612	3.76	1.4E+00	BE862107.2	EST_HUMAN	6016551B4R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
7865	17144	28677	2.89	1.4E+00	U30780.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
7865	17144	28678	2.89	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8491	18214		1.9	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
8899	18382		1.27	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen set0-2 (SE70-2), mRNA
9287	18033		1.22	1.4E+00	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) gene, complete cds
577	9826		1.79	1.3E+00	Z75840.1	NT	M.mucedo gene encoding 4-Dihydroxy-3-methylbutyrate dehydrogenase
912	10147	19308	2.87	1.3E+00	AJ271182.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1137	10380		17.3	1.3E+00	Y18213.1	NT	Homo sapiens putative psilinHBA pseudogenes for hair keratin exons 2 to 7
1304	10520	19879	11.83	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF-22)(ZNF157) mRNA
1304	10520	18880	11.83	1.3E+00	4507988	NT	Homo sapiens zinc finger protein 157 (HZF-22)(ZNF157) mRNA
1384	10578		0.94	1.3E+00	U61730.2	NT	Coxi lacryman-jobi dihydropyridine synthase (dapa) gene, complete cds
1589	10802		1.91	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of the complete genome
2515	11704		1.75	1.3E+00	BE86735.2	EST_HUMAN	60166123R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2890	12127	21280	0.62	1.3E+00	6755821	NT	Mus musculus alpha-spectrin 1, erythroid (Spna1), mRNA
							Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete cds
3575	12788	21924	0.65	1.3E+00	AF016494.1	EST_HUMAN	PMD-C70289-29-1198-004-008 CT0289 Homo sapiens cDNA
5669	14888	24278	0.72	1.3E+00	AW362834.1	EST_HUMAN	PMD-C70289-29-1198-004-008 CT0289 Homo sapiens cDNA
5686	14888	24279	9.72	1.3E+00	AW362834.1	EST_HUMAN	Sus scrofa pip gene
6559	16755	26218	2.2	1.3E+00	AJ008912.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransfase-2 gene, complete cds
6919	16112		3.29	1.3E+00	AF042084.1	NT	S.alba phr-1 mRNA for photolase
6924	16117	25582	2.21	1.3E+00	X772019.1	NT	

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 Table 4
 Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6924 16117	25583	2.21	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase	
6932 16160	25631	2.37	1.3E+00	Q00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)	
7028 16203	25982	5.78	1.3E+00	BEB63378.2	EST_HUMAN	601657143R1 NIH_3T3	
7284 16503		4.92	1.3E+00	Q14117	SWISSPROT	DHYDROXYPRIMIDINASE (DHPS) (HYDANTOINASE) (DHP)	
7450 16888	28170	2.44	1.3E+00	P25289	SWISSPROT	mRNA 3'-END PROCESSING PROTEIN RNA15	
7501 16708	28195	2.28	1.3E+00	Z18892.2	NT	Mus musculus desmin gene	
8072 17207	26740	3.07	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds	
8144 17276	26820	2.63	1.3E+00	Z88682.1	NT	Bacillus subtilis genomic DNA 23 kB fragment	
8639 17627		2.98	1.3E+00	AF187873.1	NT	Cavia porcellus inward-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds	
8821 17738	23930	4.23	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158452 5'	
8833 18108		2.07	1.3E+00	Z93464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)	
8832 17814		1.4	1.3E+00	AF187035.1	NT	Sturisoma liliifolium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product	
656 8902	18028	8.36	1.2E+00	AA4876248.1	EST_HUMAN	Z122d08 S1 Soares fetal liver_soleen_1NFL_S1 Homo sapiens cDNA clone IMAGE:431535 3'	
833 10071	19226	1.12	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	
833 10071	19227	1.12	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	
833 10071	19228	1.12	1.2E+00	PO5228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)	
888 10123		1.52	1.2E+00	8924234	NT	Hom sapiens hypothetical protein PRO3077 (PRO3077), mRNA	
1169 10390	19542	3.71	1.2E+00	AF080245.2	NT	Eleutherodactylus coquiiferape synthase mRNA, complete cds	
1213 10431	19587	1.74	1.2E+00	A1252242.1	NT	pea seed-borne mosaic virus complete genome	
1213 10431	19588	1.74	1.2E+00	A1252242.1	NT	pea seed-borne mosaic virus complete genome	
1978 11182	20380	1	1.2E+00	AF140631.1	NT	Human sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds	
3074 12310	21431	1.07	1.2E+00	AB020881.1	NT	Human sapiens mRNA for KIAA0874 protein, partial cds	
3128 12384	21494	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63	
3129 12364	21495	6.74	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63	
32254 12487		2.72	1.2E+00	P54910	SWISSPROT	CONUGAL TRANSFER PROTEIN TRBE PRECURSOR	
3331 12580	21698	0.66	1.2E+00	AF188740.1	NT	Human sapiens LHx2 gene, intron 2	
3363 12813	22031	7.58	1.2E+00	U75802.1	NT	Mus musculus subtilisin-like serine protease Lpc (PC7) gene, exons 1 to 8; partial cds	
3964 13179	22282	2.14	1.2E+00	BF373370.1	EST_HUMAN	MRO-F10175-05090-203-q06_1 F10175 Homo sapiens cDNA	
4296 12560	21698	1.04	1.2E+00	AF188740.1	NT	Human sapiens LHx2 gene, intron 2	
4487 13665		2.05	1.2E+00	MB7060.1	NT	Rattus rattus cardiac ALC3 gene, exons 1-23	
4559 13753	22851	1.8	1.2E+00	AF156495.1	NT	Human sapiens post-synaptic density 85 (DLG4) gene, complete cds	
4587 13781		6.87	1.2E+00	Y09200.1	NT	T-phrmatum chloroplast rbcL gene, partial	
5468 14695	24048	2.03	1.2E+00	AW813278.1	EST_HUMAN	MRF-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA	

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Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
6734	14953	24351	2.5	1.2E+00	X74885.1	NT	D. <i>hydei</i> 3'1 repeat cluster DNA, fragment D	
5758	14977	24379	4.03	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0080-270400-180-a03 BN0080 Homo sapiens cDNA	
5804	15021	24422	37.27	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Scores: testis_NHT Homo sapiens cDNA clone 1322374 3'	
5877	15094	24508	2.08	1.2E+00	AW813376.1	EST_HUMAN	MR3-ST0181-1402000-013-d05 ST0181 Homo sapiens cDNA	
6055	15223	24642	2.84	1.2E+00	AJ002141.1	NT	<i>Mus musculus</i> DSPP gene	
6358	15536	24990	2.81	1.2E+00	X74207.1	NT	L. <i>lactis</i> pyD and pyF genes	
6844	15839	25299	5.07	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds	
6772	15987	25425	2.49	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201090-001-e07 CT0222 Homo sapiens cDNA	
6876	16087	25536	2.56	1.2E+00	Z32850.1	NT	R. <i>communis</i> gene for pyrophosphate-dependent phosphofructokinase beta subunit	
6965	16143	25612	2.48	1.2E+00	D11745.1	EST_HUMAN	HUMHM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01	
7048	16225	25700	4.49	1.2E+00	X56832.1	NT	H. <i>sapiens</i> ENO3 gene for muscle specific endase	
7889	17102	26633	2.36	1.2E+00	AW817817.1	EST_HUMAN	PM0-ST0284-161193-001-d01 ST0284 Homo sapiens cDNA	
7923	17136		5.4	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-910 HT0422 Homo sapiens cDNA	
7982	16427	25914	3.52	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds	
8605	18185	23757	20.83	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003	
8825	17618		2.04	1.2E+00	AP001515.1	NT	Bacillus halodurans genomic DNA, section 9/14	
470	9723	18854	1.47	1.1E+00	DR6980.1	NT	Human mRNA for KIAA0227 gene, partial cds	
1733	10945	20128	2.18	1.1E+00	AW885393.1	EST_HUMAN	QV0-BN0042-170300-163-912 BN0042 Homo sapiens cDNA	
3303	12534	21668	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013	
3303	12534	21667	8.21	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013	
3461	12686	21822	0.85	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA	
3555	12778	21807	1.18	1.1E+00	AI808380.1	EST_HUMAN	wf54h11_x1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P531_HUMAN_Q12888_P53-BINDING PROTEIN 53BP1	
3689	12819	22036	1.52	1.1E+00	AE003888.1	NT	Xylella fastidiosa, section 32 of the complete genome	
3699	12819	22037	1.52	1.1E+00	AE003888.1	NT	Xylella fastidiosa, section 32 of the complete genome	
3807	13025		0.75	1.1E+00	X85374.1	NT	H. <i>parasuis</i> hypothetical protein hphIM(C), hphIR and menB genes	
3919	13135	22252	1.03	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA	
3997	13210	22315	0.89	1.1E+00	8755205	NT	Mus musculus proteasome (prosome, macrospain) subunit, beta type 7 (Psmgb7), mRNA	
4198	13402		7.67	1.1E+00	5835331	NT	R. <i>unicoloris</i> complete mitochondrial genome	
4688	13880		1.06	1.1E+00	U34992.1	NT	Carcharhinus plumbeus Ig lambda light chain gene, complete cds	
5016	14203	23290	3.61	1.1E+00	U18486.1	NT	African swine fever virus, complete genome	
5102	14282	23367	1.13	1.1E+00	X78425.1	NT	E. <i>faecalis</i> ppb5 gene	
5251	14424	23501	0.82	1.1E+00	P25396	SWISSPROT	TELLURITE RESISTANCE PROTEIN TEHA	
5335	14566	23640	1.89	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5497	14723	24081	22.14	1.1E+00	BE860184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
6286	15487	24908	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6286	15487	24909	2.18	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6294	15475	24917	7.18	1.1E+00	AI-161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6503	15700	25168	4.96	1.1E+00	BF-693986.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3246628 5'
7052	16228	25705	7.08	1.1E+00	AI-161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7073	16250	25723	22.71	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
7244	18464	25854	2.89	1.1E+00	11087384	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
7298	16515		4.08	1.1E+00	AF068894.2	NT	Klebsiella pneumoniae cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
7664	14493		5.88	1.1E+00	8922873	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
7669	16868	26370	3.89	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (CG6PDH1) mRNA, complete cds
7669	16868	26371	3.89	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (CG6PDH1) mRNA, complete cds
7895	17111	26842	5.2	1.1E+00	AI085899.1	EST_HUMAN	w76e11_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2381548 3'
8103	17237	26774	1.83	1.1E+00	DB8501.1	NT	Human PBI gene, complete cds
8103	17237	26775	1.83	1.1E+00	DB8501.1	NT	Human PBI gene, complete cds
8575	17591		2.88	1.1E+00	PF07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
8682	17852	23979	2.49	1.1E+00	AF216598.1	NT	Tetraena solium immunogenic protein Ts76 mRNA, partial cds
8811	18182		1.81	1.1E+00	AF234189.1	NT	Dichrostachys cinerea isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
99	83892		2.09	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
113	9401	18530	1.22	1.0E+00	DB85425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
424	96777		2.34	1.0E+00	AB021684.1	NT	Marchantia polymorpha genes for 2S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
583	98332	18950	1.38	1.0E+00	AJ251660.1	NT	Girardia ligula mRNA for homeodomain transcription factor (so gene)
633	98228	18057	6.39	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
635	98228		0.94	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1392	11893		1.65	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1728	10940	20123	1.15	1.0E+00	AB006531.1	NT	Plautia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2643	11826	21041	0.85	1.0E+00	AF131205.1	NT	Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Smn), neuronal apoptosis inhibitory protein-1s3 (Nrip-1s3) genes, complete cds

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2829	12068	21189	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2829	12068	21190	4.6	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2922	12160		1.25	1.0E+00	O14226	SWISSPROT	HYPOTHEtical 67.9 kD PROTEIN C6F12.08C IN CHROMOSOME 1
3163	12398	21533	1.17	1.0E+00	AAB28453.1	EST_HUMAN	bir26q05.s1 Soares fetal fetus Nb2Hf8 9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to W.P.:C4208.3 CE04204 :contains element MER22 MER22 repetitive element;
3577	8392		1.17	1.0E+00	U22808.1	NT	Xenopus laevis ribosomal gene, complete cds
3661	12882	22003	1.81	1.0E+00	A222816.1	NT	Agaricus bisporus mRNA for tyrosinase
4046	13256	22357	0.84	1.0E+00	A223391.1	NT	Homo sapiens calcium channel alpha 1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5185	14361		0.87	1.0E+00	A2200517.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5279	14450		0.6	1.0E+00	AL1 63218.2	NT	Homo sapiens chromosome 21 segment HS21C018
5315	14547	23616	2.5	1.0E+00	Z37022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5532	14816	24190	4.53	1.0E+00	A248054.1	NT	Bos taurus microtubular calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5592	14816	24191	4.53	1.0E+00	A248054.1	NT	Bos taurus microtubular calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5715	14933	24229	4.68	1.0E+00	PI4501	SWISSPROT	FIBER PROTEIN
5716	14934	24330	1.62	1.0E+00	AV452782.1	EST_HUMAN	UI-H-B13-alk-d-09-o-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
5870	15088	24601	1.87	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LIP (PC) gene, exons 1 to 8, partial cds
6224	15465		8.44	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
6387	15587	25024	8.14	1.0E+00	AA775191.1	EST_HUMAN	sc79b08.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:3887813'
6505	14498		2.37	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
6580	15776	25235	3.41	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6580	15776	25236	3.41	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6634	18073		2.74	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0226-[B1098-011-e08 HT0228 Homo sapiens cDNA
6959	16147	25618	2.2	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYTA11 5'
7209	16586	25887	32.49	1.0E+00	AA04982.1	EST_HUMAN	Zhgae022.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7209	16388	25888	32.49	1.0E+00	AA004982.1	EST_HUMAN	ZB94a02.11 Soares_fetal_liver_spleen_1NFLS_S1_Homo sapiens cDNA clone IMAGE:428906 5'	
7545	16750	26244	1.94	1.0E+00	SG0825.1	NT	PBR1=proline-rich protein [intron 3] [human, Genomic, 688 nt]	
8086	17201		1.66	1.0E+00	L47613.1	NT	Picea glauca Emb13 mRNA	
8457	17514		3.4	1.0E+00	P16306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)	
8801	17726		2.13	1.0E+00	AW976184.1	EST_HUMAN	EST388283 MAGE resequences, MAGN Homo sapiens cDNA	
2601	11785	21005	1	9.8E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102	
3583	12805		1.14	9.8E-01	AF174985.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds	
5505	14730	24092	8.2	9.8E-01	PA9657	SWISSPROT	SERINE/THYROINE PROTEIN KINASE MINIBRAIN	
6938	16082		3.4	9.8E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)	
5229	9780	18903	2.91	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYL TRANSFERASE (N-ACYL GLUTAMATE SYNTHASE) (AGS) (NAGS)	
2259	11454		1.63	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBEE gene derived retroposon on the Y chromosome	
3787	13005	22120	0.63	9.8E-01	BE987439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	
3787	13005	22121	0.63	9.8E-01	BE987439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'	
6184	15347	24784	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroEL-like protein isolate JM983	
6184	15347	24785	4.67	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroEL-like protein, isolate JM983	
7588	16771	26282	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'	
7588	16771	26283	4.32	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350750 5'	
8688	17687						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ccz2+Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >	
6147	15331	24767	3.07	9.7E-01	U52111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds	
7728	16927		1.28	9.8E-01	BF511209.1	EST_HUMAN	U1-H-B14-acr-e07-0-U1_s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'	
9272	18035		1.38	9.7E-01	AL114281.1	NT	Batrachoseps cinereus strain T4 cDNA library under conditions of nitrogen deprivation	
9289	18047	23827	5.82	9.7E-01	AL161549.2	NT	Arabidopsis thaliana DNA, chromosome 4, contig fragment No. 49	
4430	13630	22724	1	9.6E-01	AF187925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds	
4430	13630	22725	1	9.6E-01	AF187925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds	
4452	13851	22746	1.53	9.6E-01	AW789874.1	EST_HUMAN	PM2-UJ0053-240300-005-12 UJ0053 Homo sapiens cDNA	
5552	14776	24143	3.47	9.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2894	
5552	14776	24144	3.47	8.6E-01	Z70556.1	NT	Panovirus B19 DNA, patient C, genome position 2448-2894	
6598	15782		2.23	9.6E-01	X85275.1	NT	P.feliperum complete gene map of plesid-like DNA (IR-A)	
7654	16854	26353	1.69	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds	

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8051	17187	26726	4.97	9.6E-01	AV782605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG08 5'
8051	17187	26727	4.97	8.9E-01	AV782605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG08 5'
8358	17449		1.59	9.6E-01	11421722 NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA	Sphynx fibro NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8010	18260	23860	2.28	9.6E-01	U91423.1	NT	Hom sapiens CCG-1-25 protein (LOC51003), mRNA
2438	11629	20850	1.21	9.5E-01	770591 NT	Hom sapiens	Hom sapiens CCG-21 Homo sapiens cDNA clone IMAGE-3958473 5'
3765	12983	22097	2.08	9.5E-01	BE902340.1	EST_HUMAN	601675839F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE-3958473 5'
3765	12983	22098	2.08	9.5E-01	BE902340.1	EST_HUMAN	601675839F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE-3958473 5'
7798	16889	28504	1.78	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE-4103630 5'
7987	16422	25909	1.65	9.5E-01	AW283798.1	EST_HUMAN	UI-H-B12-ahp-f03-0-U1.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE-2727677 3'
3165	12400		3.64	9.4E-01	AF165980.1	NT	Bartonella claridgeiabs RNA polymerase beta subunit (rpB) gene, partial cds
3184	12418		2.15	9.4E-01	AF080598.1	NT	Pimelinating zinc finger protein (ZFP-1) mRNA, complete cds
8830	17622		1.85	9.4E-01	BE781251.1	EST_HUMAN	601465703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE-3869828 5'
9009	18178		1.61	9.4E-01	11419857 NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1705	10917		1.15	9.3E-01	AF242382.1	NT	Hom sapiens phosphoryl-CoA hydroxylase (PHYH) gene, exon 5
2598	11783	21003	1.61	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271194-01-B01 BT0503 Homo sapiens cDNA clone IMAGE-3916184 3'
40113	13225	22325	0.76	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
40113	13225	22328	0.76	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
5524	14749	24116	4.02	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylesterhydrofolate dehydrogenase mRNA, complete cds
9126	17839	23879	1.56	9.3E-01	11440298 NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (IPR2), mRNA	Inositol 1,4,5-triphosphate receptor, type 2 (IPR2), mRNA
9135	17944		2.19	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3205	12439	21574	3.6	9.2E-01	BE622702.1	EST_HUMAN	60144133811 NIH_MGC_72 Homo sapiens cDNA clone IMAGE-3916184 3'
4894	14082		0.79	9.2E-01	BF128973.1	EST_HUMAN	6018117814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4041363 5'
5649	14872	24259	4.49	9.2E-01	BF031586.1	EST_HUMAN	601481153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE-3864661 5'
7158	16333	25816	6.03	9.2E-01	11430063 NT	Homo sapiens lysosomal arylsulphatase-like protein 1 (ALSP1), mRNA	Hom sapiens lysosomal arylsulphatase-like protein 1 (ALSP1), mRNA
7240	16460	25949	1.69	9.2E-01	BE563811.1	EST_HUMAN	601334843F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE-3688714 5'
8213	17344	26883	2.06	9.2E-01	BF132402.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4052018 5'
1602	10816	18992	1.14	9.1E-01	196675.1	EST_HUMAN	ye2f01.s1 Sceires fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE-121369 3' similar to contains Alu repetitive element;
2094	11294		1.18	9.1E-01	8923056 NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3170	12405	21538	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200GBR Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200GB 5'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3170	12405	21539	1.28	9.1E-01 T26418.1	EST_HUMAN	AB2000G8R Infant brain, LNL array of Dr. M. Soares cDNA clone LLAB2000G8.5'	
5878	15095	24509	2.86	9.1E-01 Q61704	SWISSPROT	INTERALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)	
6325	15506	24852	17.88	9.1E-01 AAB06623.1	EST_HUMAN	0671g08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:13358862 3'	
6333	15573	25028	2.35	9.1E-01 U72895.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein-3 (UCP3) gene, complete cds	
8726	16554		15.31	9.1E-01 AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds	
3172	12407	21542	0.6	9.0E-01 7861625	NT	Homo sapiens DKFZp64M2423 protein (DKFZp64M2423), mRNA	
4373	13575	22671	2	9.0E-01 AF099810.1	NT	Homo sapiens neuron III-sapta gene, partial cds	
5288	14441	23514	0.61	9.0E-01 AF086302.1	EST_HUMAN	cx01b5.51 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1655889 3' similar to contains Alu repetitive element;	
5334	14758	24125	2.39	8.9E-01 AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit 2	
8251	17379	26913	2.68	8.9E-01 AE003944.1	NT	Xylella fastidiosa section 90 of 229 of the complete genome	
8557	17579		4.11	8.9E-01 AE002188.2	NT	Chlamydomonas pneumonophila AR39 section 21 of 94 of the complete genome	
4538	13134	22832	1.91	8.8E-01 O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE	
5205	14380	23486	3.88	8.8E-01 AW856840.1	EST_HUMAN	RC2-C0288-10200-015-601 C10288 Homo sapiens cDNA	
7847	16847	26345	3.08	8.8E-01 Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1	
8372	18344		2.12	8.8E-01 D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576583-1719643	
471	9724	18855	1.29	8.7E-01 AF106953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds	
2827	12066	21187	5.87	8.7E-01 AA595863.1	EST_HUMAN	nn0561_s1 NCI CGAP Pr4-1 Homo sapiens cDNA clone IMAGE:1076877	
5031	14216		2.76	8.7E-01 AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzozate 1,2-dioxogenase beta-ISPr protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzozate 1,2-dioxogenase alpha-ISPr protein OhbB (ohbB), and put>	
7408	16820	26112	6.23	8.7E-01 BF163970.1	EST_HUMAN	QV0-NN1021-100806-337-c03 NN1021 Homo sapiens cDNA	
8226	17558	26894	3.87	8.7E-01 BF107694.1	EST_HUMAN	601823_684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'	
8228	17358	26895	3.87	8.7E-01 BF107694.1	EST_HUMAN	601823_684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'	
8775	18144		2.27	8.7E-01 AV861688.1	EST_HUMAN	AV861688 GLC Homo sapiens cDNA clone GLCGGYGD7 3'	
481	9733		1.49	8.6E-01 X77012.1	NT	Rat Igf1 gene for insulin-like growth factor II	
808	10104	19287	7.46	8.6E-01 W69089.1	EST_HUMAN	Zd44603.1 Soares_fetal_hear_NbHH14SW Homo sapiens cDNA clone IMAGE:342516 5'	
2235	11430	20855	0.95	8.6E-01 4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 21-hydroxylase, cerebroendocrine xanthanogenesis), polypeptide 1 (CYP27A1b) mRNA	
3599	12820	21941	1.09	8.6E-01 AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	
3784	13002	22117	1.49	8.6E-01 U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5614	14837	24214	7.83	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5614	14837	24215	7.83	8.6E-01	XC0547.1	NT	Chicken lipoprotein lipase gene
5989	15184	24600	1.77	8.6E-01	AF143732.1	NT	Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
5989	15184	24801	1.77	8.6E-01	AF143732.1	NT	Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
8892	18092		1.96	8.6E-01	AL112162.1	NT	Batrachoides cinereus strain T4 cDNA library under conditions of nitrogen deprivation
4491	13689	22781	0.85	8.5E-01	AT701028.1	EST_HUMAN	wo08102x1 NCI CGAP_Lu24 Homo sapiens cDNA clone MAGE:2340627 3'
6301	15482	24826	2.42	8.5E-01	BE42812.1	EST_HUMAN	wo081027F1 NIH_MGC_10 Homo sapiens cDNA clone MAGE:3453505 5'
7180	16357	25835	2.22	8.5E-01	AB006799.1	NT	Cyanidium calderarium gene for SlgC, complete cds
7180	16357	25836	2.22	8.5E-01	AB006799.1	NT	Cyanidium calderarium gene for SlgC, complete cds
8711	18256		2.74	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
8717	17672		4	8.5E-01	95070098	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (PTPN5), mRNA
5440	18055	23820	2.81	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5440	18055	23821	2.81	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7057	16234		4.37	8.4E-01	A1248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
749	8890	19133	2.79	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cytC) and CytB (cytB) genes, complete cds
3060	12286	21420	3.24	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3798	13016	22128	0.71	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3988	13202	22310	3.75	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5309	14540	23545	2.38	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7140	16317	25789	4.76	8.3E-01	AF108133.1	NT	Mus musculus neuro-d1 gene, exons 3 through 12 and partial cds
7298	18485	25977	2.68	8.3E-01	AE000903.1	NT	Methanobacterium thermoeutrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
7292	16501		2.2	8.3E-01	7212472	NT	Phytopthora infestans mitochondrial genome
7851	17041	26558	2.88	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2019	11220	20428	2.47	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2059	11260		1.69	8.2E-01	AF145689.1	NT	Mus musculus trophillin (Tnn) gene, complete cds
2639	11822		1.02	8.2E-01	AW376890.1	EST_HUMAN	IL3-CT0219-161186-031-C08 CT0219 Homo sapiens cDNA
3879	13095	22212	0.61	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
4111	13318	22417	0.89	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
4111	13318	22418	0.89	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL062w
6040	15248	24670	3.49	8.2E-01	AW370433.1	EST_HUMAN	CM4-HT0243-081198-037-se01 HT0243 Homo sapiens cDNA
6198	18072	24818	4.4	8.2E-01	Z12126.1	NT	S.cerevisiae MET4, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthase (partial), and DNA polymerase alpha (partial)

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7094	16271	25748	2.43	8.2E-01	AF052859.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
7134	16361	25840	3.29	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
7184	16361	25841	3.29	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8155	17287	26831	3.09	8.2E-01	U0127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
8221	17351	26889	7.78	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8227	17357	26896	6.68	8.2E-01	HB7398.1	EST_HUMAN	yw1402.1f Soares,Placenta_8to9weeks_2NbHPtG9W Homo sapiens cDNA clone IMAGE:252195'5'
8754	17680	23952	1.91	8.2E-01	A001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2714	11893			8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3435	12660	21791	3.11	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
3435	12660	21792	3.11	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
4941	14128			0.62	8.1E-01	AF202634.1	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (Ybeta2) mRNA, complete cds
5943	15159	24571	2.59	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
5943	15159	24572	2.59	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M6-B
8017	17158	28691	3.58	8.1E-01	BE338558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8017	17158	28692	3.58	8.1E-01	BE338558.1	EST_HUMAN	RC0-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
8430	17486	24013	1.53	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
180	9460			2.95	8.0E-01	A027150.1	NT
283	9587	18698	9.28	8.0E-01	AJ32772.1	NT	Staphylococcus aureus partial pia gene for phosphate acyltransferase allele 15
2003	11206			1.53	8.0E-01	BF530962.1	EST_HUMAN
3284	12515	21646	1.71	8.0E-01	AB006193.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
4530	13126	22823	5.84	8.0E-01	X33739.2	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5001	14188	23278	1.29	8.0E-01	7657352	NT	Mus musculus myosin Xb (Myo9b), mRNA
6628	15825	25287	2.21	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
490	9713	18848	1.61	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
7222	8984			1.09	7.9E-01	AE002130.1	Ureaplasma urealyticum section 31 of 59 of the complete genome
1584	10797			26.24	7.9E-01	AB040985.1	NT
1631	10845			1	7.9E-01	U32739.1	Haeomophilus influenzae Rd section 54 of 163 of the complete genome
2228	11424	20650	6.52	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin-29, complete cds
2229	11425	20651	2.33	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1 (tap1) mRNA, complete cds
3490	12714	21880	2.71	7.9E-01	AF228984.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4287	13489			0.71	7.9E-01	BE263612.1	EST_HUMAN
4813	13807	22899	1.03	7.9E-01	9753745	NT	Mus musculus embryo (Emb), mRNA
4613	13807	22900	1.03	7.9E-01	9753745	NT	Mus musculus embryo (Emb), mRNA

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 Table 4
 Single Exon Probes Expressed in HELa Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6497	15694	25158	4.39	7.9E-01	X00986.1	NT	P. sativum GR gene
6934	16126	25594	4.56	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3MB-B (vspG3MB-B) mRNA, partial cds
7089	16268	25742	2.89	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
7577	16782		2.29	7.9E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7784	16980	28470	3	7.9E-01	P180222	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
886	10121		2.22	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2240	11435	20859	4.11	7.8E-01	AW955687.1	EST_HUMAN	EST377637 MAGE resequencing, MAGF Homo sapiens cDNA
4712	13983	23003	0.74	7.8E-01	UB7305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5062	14242		1.12	7.8E-01	AW753353.1	EST_HUMAN	RC3-C70254-130100-023-c02 CT0254 Homo sapiens cDNA
5227	14401		1.33	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
5697	14917	24311	2.41	7.8E-01	AF115858.1	NT	Sophorodon punctatus alpha enolase mRNA, partial cds
8705	18234		1.54	7.8E-01	L28280.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACSS) gene, complete cds
141	9423	18556	5.67	7.7E-01	AF184345.1	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
733	9974						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (I(Alpha)) and major histocompatibility protein class II beta chain (I(Beta)) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
2672	11654	21070	2.1	7.7E-01	AF050157.1	NT	
3578	12800	21928	1.39	7.7E-01	Q38916	SWISSPROT	CITRATE SYNTHASE
4380	13591	22683	4.2	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4390	13581	22684	3.15	7.7E-01	AF199488.1	NT	Catunrix columnis japonica sub-species japonica beta-actin mRNA, partial cds
5283	14436		3.15	7.7E-01	AF199488.1	NT	Catunrix columnis japonica sub-species japonica beta-actin mRNA, partial cds
8479	9423	18556	1.46	7.7E-01	L78833.1	NT	Rho7 and vati genes, complete cds, and ip35 gene, partial cds
8588	17596		1.35	7.7E-01	AF184345.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and ip35 gene, partial cds
5707	14926	24320	5.33	7.7E-01	11497621	NT	Lycopersicon hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
5707	14926	24321	4.05	7.6E-01	AF059510.1	NT	Archaeoglobus fulgidus, complete genome
8501	15698	25163	4.05	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6501	15698	25164	2.5	7.6E-01	8857752	NT	Mus musculus adillin (Adil-pending), mRNA
6849	16038	25502	2.6	7.6E-01	8857752	NT	Mus musculus adillin (Adil-pending), mRNA
6849	16038	25503	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7897	17113	28844	7.49	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
			2.88	7.6E-01	X86347.1	NT	Haespera mRNA for neurofilament NF70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7897	17113	26845	2.88	7.6E-01	X86347.1	NT	H.aspera mRNA for neurofilament NF70
8201	17333		6.71	7.6E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8334	17432		3.62	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
519	9770		1.25	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
591	9839	18958	1.51	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7768	16984	26477	1.71	7.5E-01	AB047819.1	NT	Homo sapiens GCMα/GCM1 gene for chorion-specific transcription factor GCMα, complete cds
8658	17635		4.34	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
9204	17989	23863	1.8	7.5E-01	AE009823.1	NT	Methanobacterium thermoautotrophicum from bases 317350 to 328792 (section 29 of 148) of the complete genome
1138	10361	19510	1.28	7.4E-01	AJ698146.1	EST_HUMAN	In 148..x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element;contains element MIR repetitive element;
2311	11505	20728	0.93	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3707	12927	22045	0.59	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4289	13500	22596	6.84	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6804	15899	25458	0.91	7.4E-01	BE747503.1	EST_HUMAN	60157026f1 NIH 3T3 cell line IMAGE:3834174 5'
8168	17300	26843	1.84	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8168	17300	26844	1.64	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
8302	17410		2.98	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1n), mRNA
8415	17488		1.42	7.4E-01	AJ472841.1	EST_HUMAN	Ia13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
3952	13167		0.68	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 57
4618	13812	22802	0.67	7.3E-01	AE001168.1	NT	Borelia burgdorferi (section 52 of 70) of the complete genome
4711	13902	23002	5.65	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5130	14308	23398	0.91	7.3E-01	Q43103	SWISSPROT	FERRICRHOME SIDEROPHORE PEPTIDE SYNTHETASE
5936	15152	24562	0.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
5936	15152	24563	6.03	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6310	15491	24935	8.23	7.3E-01	M26511.1	NT	V. alginicificus sucrase (scrB) gene, complete cds
6310	15491	24936	8.23	7.3E-01	M26511.1	NT	V. alginicificus sucrase (scrB) gene, complete cds
7968	17147	26681	3.69	7.3E-01	AA678019.1	EST_HUMAN	Z125608.s1 Soares fetal liver spleen 1NF/S_S1 Homo sapiens cDNA clone IMAGE:431799 3'
7968	17147	26682	3.69	7.3E-01	AA678019.1	EST_HUMAN	Z125608.s1 Soares fetal liver spleen 1NF/S_S1 Homo sapiens cDNA clone IMAGE:431799 3'
841	10078		2.68	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (elf-2a) mRNA, complete cds
1927	11131	20326	4.35	7.2E-01	X779140.1	NT	N.tabacum Nef-4A13 mRNA
2424	11615	20837	2.18	7.2E-01	AB0098605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3031	12287	21394	1.35	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3420	126555	21785	3.04	7.2E-01	Af065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-I allele, complete cds
3592	12813	21834	1.13	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
4039	13249		0.81	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18
4780	13969	23071	3.88	7.2E-01	D90314.1	NT	L.mesenteroides gene for sucrose phosphorylase [EC 2.4.1.7]
6335	15515		6.78	7.2E-01	8625875	NT	Human herpesvirus 3, complete genome
7325	16541	26030	6.98	7.2E-01	U92623.1	NT	Rettus norvegicus cytochrome c mRNA, complete cds
7715	16914	28423	1.7	7.2E-01	S76838.1	NT	Dbs=Dbl guanine nucleotide exchange factor homolog [mice, 32D murine hemopoietic cell line, mRNA, 3923 nt]
8857	17760		4.26	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
699	9841	19075	12.1	7.1E-01	DA1070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds
3027	12263	21391	15.87	7.1E-01	A227077.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor 4, exons 1-5/16
4190	13394	22493	3.47	7.1E-01	7305380	NT	Mus musculus otogelin (Otag), mRNA
4190	13394	22494	3.47	7.1E-01	7305380	NT	Mus musculus otogelin (Otag), mRNA
6053	15253	24877	7.74	7.1E-01	U38232.1	NT	Drosophila melanogaster 6-pyruvoyl tetrahydropterin synthase (prt) gene, complete cds
8640	18160		1.97	7.1E-01	AA421492.1	EST_HUMAN	Z005h11.61 Soares, testis_NTH Homo sapiens cDNA clone IMAGE:731109.3'
1238	10453	18811	2.66	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1238	10453	18812	2.66	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2412	11604	20825	1.49	7.0E-01	N82412.1	EST_HUMAN	Y775e07.31 Soares_multiple_sclerosis_2NBHMSP_Homo sapiens cDNA clone IMAGE:288708.3' similar to Y773e07.31 Soares_multiple_sclerosis_2NBHMSP_Homo sapiens cDNA clone IMAGE:288708.3' similar to Y773e07.31 Soares_multiple_sclerosis_2NBHMSP_Homo sapiens cDNA clone IMAGE:288708.3' similar to gb:K03020
2412	11604	20926	1.49	7.0E-01	N82412.1	EST_HUMAN	contains Alu repetitive element;
5038	14268		2.07	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5207	14382	23468	0.61	7.0E-01	AE003921.1	NT	Xylella fastidiosa, section 67 of 229 of the complete genome
5253	14426	23502	8.3	7.0E-01	T68328.1	EST_HUMAN	yc411h03.51 Streptomyces liver (#837224) Homo sapiens cDNA clone IMAGE:83285.3' similar to gb:K03020
6589	15785		9.8	7.0E-01	AE000253.1	NT	PHENYLALANINE-4-HYDROXYLASE (HUMAN)
7680	16878	26385	2.01	7.0E-01	AV763842.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 1-43 of 400 of the complete genome
7680	16879	26386	2.01	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCHE04.5'
9177	10209	19364	11.39	6.9E-01	U69674.1	NT	Candida albicans squaleine epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
9177	10209	19365	11.39	6.9E-01	U69674.1	NT	Candida albicans squaleine epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds

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 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1317 10533	19895		2.41	6.9E-01 AA593530.1	EST_HUMAN	nn28a9 s1 NCI CGAP Gas1 Homo sapiens cDNA clone IMAGE:10851763'	
3185 12420	21653		1.68	6.9E-01 AE002271.2	NT	Chiarmata mundarum, section 3 of 85 of the complete genome	
5248 14419	23486		0.62	6.9E-01 BE782751.1	EST_HUMAN	601485594F1 NIH MGC_67 Homo sapiens cDNA clone IMAGE:38889435'	
6455 15832	25120		3.94	6.9E-01 AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	
8455 16862	26121		3.94	6.9E-01 AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69	
7810 17003	26518		2.35	6.9E-01 D89013.1	NT	Homo sapiens DAN gene, complete cds	
7810 17003	26517		2.35	6.9E-01 D89013.1	NT	Homo sapiens DAN gene, complete cds	
8278 18154			3.81	6.9E-01 Q89B58	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)	
964 10197	19352		0.92	6.8E-01 AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds	
2634 11817			1.32	6.8E-01 D80917.1	NT	Synecocystis sp. PCG8803 complete genome, 27/27, 3418852-3573470	
2781 10807	19883		1.28	6.8E-01 AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_m1a1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);	
4569 13763	22859		1.35	6.8E-01 J00762.1	NT	Rat(hooded) prolectin gene : exon iii and flanks	
6876 16154	26625		3.23	6.8E-01 AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds	
7653 16853	28351		2.57	6.8E-01 AJ276875.1	NT	Slagangspora avenae bg11 gene for beta-glucosidase, exons 1-4	
7653 16853	28352		2.57	6.8E-01 AJ276875.1	NT	Slagangspora avenae bg11 gene for beta-glucosidase, exons 1-4	
7675 16874	28378		2.41	6.8E-01 AF038939.1	NT	Mus musculus zinc finger protein (Feg3) mRNA, complete cds	
7675 16874	28380		2.41	6.8E-01 AF038939.1	NT	Mus musculus zinc finger protein (Feg3) mRNA, complete cds	
7846 17037	28553		1.85	6.8E-01 AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (elF-4C) mRNA, complete cds	
303 8576	18709		27.9	6.7E-01 AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds	
344 9612	18739		21.23	6.7E-01 AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds	
1876 11083			1.07	6.7E-01 M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds	
2115 11314	20530		1.38	6.7E-01 AA451884.1	EST_HUMAN	zr12g12.s1 Scarves_total_ferus_Nb2hIF8_9W Homo sapiens cDNA clone IMAGE:788310 3' similar to contains element TATA repetitive element ;	
2132 12011	20550		3.16	6.7E-01 AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced	
2953 12191	21325		4.16	6.7E-01 6875580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp) mRNA	
4447 13648	22742		0.8	6.7E-01 X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase	
4985 14172	23262		1.04	6.7E-01 AW079110.1	EST_HUMAN	xes95g12.x1 NCI CGAP_Co17 Homo sapiens cDNA clone IMAGE:25745588 3'	
6215 15398			4.48	6.7E-01 AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome	

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7527	16732	26222	2.59	6.7E-01	BF354649.1	EST_HUMAN	CM3-HT0769-010600-197-c03 HT0769 Homo sapiens cDNA N-ACETYLGLUCOSAMINYLPHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GFI1
7994	16428	25916	3.48	6.7E-01	O14357	SWISSPROT	Homo sapiens SLT1 protein (SLT1) mRNA, partial cds
2465	11656	20877	0.91	6.6E-01	AF075240.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2661	11842	21056	1.09	6.6E-01	AF189339.1	NT	Homo sapiens seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3484	12889	21825	1.22	6.6E-01	4500880	NT	C. albicans random DNA marker, 282bp
3638	12859	21978	3.96	6.6E-01	Y07669.1	NT	
4087	13298		1.19	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RReT gene, and sodium phosphate transporter (NPT3) gene, complete cds
5803	15020	24421	4.35	6.6E-01	6880577	NT	Mus musculus kinase light chain 2 (Klc2), mRNA
6369	15549	25005	3.49	6.6E-01	AV680506.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLCGID04 3'
6228	9874	18895	2.11	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
6229	9874	18908	2.11	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3411	12687	21768	5.25	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4267	13470	22563	4.63	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4301	13502	22598	0.97	6.5E-01	AL181539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
5095	14275	23358	1.84	6.5E-01	U28921.1	NT	
5413	18054	23773	2.09	6.5E-01	P18480	SWISSPROT	Phascolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
7177	16354	25832	3.78	6.5E-01	AF119676.1	NT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5)
7228	16449	25938	3.68	6.5E-01	HB7583.1	EST_HUMAN	yw1706.11 Scarecrows_Btg2weeks_2NbHPBtg2W Homo sapiens cDNA clone IMAGE:252515 5'
7278	16497	25989	4.84	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone PLACE1007810 5'
7371	16587		4.71	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
8127	17261	26804	2.85	6.5E-01	AF014115.1	NT	Plasmid medium berghel cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
8700	17688		3.08	6.5E-01	BE465050.1	EST_HUMAN	hv74a10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
8946	18058		1.75	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL087C
256	9532	18663	8.75	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3433	12858	21759	2.87	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 end 2 and complete cds
4490	13688	22779	0.73	6.4E-01	Y12488.1	NT	M.musculus whn gene
4490	13688	22780	0.73	6.4E-01	Y12488.1	NT	M.musculus whn gene

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ('top') Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7105	16282	25762	0.92	6.4E-01	U82828.1	NT	Homo sapiens atavia telangiectasia (ATM) gene, complete cds
8818	17734		7.45	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCGC09 5'
440	8684	18833	4.65	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
541	9792	18915	2.33	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2128	11327	20545	2.37	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2542	11730	20948	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP-1) mRNA, partial cds
2542	11730	20849	2.44	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP-1) mRNA, partial cds
2979	12216		0.69	6.3E-01	Y12275.1	NT	Lycopersicon esculentum p69a gene, complete CDS
6886	16077	25545	4.49	6.3E-01	9627521	NT	Variola virus, complete genome
6886	16077	25546	4.49	6.3E-01	9627521	NT	Variola virus, complete genome
7627	16829	26326	1.96	6.3E-01	AA877715.1	EST_HUMAN	nr05h06_s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:11613713 similar to TR:002916 O02916
7878	17067	26592	14.1	6.3E-01	A904160.1	EST_HUMAN	CM-BT043-090289-046 BT043 Homo sapiens cDNA
7983	17142	26875	2.07	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
8116	17250	28790	1.95	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
8392	18320	23596	8.88	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 6q (Krt2-6q), mRNA
8490	17534		1.48	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphotransferase (PAPSS) mRNA, complete cds
8718	18230	2.12	6.3E-01	X88528.1	NT	Clinicalca psCD gene	
5800	14824	24200	1.94	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 14.25 KD PROTEIN C23E2.02 IN CHROMOSOME 1
6289	15469		2.85	6.2E-01	AF022263.1	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-4) mRNA, partial cds
6581	15757	25220	6.38	6.2E-01	H72255.1	EST_HUMAN	J501608_s1 Severe, fatal liver sphingolipidosis in INF1S.Homo sapiens cDNA clone IMAGE:213542 3'
6915	16103		3.47	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
7100	16277	25757	10.3	6.2E-01	AL1615112	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
7215	16382	25874	5.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
7215	16392	25875	5.08	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
2358	11551		6.54	6.1E-01	6876076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
6025	16233	24854	3.81	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6025	15233	24855	3.81	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6537	15733	25197	4.89	6.1E-01	AF03555.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
6885	16076	25543	26.49	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
6885	16076	25544	26.49	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8225	17355	28892	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8225	17355	28893	2.27	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8486	18116	23810	1.39	6.1E-01	AB041350.1	NT	Mus musculus Colfats mRNA for type IV collagen alpha 5 chain, complete cds
9150	17853		1.36	6.1E-01	X85287.1	NT	M. mazai orfA, orfB, and orfC of archaean ABC-transporter system
501	9753	18881	0.83	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
568	9618		2.86	6.0E-01	5802999	NT	Homo sapiens adapter-related protein complex 3, mu/2 subunit (CLAP2), mRNA
1370	10584	19751	1.71	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH53-53b attachment protein (G) gene, complete cds
3804	13022	22133	0.92	6.0E-01	AJ233398.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, NV, L genes, French strain 07-71
4011	13223	22324	1.39	6.0E-01	X16842.1	NT	Xenopus mRNA for desmin
4170	13374		1.31	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 28, 27, and 28
6314	14548	23615	1.92	6.0E-01	P20288	SWISSPROT	D2) DOPAMINE RECEPTOR
5412	14641	23772	2.63	6.0E-01	AW139713.1	EST HUMAN	U-H-B1-seb-e-10-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:27186193
5897	15114	24525	2.64	6.0E-01	U38913.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6232	15413	24854	6.27	6.0E-01	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
6500	15697	25161	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
6600	15697	25162	5.08	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7019	16198	25872	2.68	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT1, complete cds
7159	16336		2.39	6.0E-01	C01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER9 (PEROXIN-3)
7624	16826	28323	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperin protein, 419 kD isoform
7624	16826	28324	1.98	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperin protein, 419 kD isoform
8085	17220	26756	2.66	6.0E-01	AI420623.1	EST HUMAN	I08f07_x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:20956213'
8788	17715	23980	1.73	6.0E-01	11421983	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
8896	17780		1.55	6.0E-01	AA706087.1	EST HUMAN	Z98g05_s1 Soares_fetal_liver_spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:4627763'
9052	18161		2.82	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
9093	18185	23755	1.87	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
9121	18090		2.38	6.0E-01	EE157617.1	EST HUMAN	RC1-H10376-03050-015-03 H10375 Homo sapiens cDNA
1008	10239	18391	2.5	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3237	12471	21602	5.43	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
3237	12471	21603	5.43	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4205	13408		3.92	5.9E-01	AF163275.1	NT	Rattus norvegicus connexin 2 mRNA, partial cds

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Probe SEQ ID NO.	Exon ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5854 15072	24483	5.05	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
8195 15377	24817	1.64	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7130 16307	26787	2.2	6.9E-01	P56284	SWISSPROT	VASCULAR ENDOTHELIAL CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
7264 16483	25976	3.21	5.9E-01	Q8X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
7269 16488	25978	1.75	5.9E-01	AF197894.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
7532 16737	26227	2.97	5.9E-01	AW937175.1	EST_HUMAN	PMI-DT0041-190100-Q02-h03 DT0041 Homo sapiens cDNA
7749 16944	28456	2.23	5.9E-01	AF064626.1	NT	Mus musculus strain SFRET/Ei CD48 antigen (Cd48) gene, partial cds
8429 17485	24012	1.67	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
8684 17653		1.53	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyruvate pyrophosphate decarboxylase, complete cds
8910 17798		6.21	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1873 11080	20270	0.93	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3982 13177	22280	0.95	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4515 13711	22804	2.77	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4808 13987		1.44	5.8E-01	AF110846.1	NT	Megastigmus scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
6003 15285		2.43	5.8E-01	SB5091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
6525 15721	26785	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6525 15721	25186	2.9	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
6741 15638	25387	12.15	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor -4, exons 6-11
7581 16768	28287	9.84	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7606 16809		3.72	5.8E-01	BF700982.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
7701 16890		2.14	5.8E-01	BF700082.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3008 12244		0.68	5.7E-01	8755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3189 12424	21557	1.5	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVOT1)
3478 12702		3.08	5.7E-01	AB033503.1	NT	Populus tremuloides mRNA for 1-amino cyclopropane-1-carboxylate synthase, complete cds
3881 13087	22214	1.81	6.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S7-2-BJ1S1) mRNA, partial cds
5816 15033	24454	4.41	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3058550 5'
6400 15581	25038	2.26	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (IP5CR) (P5CR) (PSC REDUCTASE)
8386 17487		1.31	5.7E-01	BE715051.1	EST_HUMAN	MR3-H170736-180700-003-a02 HT0736 Homo sapiens cDNA
3340 12569	21707	1.22	5.8E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3340 12569	21708	1.22	5.8E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
6718 16913	26312	4.84	5.8E-01	AV884703.1	EST_HUMAN	AV884703 GKC Homo sapiens cDNA clone GKCFSF05 5'
6718 15913	25313	4.84	5.8E-01	AV884703.1	EST_HUMAN	AV884703 GKC Homo sapiens cDNA clone GKCFSF05 5'

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8284	17400			2.94	5.6E-01 BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
8401	17479	28595		1.58	5.6E-01 AA193535.1	EST_HUMAN	ng75g10_s1 NCI_CGAP_Pt8 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element;
8786	14494	23583		1.7	5.6E-01 AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
8812	17732			2.41	5.6E-01 P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9238	18010			4.08	5.6E-01 BF573829.1	EST_HUMAN	602132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1219	10437	19593		1.49	5.5E-01 8393912NT	Rattus norvegicus Propion Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2682	11843	21057		2.75	5.5E-01 P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2682	11843	21058		2.75	5.5E-01 P03341	SWISSPROT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
2869	12107	21238		1	5.5E-01 5902085 NT	EST_HUMAN	301810_s1 Seares adult brain N2b5hB55Y Homo sapiens cDNA clone IMAGE:1782868 3'
3030	12268			1.75	5.5E-01 H46219.1	NT	Rabbit oral papillomavirus, complete genome
3200	12435	21570		3.16	5.5E-01 AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3671	12892	22913		1.23	5.5E-01 P48755	SWISSPROT	FOS-RELATED ANTICEN-1
5171	14350			1.05	5.5E-01 AF063868.1	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
142	9424	18557		10.17	5.4E-01 7657268 NT	Homo sapiens KIAA0928 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	
142	9424	18558		10.17	5.4E-01 7657268 NT	Homo sapiens KIAA0928 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	
592	8840	18959		1.64	5.4E-01 AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GstA (gstA) genes, complete cds; and unknown genes
592	8840	18960		1.64	5.4E-01 AF232006.1	NT	Homo sapiens KIAA0928 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1278	10493	19652		3.59	5.4E-01 AW8986087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2076	11276			2.48	5.4E-01 AE002247.2	NT	Chlamydomonas pneumonias AR39 ; section 74 of 94 of the complete genome
2219	11416	20841		2.25	5.4E-01 AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5260	14433			1.89	5.4E-01 X85873.1	NT	A. italiana mRNA for phospholipid-e-specific phospholipase C
5514	14739	24104		1.87	5.4E-01 AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
7070	16247			2.44	5.4E-01 BF572536.1	EST_HUMAN	602076545F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243690 5'
7644	16844	26312		3.44	5.4E-01 P38858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
8141	17273	26817		6.26	5.4E-01 Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8141	17273	26818		6.26	5.4E-01 Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8348	17443			2.44	5.4E-01 A 858398.1	EST_HUMAN	w 37904.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb M13452 LAMIN A (HUMAN);
522	9773	18988		1.4	5.3E-01 AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 2B hydroxylase (CYP2B), complement component C4 (C4B) C11, helicase (SKI2N), RD, complement factor B (B), and complement component C2 (C2) genes, >
2737	11916	21128		7.07	5.3E-01 4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptides 1 (PTPRZ1) mRNA
2737	11916	21130		7.07	5.3E-01 4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3298	12443	21575		3.37	5.3E-01 AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4194	13398			1.36	5.3E-01 U39687.1	NT	Mycobacteria genitalium section 9 of 51 of the complete genome
5423	14850	23785		1.82	5.3E-01 A 820921.1	EST_HUMAN	ZU42112.y5 Scores over tumor NB1HOT Homo sapiens cDNA clone IMAGE:7407115'
6423	14860	23786		1.82	6.3E-01 A 820921.1	EST_HUMAN	ZU42112.y5 Scores over tumor NB1HOT Homo sapiens cDNA clone IMAGE:7407115'
5510	14735	24097		2.05	5.3E-01 BE645620.1	EST_HUMAN	7 673612.x1 NCI_CGAP_P 28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5510	14735	24098		2.05	5.3E-01 BE645620.1	EST_HUMAN	7 673612.x1 NCI_CGAP_P 28 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
6745	15340			2.53	5.3E-01 LD1950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds; chloroplast genes for chloroplast product
8095	17229	26767		6.26	5.3E-01 BE666291.1	EST_HUMAN	6 01339867/F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:36882168 5'
8277	18162			3.58	5.3E-01 A 916053.1	EST_HUMAN	cg30605.s1 NCI_CGAP_B 7 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb J02811 APOLIPOPROTEIN D PRECURSOR (HUMAN);
828	10084	19216		10.97	6.2E-01 L 20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1172	10383	19545		11.35	5.2E-01 Q 9WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NFAT5)
1198	10419	18572		2.73	5.2E-01 AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1851	11058			3.84	5.2E-01 AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2114	11313	20528		2.33	5.2E-01 AB016283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
2461	11652	20873		10.39	5.2E-01 AF189339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2461	11652	20874		10.39	6.2E-01 AF189339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3083	12318	21440		1.91	5.2E-01 U65942.1	NT	Chlamydomonas abortus strain S283 POMF91A and POMF90A precursor, genes, complete cds
3203	12428			0.77	5.2E-01 D 73443.1	NT	Azotobacter vinelandii ldc gene for isocitrate dehydrogenase, complete cds
3383	12610			1.54	5.2E-01 AL116780.1	NT	Betula is cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3421	12846	21776		2.28	5.2E-01 AA984105.1	EST_HUMAN	am 77905.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3610	12831			0.6	5.2E-01 AF020289.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mndh) mRNA, nuclear gene encoding chloroplast protein, complete cds

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
4482	13680			1.07	5.2E-01 AF093798.1	NT	Avian infectious bronchitis virus isolate variant 2 S1 spike glycoprotein gene, partial cds	
4608	13802	22892		0.7	5.2E-01 6752947	NT	Mus musculus acetylcholine receptor beta (Acrb). mRNA	
9208	17891			4.88	5.2E-01 P18616	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)	
623	9868	18980		1.62	5.1E-01 M58309.1	NT	Human adrenodoxin reductase gene, exons 3 to 12	
654	9880	18025		4.65	5.1E-01 AJ233844.1	NT	Polychaetum vitellinum (strain PI_Vt1) 16S rRNA gene	
654	9890	18028		4.65	5.1E-01 AJ233844.1	NT	Polychaetum vitellinum (strain PI_Vt1) 16S rRNA gene	
1992	11195			1.2	5.1E-01 BF683095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:42981175'	
4054	13264	22367		4.8	5.1E-01 A1856495.1	EST_HUMAN	wi39b12.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2427283 3'	
4168	13372	22471		3.35	5.1E-01 P95380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	
6049	16217	24637		1.74	6.1E-01 R80873.1	EST_HUMAN	y64805.s1 Soares placentae Nb2HP Homo sapiens cDNA clone IMAGE:1468723'	
6988	16164	25638		6.52	5.1E-01 J05412.1	NT	Human regenerating protein (rgr) gene, complete cds	
6987	16165	25637		4.7	5.1E-01 W22302.1	EST_HUMAN	66B1 Human retina cDNA Tsp509/cleaved sublibrary Homo sapiens cDNA not directional	
8501	18084	3.24			5.1E-01 BF030207.1	EST_HUMAN	601556863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'	
8759	17700			2.09	5.1E-01 BF439982.1	EST_HUMAN	mc51f10.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TARI repetitive element;	
2104	11304	20517		1.08	5.0E-01 488552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA	
2104	11304	20518		1.08	5.0E-01 488552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA	
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (tcpCDGAHFE), and putative chromosome replication protein (grdA) genes, complete cds; and termination factor Rho (rho) genes	
2112	11311	20525		1.53	5.0E-01 AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (tcpCDGAHFE), and putative chromosome replication protein (grdA) genes, complete cds; and termination factor Rho (rho) genes	
2112	11311	20526		1.53	5.0E-01 AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (tcpCDGAHFE), and putative chromosome replication protein (grdA) genes, complete cds; and termination factor Rho (rho) genes	
3729	12948	22068		0.84	5.0E-01 U55574.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds	
3854	13070	22184		3.27	5.0E-01 AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds	
6898	15604	25068		4.28	5.0E-01 BF317212.1	EST_HUMAN	601603871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'	
8434	17500			1.82	5.0E-01 AF029215.1	NT	Mus musculus MRC_OX-2 antigen homolog gene, exons 2-5, and complete cds	
9174	17867			2.88	5.0E-01 AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102	
9185	17976			3.84	5.0E-01 O13861	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11	
789	10038	19188		2.7	4.8E-01 BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'	
1635	10849	20027		2.98	4.9E-01 AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP	
1870	11077	20267		1.33	4.9E-01 U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds	
5677	14887	24289		3.1	4.9E-01 AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10	

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5677	14897	24280	3.1	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6275	15455	24898	1.68	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8853	18389		2.73	4.9E-01	10946863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1). mRNA
8328	17428		1.61	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9187	18354		4.8	4.9E-01	AA613562.1	EST_HUMAN	nc022611.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144632 3'
9249	18019		1.47	4.9E-01	11431438	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1). mRNA
3512	12736		0.98	4.8E-01	AA912842.1	EST_HUMAN	d328e0.s1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:1626144 3'
4324	13525		0.69	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4678	13525		0.68	4.8E-01	4504850	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
5443	14869	23628	9.14	4.8E-01	J02987.1	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5961	15176		3.78	4.8E-01	AA659878.1	EST_HUMAN	nu85f08.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1217513
6218	15397		2.3	4.8E-01	5031650	NT	Homo sapiens reproduction 8 (D8S2288E) mRNA
6389	15580	25036	3.91	4.8E-01	AL181492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6389	15580	25037	3.81	4.8E-01	AL181492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
7316	16534		2.05	4.8E-01	X83502.1	NT	S.cerevisiae ORFs from chromosome X
8408	17483		1.28	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8845	18122		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
3039	12276		0.79	4.7E-01	AF192387.1	NT	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
5882	15098	24510	8.23	4.7E-01	BF217173.1	EST_HUMAN	601883880f1 NIH_MIGC_57_Homo sapiens cDNA clone IMAGE:4098387 5'
7424	18634		6.28	4.7E-01	AF102673.1	NT	Influenza A virus isolate hk51697 hemagglutinin (HA) gene, partial cds
7651	16851	26349	2.42	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
7915	17130	26660	2.99	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029_Homo sapiens cDNA
8667	17843		1.41	4.7E-01	AW341561.1	EST_HUMAN	hd11cc08.x1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2909198 3'
3724	12844	22061	1.84	4.6E-01	BF683300.1	EST_HUMAN	602081103f1 NIH_MIGC_81_Homo sapiens cDNA clone IMAGE:4245481 5'
3724	12944	22082	1.64	4.6E-01	BF683300.1	EST_HUMAN	602081103f1 NIH_MIGC_81_Homo sapiens cDNA clone IMAGE:4245481 5'
5428	14655	23792	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5428	14655	23793	3.65	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5464	14690	24042	1.86	4.6E-01	BE734781.1	EST_HUMAN	601568755f1 NIH_MIGC_21_Homo sapiens cDNA clone IMAGE:3843637 5'
5473	14689	24052	1.88	4.6E-01	A1247679.1	EST_HUMAN	qhs9h2.x1 Soares_fetal_liver_spine_1NFLS_S1_Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O16338 O16338 BUTYROPHILLIN :

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5473	14689	24053	1.88	4.6E-01	A1247679.1	EST_HUMAN	qtl59102.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN; Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
5985	15287	24892	1.84	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
5985	15287	24893	1.84	4.6E-01	U62332.1	NT	Emericella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6398	15568	25025	2.25	4.6E-01	AA493577.1	EST_HUMAN	nh4405.s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
6558	15764	25226	21.67	4.6E-01	Bf697599.1	EST_HUMAN	602130953F1 NIH MGIC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
7063	16240	25713	3.37	4.6E-01	A195834.1	EST_HUMAN	wg73e12.x1 Soares_NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7063	16240	25714	3.37	4.6E-01	A195834.1	EST_HUMAN	wg73e12.x1 Soares_NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
7563	16768		3.16	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
7571	16776	26268	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT10730-100500-075-905 HT0730 Homo sapiens cDNA
7571	16776	26269	3.63	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT10730-100500-075-905 HT0730 Homo sapiens cDNA
8007	16442	25930	5.97	4.6E-01	AF0169369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8007	16442	25931	5.97	4.6E-01	AF0169369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
8588	17597		1.24	4.6E-01	D56316.1	EST_HUMAN	HUM105F03B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-105FF35
1875	11082	20272	1.17	4.5E-01	AE0011831.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1875	11082	20273	1.17	4.5E-01	AE0011831.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
2822	12061	21184	5.81	4.5E-01	AA870086.1	EST_HUMAN	255d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:484179 3'
3289	12520	21651	4.15	4.5E-01	Q57983	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3358	12584	21723	1.2	4.5E-01	AF126378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4008	13218		1.27	4.5E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN
4052	13262	22365	0.66	4.5E-01	A1708908.1	EST_HUMAN	as98609.x1 Barsteed iota HPLRBB Homo sapiens cDNA clone IMAGE:2353480 3'
4157	14479		5.3	4.5E-01	AW873495.1	EST_HUMAN	hc609d225R1 NIH MGIC_87 Homo sapiens cDNA clone IMAGE:38869023 3'
4982	14149	23241	1.17	4.5E-01	BE963445.2	EST_HUMAN	w132602.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:24266118 3' similar to TR:Q92923 Q92923 SWI/SNF COMPLEX-170 KDA SUBUNIT
6340	15520	24987	2.51	4.5E-01	A1858849.1	EST_HUMAN	t256g11.x1 NCI CGAP_OV35 Homo sapiens cDNA clone IMAGE:2292844 3'
6802	15788	25235	4.3	4.5E-01	A1648596.1	EST_HUMAN	
6710	15905		2.22	4.5E-01	11444786	NT	Hom sapiens hypothetical protein DKE2p547G183 (DKE2p547G183), mRNA
7212	16389	25871	16.01	4.5E-01	M88606.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17
7212	16389	25872	16.01	4.5E-01	M88606.1	EST_HUMAN	EST02531 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBCY17

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7440	16848	26141	3.36	4.5E-01	AW681221.1	EST_HUMAN	x014h01_x1 NCL_CGAP_U3 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
7804	16897		1.8	4.5E-01	A771982.1	EST_HUMAN	Q84252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1]
8036	17172	26711	2.23	4.5E-01	BE068472.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
8286	18348		3.39	4.5E-01	BE871481.1	EST_HUMAN	RC3-BT0333-160300-016-a03 BT0333 Homo sapiens cDNA clone IMAGE:3852961 5'
8893	17854		1.12	4.5E-01	BF337531.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4163280 5'
9067	17894		3.3	4.5E-01	11422098	NT	602035275F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4163280 5'
2004	11207		1.98	4.4E-01	6580503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2352	11545	20767	3.37	4.4E-01	P49765	SWISSPROT	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
3287	12518	21649	1.37	4.4E-01	AF058780.1	NT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3287	12518	21650	1.37	4.4E-01	AF058780.1	NT	Rattus norvegicus Syngap-b mRNA, complete cds
3291	12522	21653	2.03	4.4E-01	BF058728.1	EST_HUMAN	781d02_y1 NCL_CGAP_BrI6 Homo sapiens cDNA clone IMAGE:3393795 5'
4219	13422		1.4	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809393 5'
5242	14416		4.05	4.4E-01	Q11082	SWISSPROT	PROBABLE G PROTEIN-COUPLED RECEPTOR B0563 6
5770	14888	24389	1.93	4.4E-01	AW080795.1	EST_HUMAN	xc27e08_x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR_O95154 O95154
6411	15808		19.38	4.4E-01	Z11679.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE. [1]
7058	16235		2.74	4.4E-01	P28922	SWISSPROT	S. tuberosum mRNA for induced stolon tip protein (partial)
7110	16287	25768	4.94	4.4E-01	P55590	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
8570	17588	23998	3.41	4.4E-01	6677874	NT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
8581	18279		4.39	4.4E-01	AI163282.2	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
8035	17879	23893	3.59	4.4E-01	96277742	NT	Homo sapiens chromosome 21 segment HS21C032
9137	17845		1.88	4.4E-01	P54725	SWISSPROT	Autophora californica nucleopolyhedrovirus, complete genome
4117	9870	18810	2.16	4.3E-01	AF565218.1	NT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
4117	9870	18811	2.15	4.3E-01	AF565218.1	NT	Callithrix jacchus MN/W opsin gene, upstream flanking region
1583	10798	18873	0.92	4.3E-01	AW856550.1	EST_HUMAN	QVA-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2824	12083		1.01	4.3E-01	AW855269.1	EST_HUMAN	CMV-DT0003-010200-077-c01 D10003 Homo sapiens cDNA
3025	12261	21389	0.87	4.3E-01	AW858477.1	EST_HUMAN	MRO-BN0070-270300-008-q04 BN0070 Homo sapiens cDNA
4133	13339	22438	1.3	4.3E-01	J00306.1	NT	Human somatosatin 1 gene and flanks
4400	9870	18810	0.89	4.3E-01	AF555218.1	NT	Callithrix jacchus MN/W opsin gene, upstream flanking region
4400	9870	18811	0.89	4.3E-01	AF555218.1	NT	Callithrix jacchus MN/W opsin gene, upstream flanking region
5618	14841	24219	2.04	4.3E-01	AF179825.1	NT	Saimiri sciureus olfactory receptor (SSOC186) gene, partial cds
5983	15183	24599	4.69	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica ifn-g gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6253	15444		1.94	4.3E-01	BT348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156286 5'
6609	15805		3.13	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-(fiaC-fia) genes, complete cds
7505	15275	24705	2.79	4.3E-01	AFO75829.1	NT	Equus caballus microsatellite LEX027
7757	16953	26460	1.8	4.3E-01	AW882658.1	EST_HUMAN	RC3-BN034-280200-L13-c12 BN0034 Homo sapiens cDNA
7757	16953	26461	1.8	4.3E-01	AW882658.1	EST_HUMAN	RC3-BN034-280200-L13-c12 BN0034 Homo sapiens cDNA
9236	18009		2.07	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor white gene
1368	11992	19747	1.62	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FITSH HOMOLOG PRECURSOR
1917	11122		0.89	4.2E-01	AA781653.1	EST_HUMAN	r22460.31 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288698 3'
3587	12808	21930	5.31	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3616	12837	21956	1.03	4.2E-01	AJ280338.1	EST_HUMAN	q194601.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879945 3'
3692	14478		0.8	4.2E-01	NB1203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE-1-K similar to R07879, Z40498
3860	13175	22289	1.16	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4707	13898	22987	7.2	4.2E-01	AA534093.1	EST_HUMAN	nig890.51 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:897777 similar to gb:M33500 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR,1 BETA CHAIN (HUMAN);
4790	13979	23083	4.06	4.2E-01	R13467.1	EST_HUMAN	y77601.r1 Soares_infant brain 1NB1 Homo sapiens cDNA clone IMAGE:28278 5'
6084	15254	24878	9.98	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE:2000470 3'
8084	15254	24878	9.98	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE:2000470 3'
8093	18071	24726	1.98	4.2E-01	SB2504.1	NT	Brcal=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
8122	15308	24739	5.87	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6461	15658	25129	5.45	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, IMAGE: Homo sapiens cDNA EST369413 MAGE resequences, IMAGE: Homo sapiens cDNA EST369413 MAGE resequences, IMAGE: Homo sapiens cDNA
6481	15658	25130	5.45	4.2E-01	AW957448.1	EST_HUMAN	Oryzias latipes OIGCT mRNA for membrane gammaM cyclase, complete cds
7612	16815	26311	2.08	4.2E-01	AB023489.1	NT	601650352R1 NIH MGIC_71 Homo sapiens cDNA clone IMAGE:3906035 3'
7933	17073	26800	2.55	4.2E-01	BE988485.2	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'
9179	17971		1.28	4.2E-01	AV731815.1	EST_HUMAN	RC-BT081-210198-142 BT091 Homo sapiens cDNA
1102	10326	19476	1.44	4.1E-01	A905481.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1111	10335	19485	0.85	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1111	10335	19486	0.85	4.1E-01	AV705243.1	EST_HUMAN	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2871	11852	21068	1.14	4.1E-01	7705283	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
2891	12128	21261	2.32	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
2891	12128	21262	2.32	4.1E-01	AL161538.2	NT	q194603.s1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3272	12505	21686	0.6	4.1E-01	AA806344.1	EST_HUMAN	EST373364 MAGG Homo sapiens cDNA
3753	12972	22087	0.74	4.1E-01	AW961282.1	EST_HUMAN	EST373364 MAGG Homo sapiens cDNA
3753	12972	22088	0.74	4.1E-01	AW961282.1	EST_HUMAN	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoC, isoF genes
4260	13463	22555	2.88	4.1E-01	AJ249207.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4292	13484			0.78	4.1E-01 AF809257.1	EST_HUMAN	om33d02_s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4670	13884	22865		1.28	4.1E-01 AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
5257	14430			0.85	4.1E-01 BF345483.1	EST_HUMAN	602018232F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155102 5'
5650	14873	24260		4.51	4.1E-01 BF581383.1	EST_HUMAN	602156580F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287319 5'
6285	15446	24885		2.7	4.1E-01 U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7416	16628	26120		50.16	4.1E-01 X58700.1	NT	Zea mays ZmPNIS2 gene for 19 kDa zein protein
7930	16406	25880		2.89	4.1E-01 Q8470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HVK1)
8919	18325			1.75	4.1E-01 D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1338	11980			3.52	4.0E-01 AW847123.1	EST_HUMAN	RC2-CT0201-2908989-012-d10 CT0201 Homo sapiens cDNA
1046	10271	19422		1.06	4.0E-01 8404858	NT	Lequeus rubellus mitochondrion, complete genome
1347	10562	19727		1.04	4.0E-01 AF203478.1	NT	Drosophila melanogaster Dalmatian (dm1) mRNA, complete cds
1478	10691			3.71	4.0E-01 6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfb), mRNA
1974	12007	20384		1.86	4.0E-01 Z66933.1	NT	Ascidobius immersus mas2 gene
1974	12007	20385		1.86	4.0E-01 Z66933.1	NT	Ascidobius immersus mas2 gene
2757	9421	18555		2.81	4.0E-01 6678480	NT	Mus musculus ubiquitin-protein ligase 63 component n-recognition (Ubr1), mRNA
2923	12161	21285		1.49	4.0E-01 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2923	12161	21288		1.49	4.0E-01 AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3673	12894	22016		2.17	4.0E-01 AF068803.1	NT	Streptococcus pneumoniae YIC (YID) YID (YID), penicillin-binding protein 2x (ppb2x), and undecapeptidyl-phospho-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptides transferase (mraY) genes, complete cds
3817	13035	22146		3.33	4.0E-01 AJ277511.1	NT	Ovis aries partial ID2 gene for T cell receptor delta chain (TCRD12), exon 1
3817	13035	22147		3.33	4.0E-01 AJ277511.1	NT	Ovis aries partial ID2 gene for T cell receptor delta chain (TCRD12), exon 1
48322	14021			9.93	4.0E-01 Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
8212	17343			3.53	4.0E-01 L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
8587	18179			2.28	4.0E-01 AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9138	17946			1.4	4.0E-01 P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-ST3 INTERGENIC REGION
1384	10568	19765		1.52	3.9E-01 AF206818.1	NT	Gorilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2805	11789	21009		3.23	3.9E-01 AB033019.1	NT	Homo sapiens mRNA for KIAA1183 protein, partial cds
2668	11847	21061		4.39	3.9E-01 X82032.1	NT	H. sapiens B-myb gene
2668	11847	21062		4.39	3.9E-01 X82032.1	NT	H. sapiens B-myb gene
3082	12288	21422		4.8	3.9E-01 AJ225886.1	NT	Sinorhizobium meliloti 4a, syfB2, crf3 genes and crf3
4055	13265	22398		1.53	3.9E-01 BF592611.1	EST_HUMAN	7161d01.X1 NCI_CGAP_B116 Homo sapiens cDNA clone IMAGE:3339169 3'
5014	14201	23298		2.1	3.9E-01 BE729687.1	EST_HUMAN	601563945F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833369 5'
5630	14854	24237		4.01	3.9E-01 BF208036.1	EST_HUMAN	601882362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Database Source
7032	16209	25986		3.45	M19879.1	NT	Human clatbindin 27 gene, exons 10 and 11, and L1 and Alu repeats	
7397	16810			1.84	3.9E-01 AF6859.4	EST_HUMAN	AV685974 GfKC Homo sapiens cDNA clone IMAGE:3028915'	
8352	18355			4.15	3.9E-01 AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds	
8415	17528			2.15	3.9E-01 Q61870	SWISSPROT	HOMEOBOX PROTEIN HUX1	
8561	17582	23987		1.37	3.9E-01 AE001811.1	NT	Thermatoga maritima section 123 of 136 of the complete genome	
9011	17985			1.31	3.9E-01 11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583). mRNA	
163	9445			16.12	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
512	9763			6.59	3.8E-01 AB029291.1	NT	Mus musculus pcm-1 mRNA for pentacentriolar material-1, complete cds	
1836	11044			1.28	3.8E-01 AE003870.1	NT	Xylella fastidiosa, section 18 of 229 of the complete genome	
2535	11723	20940		3.41	3.8E-01 AF214117.1	NT	Arabidopsis thaliana putative c-myb-like transcription factor (MYB3R-3) mRNA, complete cds	
2698	12021	21000		4.04	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2861	12189			0.92	3.8E-01 AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)	
3013	12249	21380		2.35	3.8E-01 AF033333.1	NT	Pleuroectes americanus aminopeptidase N (ampN) gene, partial cds	
3458	12683	21817		9.08	3.8E-01 AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4 contig fragment No. 30	
3513	12737			0.75	3.8E-01 AI807218.1	EST_HUMAN	wr38b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855.3'	
3528	12137			0.66	3.8E-01 AI807218.1	EST_HUMAN	wr38b12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855.3'	
3533	12779	21908		8.64	3.8E-01 AF109372.1	NT	Danio rerio blue-sensitive opsin (blueops) mRNA, complete cds	
3658	12778	21909		8.64	3.8E-01 AF109372.1	NT	Danio rerio blue-sensitive opsin (blueops) mRNA, complete cds	
3739	12859	22074		1.09	3.8E-01 BE154080.1	EST_HUMAN	PM0-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA	
3894	13110	22228		0.69	3.8E-01	6754095	NT	Mus musculus general transcription factor II (Gtf2), mRNA
5079	14259	23344		1.14	3.8E-01 AF028833.1	NT	Homo sapiens Myo17 protein (MPV17) gene, partial cds; and urocoitin gene, complete cds	
5221	14385	23480		4.31	3.8E-01 AF158635.1	NT	Triticum vernicosum Vf (Vf) gene, partial cds	
5945	15161	24574		5.59	3.8E-01 BE072399.1	EST_HUMAN	QV3-BT0537-271289-049-902 BT0537 Homo sapiens cDNA	
5984	15286	24891		4.68	3.8E-01 AI374601.1	EST_HUMAN	Ia5411-x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:2047917.3' similar to Ia5411-x1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:120539.5' similar to contains Alu repetitive element;	
6297	15478			4.51	3.8E-01 X61597.1	NT	M.musculus gene for kallikrein-binding protein	
6641	16336	25287		3.65	3.8E-01 AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds	
6944	16088			7.37	3.8E-01 T95413.1	EST_HUMAN	y43h08_r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:302893'	
8085	17200			3.41	3.8E-01 BE179219.1	EST_HUMAN	yf2h11.31 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:302893'	
8180	17322	28865		3.07	3.8E-01 R42550.1	EST_HUMAN	yf2h11.s1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:302893'	
8180	17322	28866		3.07	3.8E-01 R42550.1	EST_HUMAN	Borreia burgdorferi (section 10 of 70) of the complete genome	
8571	17589			2.97	3.8E-01 AE001124.1	NT	Human ps3 (TPS3) gene, complete cds	
8703	18276			1.58	3.8E-01 I194788.1	NT		

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8818	17736			1.91	3.8E-01 BE829256.1	EST_HUMAN	QV3ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
9237	18251			1.26	3.8E-01 AF261483.1	NT	Mus musculus vomeronasal receptor V1RA4 (V1re4) gene, complete cds
9255	18023	23852		1.24	3.8E-01 AF184972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2443	11634	20854		8.52	3.7E-01 AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3437	12662	21794		10.32	3.7E-01 AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3852	13098	22183		1	3.7E-01 AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4214	13417	22513		8.6	3.7E-01 AA218707.1	EST_HUMAN	ck39cc7-x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4311	13512	22606		1.22	3.7E-01 AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-B02 OT0007 Homo sapiens cDNA
4384	13585	22687		2.78	3.7E-01 AE002406.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
5272	14474	23516		7.85	3.7E-01 BE865837.1	EST_HUMAN	601678239F1 NIH MGIC_53 Homo sapiens cDNA clone IMAGE:3961136 5'
6135	15319	24753		3.37	3.7E-01 11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7) mRNA
6571	15787	25229		3.35	3.7E-01 11436179	NT	Homo sapiens chromosome 12 open reading frame 4 (C12orf4) mRNA
6571	15787	25230		3.35	3.7E-01 11436179	NT	Homo sapiens chromosome 12 open reading frame 4 (C12orf4) mRNA
7138	16315	25796		3.64	3.7E-01 A1336411.1	EST_HUMAN	qf46807-x1 Soares_fetal_lung_NbII-19W Homo sapiens cDNA clone IMAGE:1650897 3'
7699	16802	28295		2.8	3.7E-01 AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7699	16802	28296		2.8	3.7E-01 AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
7604	16807	26304		2.52	3.7E-01 AF149786.1	NT	Erythrocytes patatas isodate #8289 decay-accelerating factor (CD55) gene, partial cds
8002	16437	25924		4.81	3.7E-01 X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (Tdt) (EC 2.7.7.31)
8239	17398			3.16	3.7E-01 66777678	NT	Mus musculus retinoblastoma 1 (Rb1) mRNA
8268	17916			1.53	3.7E-01 J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
8441	17504			3.72	3.7E-01 AJ243525.1	NT	Chlamydia pneumoniae partial omega 1 gene for outer membrane protein 1
8542	17587			2.37	3.7E-01 D88976.1	NT	Human mRNA for KIAA0223 gene, partial cds
8831	17813			1.89	3.7E-01 AL121154.1	EST_HUMAN	DKFZp762k075_r1762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762k075 5'
8900	17860	23888		2.55	3.7E-01 Y18000.1	NT	Homo sapiens NF2 gene
9232	18210			1.23	3.7E-01 X91192.1	NT	H.sapiens PLC beta 3 gene (exon 1) and SOM172 gene (exon 1)
265	9540	18670		1.16	3.6E-01 AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1003	10234			7.24	3.6E-01 U88241.1	NT	Human mibrp gene, partial cds
1321	10536	18700		2.68	3.6E-01 T80255.1	EST_HUMAN	y036d5_r1 Soares_infant brain 1NIIB Homo sapiens cDNA clone IMAGE:24443 5'
1321	10536	18701		2.68	3.6E-01 T80255.1	EST_HUMAN	y036d5_r1 Soares_infant brain 1NIIB Homo sapiens cDNA clone IMAGE:24443 5'
1881	11088	20278		6.2	3.6E-01 AW590184.1	EST_HUMAN	hg33f02_x1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2847419 3'
1881	11088	20279		6.2	3.6E-01 AW590184.1	EST_HUMAN	hg33f02_x1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
1922	11126	20322		5.46	3.6E-01 AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2234	11429			1.19	3.6E-01 AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2353	11546			1.98	3.6E-01 X78725.1	NT	P.lirengulare (P3804) gene for actin

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	11841	20862	1.18	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181080-011-907 ST0171 Homo sapiens cDNA PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2594	11780	20998	1.3	3.6E-01	PF24208	SWISSPROT	Drosophila melanogaster sugar transporter 3 (sub3) mRNA, complete cds
2851	14478		9.22	3.6E-01	AF199485.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3446	12671	21805	2.88	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3446	12671	21806	2.88	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4492	13602	22702	1.01	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA Brassica napus mRNA for MAP4K alpha2 protein
4700	13891	22891	0.94	3.6E-01	AJ009609.1	NT	Mus musculus protein tyrosine kinase Tec ('Tec') gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4730	13921	23024	0.97	3.6E-01	AF071938.1	NT	Mus musculus protein tyrosine kinase Tec ('Tec') gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4730	13921	23025	0.97	3.6E-01	AF071938.1	NT	Z mays mRNA for casein kinase II alpha subunit
4765	13954	23055	0.71	3.6E-01	Y11526.1	NT	Bacteria from anodic bulk soil 16S rRNA gene (strain XB45)
4802	13891	23099	5.79	3.6E-01	AJJ229237.1	NT	had2g04_x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:28725563
5033	14218	23303	2.56	3.6E-01	AW338983.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5131	14309	23400	0.76	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
5862	15080	24492	1.65	3.6E-01	Y10198.1	NT	Homo sapiens PHEx genes
6138	15322		4.03	3.6E-01	R94090.1	EST_HUMAN	Y174s06.11 Scarecs fetal liver spleen thymus_NHFFT Homo sapiens cDNA clone IMAGE:2759875
6202	15383	24825	1.81	3.6E-01	AW027174.1	EST_HUMAN	W72c10_x1 Scarecs_fetal liver spleen_thymus_NHFFT Homo sapiens cDNA clone IMAGE:25130103 similar to TR:O15117
6552	15748	25209	21.1	3.6E-01	AL161583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
6765	15860	25415	5.02	3.6E-01	4504556	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
6766	15860	25416	5.02	3.6E-01	4504556	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7027	16204	25681	24.7	3.6E-01	C53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
7518	16723	26213	2.34	3.6E-01	BE802390.1	EST_HUMAN	801676418E-1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:39589975
7672	16871	26374	3.94	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
7980	16416	25902	3.79	3.6E-01	AE090856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
8305	18383		2.02	3.6E-01	Y19210.1	NT	Homo sapiens Hbb5 gene for hair keratin, exons 1 to 9
8391	17472		5.38	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
8553	17575		3.66	3.6E-01	U66388.1	NT	Mus musculus Emr1 mRNA, complete cds

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8937	17817			1.52	3.6E-01	11432598	NT
9208	18327			2.18	3.6E-01	AW190229.1	EST_HUMAN
9259	18027			1.88	3.6E-01	L27208.1	NT
115	9403	18532		0.79	3.5E-01	AL161536.2	NT
214	9494	18626		2.07	3.5E-01	6878933	NT
684	9827	19058		1.16	3.5E-01	AL161581.2	NT
732	9973	19112		1.36	3.5E-01	7706136	NT
732	9973	19113		1.36	3.5E-01	7706136	NT
789	10029	18178		3.88	3.6E-01	BF129798.1	EST_HUMAN
1617	10830	20005		1.84	3.5E-01	U35776.1	NT
2247	11442	20686		0.93	3.5E-01	P06798	SWISSPROT
2567	12020	20972		2.03	3.5E-01	AA223252.1	EST_HUMAN
2857	12195	21329		0.78	3.5E-01	AA107691.1	EST_HUMAN
3793	13011			1.23	3.5E-01	AA642138.1	EST_HUMAN
4249	13452	22543		2.33	3.5E-01	AF071253.1	NT
4953	14140	23234		4.58	3.5E-01	MM18349.1	NT
5147	14326			3.22	3.5E-01	AA825140.1	EST_HUMAN
5356	14586	23662		1.81	3.5E-01	Q96687	SWISSPROT
5356	14586	23683		1.81	3.5E-01	Q96687	SWISSPROT
6107	15201			3.68	3.5E-01	X98505.1	NT
6489	15889			3.28	3.5E-01	11448042	NT
7320	16537	26025		3.47	3.5E-01	X61084.1	NT
7592	16796	26289		2.15	3.5E-01	AJ243178.1	NT
7592	16796	26290		2.15	3.5E-01	AJ243178.1	NT
8119	17253	28794		2.04	3.5E-01	N77597.1	EST_HUMAN
8181	17313	28855		1.67	3.5E-01	LO5145.1	NT
8472	17525			2.16	3.5E-01	X64585.1	NT
8843	17628			1.55	3.5E-01	AE001774.1	NT
9263	18227	23697		2.45	3.5E-01	HB0814.1	EST_HUMAN
9263	18227	23698		2.45	3.5E-01	HB0814.1	EST_HUMAN

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
714	8968			1.67	3.4E-01 AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
983	10214	18370		5.03	3.4E-01 Y09788.2	NT	Pseudomonas fluorescens colR_cds genes, orf222 and partial lnsA gene
1334	10549	19713		1.61	3.4E-01 Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2368	11589	20781		2.41	3.4E-01 D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
2959	12197	21331		0.97	3.4E-01 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
	2959	12197		0.97	3.4E-01 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3125	12350	21489		6.49	3.4E-01 U83805.1	NT	Caris familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3317	12547	21680		0.94	3.4E-01 AF034852.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3505	12729	21866		4.83	3.4E-01 AF106353.1	NT	Methylovorus sp. strain SS1 putative GpE (gpE), DnaK (dnak), and putative DnaJ (dnaj) genes, complete cds
3772	12980			1.4	3.4E-01 BF449010.1	EST_HUMAN	7N94a01_x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:35722323' similar to TR:Q9UJ15 Q8UJ15 DJ18C9.1'
4029	13238			1.43	3.4E-01 AA584198.1	EST_HUMAN	nc011510.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:11100347.3'
4498	13684	22788		0.68	3.4E-01 AF168341.1	NT	Homo sapiens integrin alpha 8 (ITGA6) gene, exons 12 through 23
4845	13839	22929		2.14	3.4E-01 BE089912.1	EST_HUMAN	MR4-BT043-230200-202-001 BT10403 Homo sapiens cDNA
4971	14158			4.38	3.4E-01 A1240973.1	EST_HUMAN	qj98505.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:18672083' similar to contains Alu repetitive element;
5529	14753	24120		3.01	3.4E-01 AL161584.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5577	14801			5.91	3.4E-01 AA085313.1	EST_HUMAN	zn12d11.s1 Strategene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221.3'
5857	14880			1.94	3.4E-01 L02871.1	NT	Echovirus 22 1AB, 1C, 1D, 2B, 2C, 3A, 3B, 3D proteins RNA, complete mature peptides and cds
5711	14930	24324		1.99	3.4E-01 AW204505.1	EST_HUMAN	U1-H-B11-ssi-e-12-0-U1_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582.3'
5768	14987	24387		1.86	3.4E-01 AL120544.1	EST_HUMAN	DKEZp761A249_r1_761 (synonym: hany2) Homo sapiens cDNA clone DKFZp761A249.5'
6831	16025	25480		5.51	3.4E-01 P26013	SWISSPROT	INTEGRIN_BETA-8 PRECURSOR
6831	16025	25491		5.51	3.4E-01 P26013	SWISSPROT	INTEGRIN_BETA-8 PRECURSOR
6892	15598	25083		8.48	3.4E-01 U19492.1	NT	Saccharomyces cerevisiae Mar1p (MAF1) gene, complete cds
6892	15598	25084		8.46	3.4E-01 U19492.1	NT	Saccharomyces cerevisiae Mar1p (MAF1) gene, complete cds
7037	16214	25891		3.24	3.4E-01 AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
7588	16791			4.26	3.4E-01 AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
7621	16824	26320		2.84	3.4E-01 P06925	SWISSPROT	PROTABLE E4 PROTEIN

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7657	16857	26358	2.78	3.4E-01	Af045981.1	NT	Rutilus arvensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
7832	17024	26539	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
7832	17024	26540	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 38 and 37
8032	17169	26708	1.9	3.4E-01	A8035507.1	NT	Rettus norvegicus mRNA for s-glyceraldehyde-3-phosphate dehydrogenase (GAPDH), complete cds
8038	17193	28731	4.89	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosomal 4, contig fragment No. 27
8250	17378	28912	1.85	3.4E-01	BFO81948.1	EST_HUMAN	7K69d12_X1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480648 3'
8232	17598		1.9	3.4E-01	U89604.1	NT	Citrus uniflora virus putative replicase gene, partial cds
8394	17473		1.37	3.4E-01	Z21621.1	NT	S.cerevisiae RIB5 gene encoding Riboflavin synthase
8500	18118		1.58	3.4E-01	A1254351.1	NT	Schizosaccharomyces pombe Cwf8p (cw8) gene, complete cds
8623	17817		6.12	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds
8635	18149		2.88	3.4E-01	BE218852.1	EST_HUMAN	h42108_X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.3'
8713	18252		1.9	3.4E-01	9838381	NT	PTR5 repetitive element ;
8825	17739	23931	1.98	3.4E-01	A1297131.1	NT	Beta vulgaris mitochondrial, complete genome
9142	17848		2.16	3.4E-01	Af019413.1	NT	Hom sapiens HLA class III region containing Tenascin X (Tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, halicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes,>
14	8810	18412	14.06	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5U1 nodX gene
105	8810	18412	5.73	3.3E-01	X07980.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
454	9707	18845	0.77	3.3E-01	Al161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
639	9885	18010	1.85	3.3E-01	7682485	NT	Hom sapiens KIAA1100 protein (KIAA1100), mRNA
1208	10427	18584	3.17	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1314	10530	18692	3.14	3.3E-01	BF588880.1	EST_HUMAN	60218401671 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1535	10798	18974	1.04	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dtg5), mRNA
1710	10822		1.41	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week / Homo sapiens cDNA 5' end
2369	11582		4.41	3.3E-01	4507834	NT	Hom sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMP5) mRNA
2801	12139	21276	2.03	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Yeo3-12 complete genome
2977	12214		0.67	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT (CLMF/P35)
3020	12256	21385	1.04	3.3E-01	AB007832.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3470	12685	21831	0.97	3.3E-01	AB012822.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3783	13001	22116	0.8	3.3E-01	D14015.1	NT	Rat mRNA for cyclin E, complete cds

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3797	13015	22128	2.2	3.3E-01	Q84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3808	13026	22136	1	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3942	13158	22275	1.97	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3978	13192	22300	2.17	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4361	13583		2.43	3.3E-01	D31682.1	NT	Rettus norvegicus DNA for regucalcin, partial cds
4696	13887		1.58	3.3E-01	AI539114.1	EST_HUMAN	tp78p12_x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4856	14044	23138	1.36	3.3E-01	D64003.1	NT	Synecdochis sp. PCG8803 complete genome_22/27_2755703_2888766
5222	14398	23481	1.51	3.3E-01	AV884409.1	EST_HUMAN	CV3-OT0055-290301-137-911 O70055 Homo sapiens cDNA
6348	14578	23654	2.48	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5348	14578	23655	2.48	3.3E-01	X89818.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5636	14860	24244	1.76	3.3E-01	BE619850.1	EST_HUMAN	60147276871 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5636	14860	24245	1.76	3.3E-01	BE619850.1	EST_HUMAN	60147276871 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
5678	14898	24281	6.34	3.3E-01	P05691	SWISSPROT	CIRCUIMSPOROZOITE PROTEIN (CS)
6035	15243	24664	4.61	3.3E-01	AI628131.1	EST_HUMAN	ty84n01_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element;
6035	15243	24685	4.61	3.3E-01	AI628131.1	EST_HUMAN	ty84n01_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element;contains element L1 repetitive element;
6408	15589	25049	1.8	3.3E-01	NB5146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
6842	15837	25298	14.81	3.3E-01	BF683954.1	EST_HUMAN	602140372F_1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301800 5'
6916	16104	25570	3.78	3.3E-01	N698868.1	EST_HUMAN	2a67ho_51 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297649 3'
6935	16079	26549	3.25	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-01-904 TN0077 Homo sapiens cDNA
7309	16527	26017	2.71	3.3E-01	X63983.1	NT	D.mauritiana Adh gene
7309	16527	26018	2.71	3.3E-01	X63983.1	NT	D.mauritiana Adh gene
7585	16788		1.89	3.3E-01	BF528409.1	EST_HUMAN	602070802F_1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4213585 5'
7783	16978	26491	11.77	3.3E-01	BE219351.1	EST_HUMAN	hv51802_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
7885	17101	26632	4.85	3.3E-01	P47863	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
8209	17340		4.68	3.3E-01	AA808621.1	EST_HUMAN	ob71902_x1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1356850 3'
8228	8310	18412	2.53	3.3E-01	X07980.1	NT	Rhizobium leguminosarum symb plasmid pRLS1 nodX gene
8381	17485	26590	1.58	3.3E-01	6598319 NT	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9131	17941			12.3	3.3E-01 AP0000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 28700-1-544000 nt. position (27)
463	9716			2.22	3.2E-01 AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
725	9887			0.92	3.2E-01 AI_1615612	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1170	10391	19543		18.32	3.2E-01 AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA polymerase gene, complete cds
1289	10504	19885		1.74	3.2E-01 Z50202.1	NT	P. vulgaris arc5-1 gene
1394	10608	19172		6.8	3.2E-01 Q48824	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1744	10956	20139		1.28	3.2E-01 Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1754	10966	20151		5.41	3.2E-01 AW957194.1	EST_HUMAN	EST362264 MAGE resequences, MAGD Homo sapiens cDNA
1754	10986	20152		5.41	3.2E-01 AW957194.1	EST_HUMAN	EST362264 MAGE resequences, MAGD Homo sapiens cDNA
1810	11019	20211		1.34	3.2E-01 AI_111655.1	NT	Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2128	11326	20543		2.6	3.2E-01 BF203817.1	EST_HUMAN	60188804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2508	11894			2.24	3.2E-01 7710078	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxknot), mRNA
2670	11851	21067		1.35	3.2E-01 AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PZF) gene, complete cds
3548	12807	0.87		3.2E-01 D10872.1	NT	Human h NAT allele 3.2 gene for arylamine N-acetyltransferase	
4387	13588	22690		1.44	3.2E-01 M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4501	13689	22793		1.34	3.2E-01 Q10268	SWISSPROT	HYPOTHETICAL 8.1-KD PROTEIN C13G7_04C IN CHROMOSOME 1 PRECURSOR
4749	13940			7.91	3.2E-01 BF893617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4901	14089	23182		0.69	3.2E-01 Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5310	14541	23810		3.05	3.2E-01 BE173964.1	EST_HUMAN	CMD-HT0569-060300-289-f10 HT0569 Homo sapiens cDNA
6516	15712	25177		2.43	3.2E-01 M60266.1	NT	Rat ISOC-atrial natriuretic factor gene, complete cds
6585	15781	25241		13.9	3.2E-01 X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6587	15783	25244		22.45	3.2E-01 BF511635.1	EST_HUMAN	6011887107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126833 5
6645	15840	25300		2.84	3.2E-01 AE002015.1	NT	Deinococcus radiodurans R4 section 152 of 229 of the complete chromosome 1
6796	15991			2.59	3.2E-01 M88511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7071	16248	25721		2.71	3.2E-01 U44914.1	NT	Borrelia burgdorferi plasmid cp32-2; erpC and erpD genes, complete cds; and unknown genes
7170	16347			2.78	3.2E-01 AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
7281	16480	25972		3.47	3.2E-01 T08813.1	EST_HUMAN	EST1042 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBD221
8417	18278			2.4	3.2E-01 L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
8868	17838			2.92	3.2E-01 O83277	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9111	17929			1.43	3.2E-01 L59874.1	NT	Homo sapiens deoxyribonuclease gene, complete cds
9171	18319	23505		1.92	3.2E-01 BE385776.1	EST_HUMAN	6012125480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3816748 5'

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Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	11814	21033	3.26	3.1E-01	R18051.1	EST_HUMAN	yes006.11 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:125051 6' similar to gb:M64241 QM PROTEIN (HUMAN); Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2658	11955	21052	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2658	11955	21053	3.57	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2810	12050		1.15	3.1E-01	AW628036.1	EST_HUMAN	hi46h08_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3108	12373		3.8	3.1E-01	AB025069.1	NT	Mus musculus gene for Ser/Thr kinase KIAAMRE, exon 6
3885	13101	22218	1	3.1E-01	A2251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4983	14170	22260	0.98	3.1E-01	AE003984.1	NT	Xylella fastidiosa, Section 130 of the complete genome
5430	14657	23795	9.75	3.1E-01	AF178611.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5581	14784	24154	2.13	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6073	18048	23562	2.71	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:35240420 5'
7119	16298	25778	2.92	3.1E-01	AI244001.1	EST_HUMAN	q16161_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1963980 3' similar to gb:S557700
7444	16626	26119	1.86	3.1E-01	BZ216117.1	EST_HUMAN	HYDROXYMETHYL GLUTARYL-CAOLYASE PRECURSOR (HUMAN);
8069	17204	28737	2.43	3.1E-01	78622291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
8551	17574		1.55	3.1E-01	AF284308.1	NT	Analis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene
8590	17599		1.62	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
8740	17686		2.6	3.1E-01	AF198653.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP) gene, complete cds
9116	17934						Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, AA differentiation-dependent protein, triple LM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
9155	18314		1.52	3.1E-01	10946623	NT	Mus musculus peptide/glycan recognition protein-like (Pglypl-pending), mRNA
72	11935	18494	1.46	3.0E-01	6755058	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
298	9534	18685	8.86	3.0E-01	A2271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1231	10449	18605	2.2	3.0E-01	AW300400.1	EST_HUMAN	xs65fb08_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	10710	19883	5.25	3.0E-01	AJ008755.1	NT	Baleaemoptera physalus gene encoding atrial natriuretic peptide
3109	12404		0.94	3.0E-01	X33615.1	NT	S.pombe p1c1 gene
3118	12413		1.29	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alpG genes for polygluturonata lyases, complete cds
3312	12800	21736	0.62	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
3848	13063	22177	1.88	3.0E-01	AW817785.1	EST_HUMAN	PMI-ST0282-261199-001-001 ST0262 Homo sapiens cDNA
3951	13168	22280	1.08	3.0E-01	A2271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4514	13710	22803	1.89	3.0E-01	AJ008755.1	NT	Baleaemoptera physalus gene encoding atrial natriuretic peptide
5180	12660	21736	0.63	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5366	14596	23673	5.84	3.0E-01	BE741628.1	EST_HUMAN	6015949860F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5441	14687	23822	3.77	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-ad3 BT0333 Homo sapiens cDNA
5441	14687	23823	3.77	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-ad3 BT0333 Homo sapiens cDNA
5462	14888	24038	4.58	3.0E-01	U01247.1	NT	Mus musculus 12S rRNA 10 kDa protein (McC10) gene, complete cds
6011	15281	24985	2.89	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6221	15402	24843	3.34	3.0E-01	10947007	NT	Mus musculus midolloid (Mid)-pending mRNA
6290	15471	24912	1.75	3.0E-01	Af071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
6598	15784		4.69	3.0E-01	99_0161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec9b), mRNA
6620	15816	25275	2.36	3.0E-01	BE566083.1	EST_HUMAN	601339078F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3581594 5'
7188	16383	25843	2.79	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
8240	17569	26904	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8240	17569	26905	3.04	3.0E-01	H51029.1	EST_HUMAN	yp84b10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
8852	18261		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9149	18311		3.57	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Fapl), mRNA
1706	10918		1.72	2.9E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and gr2r gene for insulin-like growth factor type 2 and L41ps and Au7/6 pseudogenes
1993	11186	20405	1.33	2.9E-01	AE000736.1	NT	Aequifascia aedacina section 88 of 109 of the complete genome
3217	12451	21583	1.78	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-f12 CT0328 Homo sapiens cDNA
3217	12451	21584	1.78	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171298-001-f12 CT0328 Homo sapiens cDNA
4048	13258	22360	0.66	2.9E-01	AB016428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4061	13272		0.66	2.9E-01	AW002802.1	EST_HUMAN	w02f10.21 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2480395 3'
4483	13581	22770	1.18	2.9E-01	AA284468.1	EST_HUMAN	z55741.21 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Aliu repetitive element;
4852	14041	23134	4.7	2.9E-01	AB018028.1	NT	Mus musculus gene, complete cds, similar to EXLM1 wa06f03.21 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12.1.1
5144	14323		1.21	2.8E-01	AJ670889.1	EST_HUMAN	B. subtilis levanses operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase repetitive element;
5557	14781	24148	5.09	2.9E-01	X56098.1	NT	B. subtilis levanses operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanses
5557	14781	24150	5.09	2.9E-01	X56098.1	NT	B. subtilis levanses operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanses
5553	14787	24158	6.3	2.9E-01	6679662	NT	Mus musculus Eph receptor AB (Ephab), mRNA
5799	15016	24419	2.5	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6123	15307	24740	3.4	2.9E-01	Q04398	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C

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Single Exon Probes Expressed In HEK293 Cells

Probe SEQ.ID NO:	Exon SEQ.ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7470	168778	26160	2.13	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds	
7721	16920	26427	2.67	2.9E-01	VO1394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit	
7721	16920	26428	2.67	2.9E-01	VO1394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit	
8111	17245	26785	2.54	2.9E-01	AA835373.1	EST_HUMAN	ny35h02.51 NCI_CGAP_Pri2 Homo sapiens cDNA clone IMAGE:1273778 similar to contains LTR8.12 LTR8 repetitive element;	
8114	17248	26788	4.72	2.9E-01	AL139878.2	NT	Campylobacter jejuni NCITC11168 complete genome; segment 5/6 w286f05.x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element	
8802	17727	23929	1.34	2.9E-01	AW005871.1	EST_HUMAN	MER29 repetitive element;	
8893	17787	23920	3.11	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds	
9202	17987	23860	1.67	2.9E-01	Y088937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
9202	17987	23861	1.57	2.9E-01	Y088937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
575	9825			2.8E-01	U57136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds	
580	9828			2.8E-01	L28145.1	NT	Prunus dwarf virus movement protein, complete cds; coat protein, complete cds	
1091	10315	19469	3.05	2.8E-01	AF168050.1	NT	Gilia glauca cocoyote maturation factor Mos (c-mos) gene, partial cds	
1284	10499	19859	1.07	2.8E-01	BE313442.1	EST_HUMAN	6011148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'	
1284	10499	19860	1.07	2.8E-01	BE313442.1	EST_HUMAN	6011148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'	
1298	10513	19871	0.89	2.8E-01	DB86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds	
1702	10914	20102	1.41	2.8E-01	AW886020.1	EST_HUMAN	QV1-C70364-120200-065-b05 C10384 Homo sapiens cDNA	
1880	11184	20392	1.49	2.8E-01	AO1047620.1	EST_HUMAN	DKEZp588612321_11_586 (synonym: huta1) Homo sapiens cDNA clone DKEZp588612321	
2101	11301	20515	1.13	2.8E-01	AW511195.1	EST_HUMAN	hd44903.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'	
2435	11628	20848	2.08	2.8E-01	AE0003494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome	
2435	11626	20849	2.08	2.8E-01	AE0003494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome	
2512	11701			2.8E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65	
2825	12163			1.58	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2926	12164	21288	1.98	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)	
2828	12164	21289	1.98	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)	
3357	12585	21724	1.07	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-964000 nt. position (4/7)	
3973	13187	22295	2.91	2.8E-01	AE001180.1	NT	Battaria burgdonferi (section 66 of 70) of the complete genome	
4104	13311			0.75	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 529 of the complete genome
4180	13384			2.28	2.8E-01	A1090868.1	ov44g10.x1 Scores_ntestis_NHT Homo sapiens cDNA clone IMAGE:1640226 3 similar to contains Alu repetitive element; contains element MER22 repetitive element;	
4454	13652	22747		2.77	2.8E-01	P19815..	SWISSPROT RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN)(L PROTEIN)	
4792	13981	23005	1.17	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds	
4792	13981	23098	1.17	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4839	14028	23120	0.95	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (S2NAE12) polyprotein precursor, gene, partial cds
4846	14035	23128	2.9E-01	AF030154.1	NT	Bovine adrenovirus 3 complete genome	
4877	14065	23160	1.52	2.8E-01	BF528188.1	EST_HUMAN	6020942801F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180128 5'
4906	14094	23187	2.89	2.8E-01	AI272669.1	EST_HUMAN	q158c11_x1 Soares_NhIMPU_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5209	14384	23469	1.85	2.8E-01	AW808625.1	EST_HUMAN	MR1-ST0111-111188-01-0-907 ST0111 Homo sapiens cDNA
5240	14414	23494	0.79	2.8E-01	U85949.1	NT	Mus musculus hepatocyte growth factor-like protein receptor (Ran) gene, complete cds
5281	14482	23530	0.69	2.8E-01	6878616	NT	Mus musculus Yemaguchi sarcoma viral (yes) oncogene homolog (Yes), mRNA
5338	18051	23843	22.74	2.8E-01	AA348987.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5494	14720	24077	2.89	2.8E-01	AB016825.1	NT	Homo sapiens OCTN2 gene, complete cds
5976	15190	24607	7.37	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B41-acif-f-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30885182 3'
6531	15727	25192	3.85	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6651	15846	25846	8.12	2.8E-01	BF52987F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'	EST_HUMAN	6020922987F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
7095	16272	25749	4.31	2.8E-01	77081183	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
7329	16545	26034	2.35	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
7329	16545	26035	2.35	2.8E-01	BF241082.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108350 5'
7354	16570	26081	3.21	2.8E-01	BF585970.1	EST_HUMAN	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076028 5'
7457	16665	26154	2.95	2.8E-01	AF051682.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
78227	17019	4.12	2.8E-01	BF574023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'	
8840	17749	7.9	2.8E-01	DS3329.1	NT	Mus musculus DNA for presagittal D2 synthase, complete cds	
8952	17826	23905	4.34	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030406-001-007 HT0606 Homo sapiens cDNA
8980	17847	23915	1.23	2.8E-01	BE800118.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955968 5'
9139	18288	2.15	2.8E-01	11433628	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA	
483	9735	18868	3.37	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
618	9884	18984	3.09	2.7E-01	AA450061.1	EST_HUMAN	z239b110_s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1288	10483	18842	1.39	2.7E-01	AB004906.1	NT	Ionomera purpurea transposable element Tip100 gene for transposase, complete cds
1598	10812	1.78	2.7E-01	X78815.1	NT	Gambelia SR2 gene	
1704	10916	20103	3.78	2.7E-01	W58087.1	EST_HUMAN	z222110_s1 Soares_fetal_hear_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1746	10958	20141	1.35	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN PI2; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2105	12010		2.25	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2335	11528	20749	7.58	2.7E-01	Y18868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{cop}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2418	11609	20831	3.29	2.7E-01	AB310858.1	EST_HUMAN	ta43c11_x2_NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGENE:2046836 3' similar to contains element L1 repetitive element;
2941	12179		0.68	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-080900-385-605 HT0875 Homo sapiens cDNA clone IMAGENE:2A628288 3'
3987	13201	22309	1.88	2.7E-01	AB28015.1	EST_HUMAN	w62811_X1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGENE:2A628288 3'
4001	13214	22318	0.77	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (AE6) gene, partial cds
4001	13214	22319	0.77	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (AE6) gene, partial cds
4007	13219	22322	2.21	2.7E-01	L77589.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4814	14102	23195	1.12	2.7E-01	L27516.1	NT	Tritium aestivum (Wcs66) gene, complete cds
5088	14246		2.97	2.7E-01	AW858131.1	EST_HUMAN	RC1-CT0286-230200-018-603 CT0286 Homo sapiens cDNA
5308	14539	23544	2.45	2.7E-01	P17277	SWISSPROT	HOMEobox PROTEIN HOXA4 (HOXA-1.4)
6981	16273	24702	2.12	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6234	15415	24856	1.88	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20 kD PROTEIN B0563.3 IN CHROMOSOME X
6371	16661	26007	1.89	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6371	15551	25008	1.89	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6862	16052	26519	3.3	2.7E-01	Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
6862	16052	25520	3.3	2.7E-01	Q83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7117	16284	25776	3.68	2.7E-01	AF087434.1	NT	Mus musculus transcrifactor NFATc isoform a (NFATc) mRNA, complete cds
7389	16603	26091	2.21	2.7E-01	AV705043	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ABCD005 5'
7389	16603	26092	2.21	2.7E-01	AV705043	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ABCD005 5'
7398	16612	26102	4.34	2.7E-01	AB132269.1	NT	Homo sapiens cation channel 1-1/2 locus, Contig1, D7S522, genes CA1/2 (exons 1, 2a, and 2b), CAA1 (exons 1 and 2)
8861	17638		1.41	2.7E-01	AB012482.1	NT	Rattus norvegicus mRNA for phosphatidylinositol 3-kinase, catalytic subunit, beta isoform
9023	17874		1.5	2.7E-01	Q838627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
9122	17937		2.34	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
476	11968	18861	1.68	2.6E-01	P78411	SWISSPROT	PROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
487	9740		0.83	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1387	10811	19775	1.44	2.6E-01	BE885087.1	EST_HUMAN	601510638F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGENE:3912345 5'
1438	10852	19825	0.97	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1861	11068	20258	6.36	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1861	11068	20259	6.36	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2082	11263			10.1 2.6E-01	AW733152.1	EST_HUMAN	bb04d10_x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M36072_60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactin locus surfactin 3 protein gene (MOUSE);
2121	11320	20538		1.03 2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2436	11627			1.48 2.6E-01	Y12986.1	NT	B_martinitus rbcL gene
2511	11700			9.82 2.6E-01	BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890043 5'
3057	12283			1.03 2.6E-01	AV974531.1	EST_HUMAN	EST388635 IMAGE resequences, MAGM Homo sapiens cDNA EST_Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3557	12780	21910		1.04 2.6E-01	M22342.1	NT	Bacteriophage T2 DNA (adenine-N6)methyltransferase (dam) gene, complete cds
3822	12843	21963		1.94 2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3834	13150	22265		0.96 2.6E-01	AJ012174.2	NT	Chlamydomonas partial rmpB gene for RNase P RNA subunit
3834	13150	22266		0.96 2.6E-01	AJ012174.2	NT	Chlamydomonas partial rmpB gene for RNase P RNA subunit
4077	13287	22385		0.8 2.6E-01	AV959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4136	13342	22443		17.81 2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-04040-132-003 BT0630 Homo sapiens cDNA
4350	13552	22847		1.15 2.6E-01	AF175283.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4494	13692	22785		0.83 2.6E-01	AB021180.1	NT	Celitus galius mRNA for skeletal myosin heavy chain, complete cds
4494	13692	22786		0.83 2.6E-01	AB021180.1	NT	Celitus galius mRNA for skeletal myosin heavy chain, complete cds
4545	13740	22840		1.51 2.6E-01	AA457617.1	EST_HUMAN	aa89d0711 Strategene fetal retina 907202 Homo sapiens cDNA clone IMAGE:838477 5'
4848	13842	22932		1.45 2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhc631*) mRNA, complete cds
4726	13917	23018		1.39 2.6E-01	AF142703.1	NT	Ophrestia radicosa matrulae-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4891	14178	23269		4.02 2.6E-01	HO4858.1	EST_HUMAN	yf51605_x1 Sciaris placaenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5088	14248			0.59 2.6E-01	AA884625.1	EST_HUMAN	em33b1.51 Scarcos_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5203	14378	23485		1.24 2.6E-01	AA985392.1	EST_HUMAN	em81611.51 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629572 3' similar to contains
5689	18388			2.32 2.6E-01	AE001811.1	NT	L112_L1 repetitive element;
5754	14973	24371		2.17 2.6E-01	AI582557.1	EST_HUMAN	Thermotoga maritima section 123 of 136 of the complete genome
							ts02612_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 contains element LTR1 repetitive element;
5754	14973	24372		2.17 2.6E-01	AI582557.1	EST_HUMAN	ts02612_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1 contains element LTR1 repetitive element;
6575	15771	25233		2.72 2.6E-01	BP345588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150398 5'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6679	15874	25332	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-E70082-310500-021-F10 ET0082 Homo sapiens cDNA
6679	15874	25333	2.87	2.6E-01	BE830339.1	EST_HUMAN	RC5-E70082-310500-021-F10 ET0082 Homo sapiens cDNA
7980	17098	26628	1.89	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
8038	17191	25.68	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)	
8400	17478		2.5	2.6E-01	10180635	NT	Mus musculus Jerky (Jrk) mRNA
8603	18269		2.25	2.6E-01	BE983491.1	EST_HUMAN	601511032F1 NIH_MIGC_71 Homo sapiens cDNA clone IMAGE:3912912 5'
8672	17847	23978	2.83	2.6E-01	AT3:16898.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FATD2) gene, complete cds, alternatively spliced
9017	17869		1.39	2.6E-01	D38425.1	NT	Ceia cobaya mRNA for serine/threonine kinase, complete cds
9145	17850		1.28	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9184	17875		1.27	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
245	9523	18653	2.05	2.5E-01	4502296	NT	Homo sapiens ATP synthase H+ transporting, mitochondrial F1 complex, delta subunit (ATPSD), nuclear gene encoding mitochondrial protein, mRNA
246	9523	18653	2.52	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATPSD), nuclear gene encoding mitochondrial protein, mRNA
259	9535		7.15	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
842	10079	19237	1.27	2.5E-01	U09984.1	NT	Mus musculus ICR/1Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1087	10283		0.95	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1129	10353	19505	9.34	2.5E-01	T99837.1	EST_HUMAN	ye11907.1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1335	10599		2.16	2.5E-01	AS025343.1	NT	Olea europaea OEW mRNA for lipoic synthase, complete cds
1703	10915		5.2	2.5E-01	4885408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1848	12004	20246	1	2.5E-01	BE896604.1	EST_HUMAN	PM4-C70400-310700-005-d08 C10400 Homo sapiens cDNA
1848	12004	20247	1	2.5E-01	BE896604.1	EST_HUMAN	PM4-C70400-310700-005-d08 C10400 Homo sapiens cDNA
2371	11564		5.84	2.5E-01	AE000875.1	NT	Aequifex aequiculus section 7 of 108 of the complete genome
2459	11650		1.02	2.5E-01	AA251987.1	EST_HUMAN	Zs11a12.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:6848862 5'
3390	12617		4.31	2.5E-01	AW973471.1	EST_HUMAN	EST383464 MAGE resequences, MAGM Homo sapiens cDNA
3508	12732	21870	0.77	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3524	12748	21878	8.77	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4045	13255		0.9	2.5E-01	P52323	SWISSPROT	AAGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4309	13510		0.85	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4781	13852		1.18	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4787	13958	23057	4.65	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4791	13980	23084	2.54	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4816	14005			3.4	2.5E-01 AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
5074	14254	23337	0.61	2.5E-01 AW873588.1	EST_HUMAN	WP_7119GA_294.D_Ce22838;	hG2111_X1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041997 3' similar to T3 receptor-associated cofactor-1 [Human, fetal liver, mRNA, 2330 nt]
5349	14579	23656	12.94	2.5E-01 SB3380.1	NT		
6349	15529	24978	4.91	2.5E-01 AL163282.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21_C0B2	
6536	15732	25196	3.18	2.5E-01 BF033859.1	EST_HUMAN	601459238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862809 5'	
6686	15881	25320	4.29	2.5E-01 HS3236.1	EST_HUMAN	Y9B4f07.11 Scores fetal liver spleen 1NE1 S Homo sapiens cDNA clone IMAGE:2022501 5'	
6920	16113	25578	29.94	2.5E-01 UB98651.2	NT	Homo sapiens matrix metalloproteinase MMP_Ras1 gene, promoter region	
6920	16113	25579	29.94	2.5E-01 UB98651.2	NT	Homo sapiens matrix metalloproteinase MMP_Ras1 gene, promoter region	
7111	16288	25769	2.7	2.5E-01 AW581997.1	EST_HUMAN	RC3-S10186-130100-015-e07 ST0186 Homo sapiens cDNA	
7217	16394	25978	2.22	2.5E-01 X85491.1	NT	Mouse 1Md LINE DNA	
7643	16843	26541	3.62	2.5E-01 D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds	
8335	17433	26938	4.13	2.5E-01 AF200528.1	NT	Zearomyces cellulose synthase-4 (Cesa-4) mRNA, complete cds.	
8384	18350		6.92	2.5E-01 AI161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41	
8848	18192	23761	1.28	2.5E-01 AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds	
8892	18113		1.37	2.5E-01 AV892543.1	EST_HUMAN	AV6922543 GK2_Homo sapiens cDNA clone GKCGZF1 5'	
560	9810	18933	1.07	2.4E-01 AA836316.1	EST_HUMAN	cN70014.51 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'	
858	10094	19257	2.17	2.4E-01 BF576124.1	EST_HUMAN	6012132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:427157 5'	
1311	10527	18687	11.61	2.4E-01 AJ289880.1	NT	Homo sapiens KIAA02851 gene (partial), XT3 gene and L2TFL1 gene	
1311	10527	18688	11.61	2.4E-01 AJ289880.1	NT	Homo sapiens KIAA02851 gene (partial), XT3 gene and L2TFL1 gene	
1818	11026		21.38	2.4E-01 AF287753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds	
1864	11071	20262	1.38	2.4E-01 AF251708.1	NT	Zebocys duhamnades fructose-1,6-bisphosphatase mRNA, complete cds	
2107	11306	20520	1.03	2.4E-01 AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes	
2134	11332		1.04	2.4E-01 P46384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (ICA1 PROTEASE)	
2227	11423	20649	1.67	2.4E-01 AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome	
2349	11542	20765	1.01	2.4E-01 BF002171.1	EST_HUMAN	7h23d04.41 NCL_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA	
2502	11681	20911	1.59	2.4E-01 Z38534.1	NT	O-2588 26S PROTEASE REGULATORY SUBUNIT 6A ; D. discoidium (Ax3-K) pnaA gene	
2717	11898	21113	5.18	2.4E-01 X77783.1	NT	S. pombe swif gene	
2739	11916	21132	4.61	2.4E-01 AF030154.1	NT	Bovine adenovirus 3 complete genome	
3097	12233		3.32	2.4E-01 U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds	
3643	12884	21982	1	2.4E-01 AF169783.1	NT	Podospora anserina HET-C protein (HET-c) gene, complete cds	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3743	12863	22078	0.89	2.E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4008	13220		0.9	2.E-01	D28960.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5512	14737	24101	0.26	2.E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5512	14737	24102	0.26	2.E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5612	14836	24211	2.4	2.E-01	BF592336.1	EST_HUMAN	7154-d04_x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN Q08170 SPLICING FACTOR, ARGinine/SERINE-RICH 4 contains element TAR1 TAR1 repetitive element
5648	14871	24258	2.63	2.E-01	AF035646.1	NT	Drosophila melanogaster p58a MAP kinase gene, complete cds
5703	14922	24315	2.49	2.E-01	7681801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
5884	15111	24523	1.92	2.E-01	AI698989.1	EST_HUMAN	wc62c11_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2332320 3' similar to gb:J03484 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN)
6228	15409	24851	8.53	2.E-01	L43001.1	NT	Bos taurus glutamyl cyclase-activating protein 2 (guc2) mRNA, complete cds
6945	16089	25558	8.01	2.E-01	AI693515.1	EST_HUMAN	wd4360_2_x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22_b1 TAR1 repetitive element;
7191	16368	25847	2.4	2.E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
7351	16567	26057	3.3	2.E-01	AI161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
7412	16624	26118	2.68	2.E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
7754	16950		2.28	2.E-01	Z21847.1	NT	P.asterias mosaic virus genomic RNA
8291	17404	26931	1.22	2.E-01	AE217491.1	NT	Homo sapiens fragile X1D oxidoreductase (FOR) gene, exon 6
8426	18136		1.93	2.E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EL1) mRNA, complete cds
8492	17535		2.37	2.E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
8720	18120		2.21	2.E-01	Y01507.1	NT	Gallus gallus gene coding for e-actin
9180	17872		3.79	2.E-01	AI163281.2	NT	Homo sapiens chromosome 21 segment HS21C031
9222	18001		2.34	2.E-01	L20422.1	NT	Human 14-3-3n protein mRNA, complete cds
394	9649	18784	1.02	2.E-01	S75888.1	NT	aromatase [Poecilia reticulata] zebra finches, ovary, mRNA, 3188 nt]
643	9889		3.82	2.E-01	U39713.1	NT	Mycobacteria dentifilum section 35 of 51 of the complete genome
673	9918	18047	23.88	2.E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
942	10175	18328	4.61	2.E-01	BE311983.1	EST_HUMAN	6011420_3F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1499	10712	19884	0.92	2.E-01	667780	NT	Mus musculus vacuolar protein sorting 4b (yeast) Vps4b, mRNA
1639	10822	19998	3.69	2.E-01	Y10887.2	NT	Mus musculus cd15 gene, exon 1, partial
2012	11214		1.15	2.E-01	AI235535.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2409	11601	20821	1.57	2.E-01	BE297718.1	EST_HUMAN	601175562_2F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2776	10606	19770	2	2.E-01	AB015033.1	NT	Marmosabilla agariovora gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2818	12158	21281	0.96	2.3E-01	AA601379.1	EST_HUMAN	no16d06.51 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Aliu repetitive element;contains element THR repetitive element;
3049	12285		7	2.3E-01	R21732.1	EST_HUMAN	yh21b07.51 Soares placenta N2HP Homo sapiens cDNA clone IMAGE:130337 3'
3349	12577	21718	1.24	2.3E-01	HE8336.1	EST_HUMAN	y87h10.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3809	13125		6.19	2.3E-01	7882133	NT	Homo sapiens KIAA0450 gene product (KIAA0450). mRNA
4343	13545	22836	1.08	2.3E-01	R82292.1	EST_HUMAN	y17f01.11 Soares placenta N2HP Homo sapiens cDNA clone IMAGE:149017 5'
4394	13595		1.97	2.3E-01	L78789.1	NT	Mus musculus ferlin (Ren-1c) gene, promoter region
4445	13644	22739	1.16	2.3E-01	D801869.1	NT	Synechocystis sp. PCCE8803 complete genome, 1/27, 1-133859
4485	13683	22773	2.23	2.3E-01	A0f092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRK M13) mRNA, complete cds
4951	13746	22846	5.67	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5075	14255	23338	0.84	2.3E-01	A0B32400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5252	14425		1.06	2.3E-01	Af080322.1	NT	Bos taurus NAD(+)-isocitrate dehydrogenase subunit 1 (DH1-B precursor) (DH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
5332	14583	23637	2.38	2.3E-01	A0B040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5407	14635	23763	2.13	2.3E-01	Bf0558381.1	EST_HUMAN	7K30b08.51 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476899 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN F15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].
5456	14682	24032	4.76	2.3E-01	X86587.1	NT	C.familiaris rsm1 gene
5633	14857	24239	2.26	2.3E-01	A1708840.1	EST_HUMAN	es27e12.51 Barstead aorta HPLRB6_Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5633	14857	24240	2.26	2.3E-01	A1708840.1	EST_HUMAN	as27e12.51 Barstead aorta HPLRB6_Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6032	15240	24682	4.01	2.3E-01	A1718148.1	EST_HUMAN	as42f12.51 Barstead aorta HPLRB6_Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Aliu repetitive element;
6257	15438	24878	2.77	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM77 precursor RNA, partial cds
6339	15519		3.64	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15). mRNA
6398	15579		2.64	2.3E-01	NE09833.1	EST_HUMAN	zai2ec01.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282338 5'
6462	15659	25131	2.45	2.3E-01	M68893.1	NT	Oxytricha nova macrouclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
7049	16226	25701	3.31	2.3E-01	BE173060.1	EST_HUMAN	MR0+T0558240400-014-911 HT05582 Homo sapiens cDNA
7189	16376		5.86	2.3E-01	BF133577.1	EST_HUMAN	601648155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
7744	16940	26450	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein S34 (mg534 gene)
7744	16940	26451	1.81	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein S34 (mg534 gene)
7881	17107	26837	2.22	2.3E-01	AE002167.2	NT	Chlamydomphila pneumoniae AR39, section 4 of 94 of the complete genome

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8410	17485			3.16	2.3E-01 U45428.1	NT	Borrelia burgdorferi 2.9-8 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
8503	17542			25.49	2.3E-01 T27231.1	EST_HUMAN	HCOEST44 HT28M6 Homo sapiens cDNA clone HCCE44 5'
8527	18083			1.36	2.3E-01 AA085819.1	EST_HUMAN	chn1425 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
8536	17581			1.46	2.3E-01 AW863940.1	EST_HUMAN	PM4-SN007-02-03040-007-808 SN0072 Homo sapiens cDNA
8599	18281	23681		3.26	2.3E-01 AW303623.1	EST_HUMAN	x21d07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z715
8635	18331	23603		5.25	2.3E-01 BE882464.1	EST_HUMAN	Q9Z715 LYSYL OXIDASE-RELATED PROTEIN 2. ;contains PTR5_b2 TAR1 repetitive element;
8687	17658			1.79	2.3E-01 BF663319.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
8739	17885			2.68	2.3E-01 AJ008519.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
8834	17744			1.32	2.3E-01 U49845.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9102	17925			3.77	2.3E-01 BF47561.1	EST_HUMAN	Pleurodolus wall distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
9261	18242	23708		1.26	2.3E-01 M60675.1	NT	nac38h12_x1 Lipski_scatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MER38 repetitive element;
89	9382	18512		0.82	2.2E-01 A0592190.1	EST_HUMAN	Human von Willebrand factor gene, exons 23 through 34
1547	10761	18935		2.55	2.2E-01 AF187850.1	NT	q214810_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875280 3' similar to
1986	11189			0.99	2.2E-01 AF171901.1	EST_HUMAN	q214810_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875280 3' similar to
2058	11259	20474		2.57	2.2E-01 M34840.1	NT	Human von Willebrand factor gene, promoter region
2367	11560	20782		5.34	2.2E-01 BF677538.1	EST_HUMAN	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial product
2548	11736	20953		1.67	2.2E-01 BE819258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2548	11736	20954		1.67	2.2E-01 BE819258.1	EST_HUMAN	6020856908F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:42498969 5'
2835	12074	21198		5.33	2.2E-01 BE158625.1	EST_HUMAN	601462528F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38866190 5'
2835	12074	21187		5.33	2.2E-01 BE158625.1	EST_HUMAN	601462529F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38866180 5'
2871	12109			1.67	2.2E-01 AF020503.1	NT	PM2-HT0353-281289-003-812 HT0353 Homo sapiens cDNA
3369	12597			2.58	2.2E-01 AL161562.2	NT	PM2-HT0353-281289-003-812 HT0353 Homo sapiens cDNA clone IMAGE:38866180 5'
3735	12855	22071		0.61	2.2E-01 AL163285.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3803	13021			1.59	2.2E-01 AF155728.1	NT	Homo sapiens chromosome 21 segment HS21C055
4073	13283	22382		0.59	2.2E-01 AF215391.1	NT	Xiphophorus maculatus truncated Rxr1 reverse transcriptase (RT) pseudogene
4106	13313			0.61	2.2E-01 U681174.1	NT	Mus musculus breast/tovarian cancer susceptibility protein (BRCA1) mRNA, partial cds
4195	13399			1.05	2.2E-01 AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4203	13408	22501		6.45	2.2E-01 AF165142.1	NT	Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Descriptor
4250	13453	22544	2.81	2.2E-01	AF 117340 1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	
4250	13453	22545	2.81	2.2E-01	AF 117340 1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds	
4349	13551	22645	1.25	2.2E-01	U01307 1	NT	Human scRNA (BC200 beta) pseudogene	
4349	13551	22646	1.25	2.2E-01	U01307 1	NT	Human scRNA (BC200 beta) pseudogene	
4842	14031		1.18	2.2E-01	D50604 1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene	
4848	14037	23130	2.94	2.2E-01	AA211246 1	EST_HUMAN	228705 1 Streptagene hNT neuron (R83723) Homo sapiens cDNA clone IMAGE:848988 5	
5069	14249		1.22	2.2E-01	L13289 1	NT	Mus musculus vinculin gene, exon 3	
5549	14773	24141	1.96	2.2E-01	58030 02	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA	
5553	14777		4.03	2.2E-01	D8400 1	NT	Synecdochysp sp. PCC6803 complete genome, 18/27-2392728-2538999	
6097	152897	24729	9.28	2.2E-01	AV786238 1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5	
6204	15386	24827	1.82	2.2E-01	MD4136 1	NT	Human glycophorin B gene, exon 4	
6204	15385	24828	1.82	2.2E-01	MD4136 1	NT	Human glycophorin B gene, exon 4	
6470	158637		2.59	2.2E-01	AF 155143 1	NT	Mus musculus nm23-M1 gene, promoter region	
6742	15837	25398	2.32	2.2E-01	AE001713 1	NT	Thermobius maritimus section 25 of 158 of the complete genome	
6771	15886		2.68	2.2E-01	AW865603 1	EST_HUMAN	PM3-CT0263-241298-009-b07 CT0263 Homo sapiens cDNA	
6811	16006	25487	2.22	2.2E-01	8383247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Deaf1), mRNA	
6828	18022	25488	3.06	2.2E-01	BF376354 1	EST_HUMAN	MR1-TN0045-110800-008-a02 TN0046 Homo sapiens cDNA	
6857	18109	25675	22.93	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)	
7016	16193	25687	3.82	2.2E-01	AF197941 1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPshSP21) mRNA, complete cds; nuclear gene for chloroplast product	
7055	16232	26707	2.87	2.2E-01	BF208507 1	EST_HUMAN	601869724F NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5	
7859	17098	26628	5.39	2.2E-01	X01918 1	NT	Drosophila S8C glue gene cluster	
7886	16431	25918	2.96	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA	
8338	17436		2.98	2.2E-01	EE870959 1	EST_HUMAN	601448577F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5	
8447	18342		3.56	2.2E-01	U82671 2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2b (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDH), and Li>	
8539	17564		2.37	2.2E-01	AF188843 1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1e) mRNA, complete cds	
8558	14496	23584	3.17	2.2E-01	AV361098 1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA	
9192	18338		2.87	2.2E-01	AV694801 1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5	
9273	18036	23843	1.35	2.2E-01	BF243095 1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:410988 5	
9284	18283	23682	1.57	2.2E-01	AL161578 2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 74	
978	10210	18368	1.69	2.1E-01	AA569289 1	EST_HUMAN	nm31611.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804	
981	10212	18368	1.99	2.1E-01	AL161504 2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	(Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1132	10355		3.44	2.1E-01 AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome	
1208	10425	19580	1.31	2.1E-01 6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	
1208	10425	19581	1.31	2.1E-01 6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA	
1878	11085	20275	1.91	2.1E-01 AA806824.1	EST_HUMAN	ok73602.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1619810 3' similar to g6;X02765 COMPLEMENT C3 PRECURSOR (HUMAN);	
2124	11323	20541	4.13	2.1E-01 BF665073.1	EST_HUMAN	602083128F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'	
2875	12113	21241	2.07	2.1E-01 6912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA	
2817	12155	21280	1.12	2.1E-01 U72145.1	NT	Camplotheta acuminata 3-hydroxy-3-methylglutaryl coenzyme A reductase (hmrg3) mRNA, complete cds	
3794	13012		8.61	2.1E-01 9838361	NT	Beta vulgaris mitochondrial, complete genome	
4031	13241	22345	1.17	2.1E-01 F11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180	
4031	13241	22346	1.17	2.1E-01 F11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180	
4236	13439		2.87	2.1E-01 AF124526.1	NT	Orchestia cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds	
4370	13572		1.53	2.1E-01 AB039041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds	
4574	13768	22863	1.99	2.1E-01 AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds	
5280	14461	23529	1.2	2.1E-01 AE001173.1	NT	Bottius burgdorfen (section 59 of 70) of the complete genome	
5229	14561	23833	8	2.1E-01 BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:42893001 5'	
6558	15439		2.04	2.1E-01 AE0069872.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome	
6378	15568	26014	1.82	2.1E-01 AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds	
6776	15971	25427	5.83	2.1E-01 Z35786.1	NT	S.cerevisiae chromosome II reading frame ORF YBL022W	
6918	16111	25577	4.67	2.1E-01 J97378.1	NT	A.thaliana mRNA for AtRanBP1b protein	
7182	16359	25838	2.49	2.1E-01 P52824	SWISSPROT	DIACYL GLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)	
8098	17232		2.2	2.1E-01 11036847	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA	
8109	17243	26784	2.2	2.1E-01 BE180422.1	EST_HUMAN	RC3-HIT0622-040500-013-b11 HIT0622 Homo sapiens cDNA	
8810	17731		1.54	2.1E-01 AF217480.1	NT	Homo sapiens fragile XSD oxidoreductase (FOR) gene, exons 8, 9, and partial cds	
B034	18247		1.26	2.1E-01 J32588.1	NT	Human granulin gene	
9228	18004	23848	1.88	2.1E-01 BE672330.1	EST_HUMAN	7a58e02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'	
205	9485	18619	4.22	2.0E-01 AB017437.1	NT	Gallus gallus mRNA for avena, complete cds	
540	9791		2.28	2.0E-01 7705601	NT	Homo sapiens CG-I-18 protein (LOC51008), mRNA	
706	9948	19084	0.83	2.0E-01 M77085.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allotype VH ₈₂	
820	10058	19211	1.86	2.0E-01 AF027885.1	NT	Mus musculus Major Histocompatibility Locus class II region	
1019	10247	18988	0.76	2.0E-01 D90905.1	NT	Synecdochysis sp. FCC6803 complete genome, 7/27, 7B/449-9220915	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1133	10356	19507	3.48	2.0E-01	AL183213.2	NT	Homo sapiens chromosome 21 segment HS21C013	
1261	10476	18638	1.65	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene	
1315	10531	19693	1.37	2.0E-01	AW384837.1	EST_HUMAN	PMI-HT0422-291/289-002-006 HT0422 Homo sapiens cDNA	
1480	10680	19888	12.02	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA) mRNA	
1537	10750	19923	4.33	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505	
1542	10755	19929	1.25	2.0E-01	AF260700.1	NT	Homo sapiens sodium/fodide symporter mRNA, partial cds	
1672	10885	20069	2.02	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyo1) gene, complete cds	
1692	10804		2.15	2.0E-01	AF111170.3	NT	Homo sapiens Jagged2 gene, complete cds; and unknown gene	
1729	10941		3.16	2.0E-01	U67925.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome	
1855	11062	20252	4.96	2.0E-01	BE871330.1	EST_HUMAN	60144941f1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:38533330 5'	
1855	11082	20253	4.96	2.0E-01	BE871330.1	EST_HUMAN	60144941f1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:38533330 5'	
2316	11510		1.87	2.0E-01	X82877.1	NT	H_sapiens Na+-D-glucose cotransport regulator gene	
3462	12687	21823	1.8	2.0E-01	F46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEobox-leucine zipper protein ATHB-10) (HD-ZIP PROTEIN ATHB-10)	
3644	12767		0.7	2.0E-01	AW238005.1	EST_HUMAN	xp_15622.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element;	
3886	12807	22027	0.89	2.0E-01	F34641	SWISSPROT	CED-11 PROTEIN	
3891	12912		0.65	2.0E-01	68801797	NT	Mus musculus bone morphogenetic protein 6 (Bmp6), mRNA	
3831	13147	22284	0.71	2.0E-01	Z46906.1	NT	Sus scrofa	
4423	13823	22718	0.6	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nrip6) gene, complete cds; and Nrip3 gene, exons 2-9 and 11-16	
4583	13757		8.02	2.0E-01	BE828165.1	EST_HUMAN	QV4-EN0032-19050-223-803 EN0032 Homo sapiens cDNA	
5085	14245	23332	5.68	2.0E-01	8822080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA	
5135	14313	23405	1.02	2.0E-01	Y19216.1	NT	Homo sapiens putative psihbD pseudogene for hair keratin, exons 1 to 9	
5232	14406	23489	1.4	2.0E-01	MS9257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4	
5415	14843	23775	2.42	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase	
5547	14771	24138	2.28	2.0E-01	11432540	NT	Hom sapiens dual oxidase-like domains 2 (DUOX2), mRNA	
5653	14913	24307	5.86	2.0E-01	U15300.1	NT	Seachromomyces cervisiae Hal5p (HAL5) mRNA, complete cds	
5842	15059	24467	3.28	2.0E-01	X61033.1	NT	M. auratus mu class glutathione transferase gene	
5891	15108	24519	4.07	2.0E-01	AW360865.1	EST_HUMAN	PMI-C70247-141059-001-006 C10247 Homo sapiens cDNA	
6443	15640		8.48	2.0E-01	AF028026.1	NT	Andes virus strain O12313 glycoprotein G1 and G2 precursor, gene, partial cds	
6528	15725	25190	4.35	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14	
6839	16083		4.41	2.0E-01	AEG01278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome	
7038	16215		2.78	2.0E-01	AF46892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7417	16829	26121	2.97	2.0E-01	D89088.1	NT	Salvelinus fluvialis mRNA for transferin, complete cds
7417	16829	26122	2.97	2.0E-01	D89088.1	NT	Salvelinus fluvialis mRNA for transferin, complete cds
9051	17923	23874	2.36	2.0E-01	AL023592.1	EST_HUMAN	ov68a10_s1_Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
9074	17800		7.52	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
9248	17987	23986	1.9	2.0E-01	11528495	NT	Mus musculus fructosamine 3 kinase (Fn3k) mRNA
1110	8998		9.7	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahntr) mRNA
357	9825	18755	7.17	1.9E-01	AF04353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
682	8908	18638	1.12	1.9E-01	U32581.2	NT	Homo sapiens lambdoidota protein kinase C-interacting protein mRNA, complete cds
652	8908	18037	1.12	1.9E-01	U32581.2	NT	Homo sapiens lambdoidota protein kinase C-interacting protein mRNA, complete cds
869	8915	18044	5.78	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251:198-01-d01 BT0502 Homo sapiens cDNA
870	8915	18044	6.13	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251:198-01-d01 BT0502 Homo sapiens cDNA
883	10224		1.39	1.8E-01	7305180	NT	Mus musculus interleukin-2 receptor, gamma chain (Il2g) mRNA
1112	10338	19487	13.08	1.9E-01	AA358813.1	EST_HUMAN	EST8784 Fetal lung II Homo sapiens cDNA 5' end
1378	10562	19758	2.31	1.9E-01	AF061292.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1437	10651		3.35	1.9E-01	AF184623.1	NT	Plasmidium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2348	11541	20784	5.01	1.9E-01	8922533	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581) mRNA
2873	12111	21239	4.06	1.9E-01	U66086.1	NT	Sigmodon hispidus p53 gene, partial cds
2889	12126		6.97	1.9E-01	J00922.1	NT	Galus gallus ovelbumin (Y) gene, complete cds
2860	12198	21333	1.11	1.9E-01	U25148.1	NT	Rattus norvegicus brush border myosin-1 (BBM) mRNA, partial cds
3373	12601	21737	4.46	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3455	12680	21815	5.59	1.9E-01	R16487.1	EST_HUMAN	Y4210_1 Soares fetal liver spleen 1NF-S Homo sapiens cDNA clone IMAGE:1295475'
3792	13010	22125	0.72	1.9E-01	AF264017.1	NT	Rattus norvegicus arylacetamido deacetylase gene, complete cds
3970	13185	22294	3.62	1.9E-01	AB006784.1	NT	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4059	13270	22372	1.63	1.9E-01	AW754108.1	EST_HUMAN	CM3-C70315-271199-045-b11 CT0315_Homo sapiens cDNA
4216	13419	22514	1.02	1.9E-01	BE834943.1	EST_HUMAN	MR1-FN0010-28070-007-d04 FN0010 Homo sapiens cDNA
4465	13663	22758	0.59	1.9E-01	AL161493.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
4783	13972	23075	0.78	1.9E-01	Z931780.1	NT	Fugu rubripes genes encoding carboxamoy phosphate synthase III, myosin light chain, MAP2
5035	14220		1.08	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5243	14480		3.78	1.8E-01	AE004594.1	NT	Pseudomonas aeruginosa PA01, section 155 of 559 of the complete genome
5492	14718		4.47	1.9E-01	AW150148.1	EST_HUMAN	x28a07_x1_NCI_CGAP_U1_Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETNOIC ACID RECEPTOR ALPHA-1 (HUMAN)
5509	14734	24086	7.78	1.9E-01	AF127637.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5607	14831		2.29	1.8E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4_Homo sapiens cDNA clone NT2RP-401328 5'
6306	15487	24932	2.74	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme I (sbe1) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6876	15870	25329	15.9	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
7237	18458	25946	1.98	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7237	18458	25947	1.98	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
7340	16556	26044	2.08	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds; alternatively spliced
8215	17348	26886	2.81	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9239	18175	1.52	1.9E-01	7524759	NT	Chlorella vulgaris chloroplast, complete genome	
9328	18434	3.28	1.8E-01	U73200.1	NT	Mus musculus p16Rip mRNA, complete cds	
284	11984	18669	2.47	1.8E-01	AB022080.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit (CACNB2) mRNA, and translated products
375	9841	18776	1.41	1.8E-01	4502532	NT	Oryza sativa genes for membrane guanylyl cyclase OIGC1, complete cds
754	9885	19140	0.76	1.8E-01	AB021490.2	NT	wd1f022.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3.
889	10220	19374	0.88	1.8E-01	AJ912212.1	EST_HUMAN	Dicyostellum discoidineum plasmid Dsp5, complete genome
1089	10322	19473	3.09	1.8E-01	AF000580.1	NT	Yersinia pestis plasmid pCD1
1295	10510	19670	8.42	1.8E-01	AL117169.1	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1814	11022		1.71	1.8E-01	4505036	NT	qg22d10 x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:17618113 similar to TR:OT5936 OT5936 GAMMA BUTYROBETAIN HYDROXYLASE
1832	11040		1.82	1.8E-01	AJ733708.1	EST_HUMAN	
							Mus musculus Scyag8, Scyag9, Scyag16-ps, Scyag genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scyag16 pseudogene, small inducible cytokine A5 precursor, complete cds
1880	11087	20277	1.62	1.8E-01	AB051897.1	NT	Inducible cytokine A9 precursor, Scyag16 pseudogene, small inducible cytokine A5 precursor, complete cds
2652	11835		2.24	1.8E-01	AV935728.1	EST_HUMAN	QV3-LT0018-081289-036-904 DT0018 Homo sapiens cDNA
2850	12089		1.85	1.8E-01	AF184589.1	NT	Jonopodium aculeate LEAFY protein (LEAFY2) gene, partial cds
2855	12093	21223	1.11	1.8E-01	AW182300.1	EST_HUMAN	X41603.x1 Soares, NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3098	12324	21446	1.86	1.8E-01	AW9865178.1	EST_HUMAN	QV0-EH0041-07030-147-604 BN00041 Homo sapiens cDNA
3344	12572	21711	0.8	1.8E-01	BF183582.1	EST_HUMAN	601609/23R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3600	12821	21942	0.97	1.8E-01	HC3368.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
3600	12821	21943	0.97	1.8E-01	HO3369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element;
4325	13526		1.2	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BcLA-DQB), complete cds
4553	13748	22847	5.71	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4784	13973	23076	2.53	1.8E-01	AB051897.1	NT	Mus musculus Scy6, Scy8, Scy16-ps, Scy16 pseudogene, Scy16 precursor, Scy16 pseudogene, small inducible cytokine A6 precursor, small inducible cytokine A8 precursor, Scy16 precursor, Scy16 pseudogene, small inducible cytokine A5 precursor, complete cds
5072	14232	23335	2.38	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151_289-112-906 ST0203 Homo sapiens cDNA clone IMAGE:1700028 5'
5091	14271	23355	4.94	1.8E-01	AJ792382.1	EST_HUMAN	an:28907.y5 Gassier Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5126	14305	23395	7.48	1.8E-01	AF181258.1	NT	Mesocottetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5143	14322	23414	1.28	1.8E-01	AJ439881.1	EST_HUMAN	it:57604.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134580 3'
5254	14427	23503	11.75	1.8E-01	AW809402.1	EST_HUMAN	MIR4-ST0121-0411802-019-b01 ST0121 Homo sapiens cDNA clone IMAGE:278163 5'
5904	15121		2.11	1.8E-01	NR4853.1	EST_HUMAN	Y622012.r1 Seares, multiple_sclerosis_2NBHM/SFP Homo sapiens cDNA clone IMAGE:278163 5'
7231	16452	25942	2.63	1.8E-01	X777336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
7270	16489	25979	7.41	1.8E-01	UJ38906.1	NT	Bacteriophage 111 integrase, repressor protein (rro), dUTPase, holin and lysin genes, complete cds
7322	15289	24721	2.94	1.8E-01	AB018561.1	NT	Citrus limonus mRNA for wus, complete cds
7322	15289	24722	2.94	1.8E-01	AB018561.1	NT	Citrus limonus mRNA for wus, complete cds
7323	16539	28028	4.55	1.8E-01	AF019107.1	NT	Dichotomium discideum unknown (DG1041) gene, complete cds
7888	16792	28284	1.69	1.8E-01	M59257.1	NT	Human carcinogenomic antigen (CEA) gene, exon 4
7898	16433	25921	4.57	1.8E-01	X57033.1	NT	B.laurus mRNA for potassium channel
8236	17365	28903	2.48	1.8E-01	6394421	NT	Rattus norvegicus Thromboxane receptor (Tbxex2), mRNA
8371	17458		1.24	1.8E-01	10088681	NT	Bovine ephemeral fever virus, complete genome
8433	17499	24014	1.38	1.8E-01	BF349823.1	EST_HUMAN	602018928F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
8519	17805		2.59	1.8E-01	Q86682	SWISSPROT	DN TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
9042	17884		9.36	1.8E-01	R24494.1	EST_HUMAN	Yh48h10.r1 Seares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
9084	17908		1.98	1.8E-01	YI1114.1	NT	E.spar mRNA for hexokinase (hk1)
984	9833	18951	1.41	1.7E-01	BE385164.1	EST_HUMAN	601274504.F1 NIH MGCC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
985	10053	19207	2.22	1.7E-01	K53359.1	NT	P.dumerili histone gene cluster for core histones H2A, H2B, H3 and H4
988	10201		1.63	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE)(NF-L)
1065	10291	18441	0.82	1.7E-01	AF081810.1	NT	Lymetta dispar nucleopolyhedrovirus, complete genome
1065	10291	18442	0.82	1.7E-01	AF081810.1	NT	Lymetta dispar nucleopolyhedrovirus, complete genome
11798	10986	20182	1.31	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
11930	11154		3.02	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2812	12052	21173	1.9	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2812	12052	21174	1.9	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL_VIBCO gene, partial cds
2877	12115	21244	1.75	1.7E-01	AA336809.1	EST_HUMAN	EST_141651 Endometrial tumor Homo sapiens cDNA 5' end
2954	12192	21328	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cdk-1 gene, exons 1-3
2954	12192	21327	1.34	1.7E-01	AJ238736.1	NT	Naja naja atra cdk-1 gene, exons 1-3
3089	12305	21427	1.82	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3343	12571	21710	0.67	1.7E-01	NC_005763.1	EST_HUMAN	J23485 Human fetal heart, LambdaZAP Express Homo sapiens cDNA clone J2346 5'
3423	12648	21778	1.51	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3605	12828		0.66	1.7E-01	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3912	13128	22245	6.85	1.7E-01	AF235377.1	NT	Homo sapiens derivative 11 breakpoint fragment partial intron 10 of the ALL-MLL/HRX gene fused to inton 5 of the AF-4/FEL1 gene
4453	12052	21173	3.09	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL_VIBCO gene, partial cds
4453	12052	21174	3.09	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hpr) gene, complete cds, and YRAL_VIBCO gene, partial cds
4558	13752		1.93	1.7E-01	X52836.1	NT	Schistocerca gregaria alpha repetitive DNA
4773	13882	23084	0.73	1.7E-01	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
4857	14045	23138	1.13	1.7E-01	AF027635.1	EST_HUMAN	q57e08_x1 Soares_fetal_liver_splice_1NFLS_S1 Homo sapiens cDNA clone IMAGE_1848308 3 similar to Zea mays starch branching enzyme II (be) gene, complete cds
5154	14333		1.49	1.7E-01	AF0272725.1	NT	Zea mays starch branching enzyme II (be) gene, complete cds
5901	15018	24420	11.05	1.7E-01	H72118.1	EST_HUMAN	ys02g06_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE_213658 3
6033	15241		2.09	1.7E-01	AF026552.3	NT	Mesocricetus auratus orindin precursor (OVI) gene, complete cds
6205	15388	24828	8.82	1.7E-01	BE734178.1	EST_HUMAN	601568022F_NIH_MGC_21 Homo sapiens cDNA clone IMAGE_3843964 5'
6551	15747	25207	5.6	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6551	15747	25208	5.6	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6689	15884	25344	3.97	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
6956	16134	25604	11.14	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
6985	16173	25644	2.61	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7143	16320		3.39	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7272	16491	25982	6.77	1.7E-01	BE39035.1	EST_HUMAN	601286547F1NH_IMGC_44 Homo sapiens cDNA clone IMAGE_3613258 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7384	16598	26086	3.22	1.7E-01	AA814617.1	EST_HUMAN	orf48a03.s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426824 3'
7673	16872	26375	8.77	1.7E-01	7105300	NT	Mus musculus adrenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
7673	16872	26376	8.77	1.7E-01	7105300	NT	Mus musculus adrenomatosis polyposis cell binding protein Eb1 (Eb1), mRNA
8202	17334		1.64	1.7E-01	P152772	SWISSPROT	AMP NUCLEOSIDASE
8270	17918		1.34	1.7E-01	AJ272584.1	NT	Bilobella aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II
8274	17395	26929	3.52	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA1I), mRNA
8404	18282		1.48	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
8701	18124		1.59	1.7E-01	AB244404.1	EST_HUMAN	b65905.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73770 RETINOID ACID RECEPTOR ALPHA-1 (HUMAN);
8905	17853	23889	9.13	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
124	9409	18543	1.74	1.6E-01	AF217532.1	NT	Homo sapiens myelin basic protein gene, exon 6 and 7
686	11941	18050	1.2	1.6E-01	R31497.1	EST_HUMAN	YH75112.r1 Soares placenta NB2H1P Homo sapiens cDNA clone IMAGE:135569 5'
1509	10722	19894	3.18	1.6E-01	AF288117.1	NT	Homo sapiens homeobox protein OTz2 gene, complete cds
1892	11089	20290	1.84	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONIN GLYCOPROTEIN TAG-1)
1963	11167		1.12	1.6E-01	U10334.1	NT	Craspedolepta gigas RNA polymerase II largest subunit mRNA, partial cds
2458	11847	20898	1.25	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2844	12083	21208	11.43	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2844	12083	21210	11.43	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2868	12206	21342	1.77	1.6E-01	AE001862.1	NT	Dendrocyclus radioductans R1 section 1 of 2 of the complete chromosome 2
3611	12832	21852	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3611	12832	21953	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3754	12873	22089	0.73	1.6E-01	AE000962.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
3977	13181		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4320	13521	22816	11.43	1.6E-01	AF178680.1	NT	Homo sapiens apelin gene, complete cds
4450	13849		3.4	1.6E-01	AW688601.1	EST_HUMAN	EST380677 MAGE sequences, MAGJ Homo sapiens cDNA
4459	13657		4.67	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4645	14132	23227	0.79	1.6E-01	P40831	SWISSPROT	MICRONECLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
4684	14151	23242	1.37	1.6E-01	AA086343.1	EST_HUMAN	Z84h09.s1 Strategene clone (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
4688	14175	23265	1.3	1.6E-01	AJ008356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
4688	14175	23266	1.3	1.6E-01	AJ008356.1	NT	Lycopersicon esculentum RsaI fragment 2, satellite region
5451	14677	23836	3	1.6E-01	AW197498.1	EST_HUMAN	xm43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2586969 3' similar to TR:075884 075884 HYPOTHICAL 127.6 KD PROTEIN

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5451	14677	23837	3	1.8E-01	AW197496.1	EST_HUMAN	xmt43f01.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:26866989 3' similar to TR075984 O75984
5459	14685	24035	2.4	1.6E-01	AF034716.1	NT	HYPOTHETICAL_127_6_KD PROTEIN; Rattus norvegicus CCATA/enhancer binding protein epsilon (cebp) gene, complete cds
5841	15058	24465	2	1.8E-01	AL181588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
5841	15058	24468	2	1.8E-01	AL181588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
6069	14516	23558	4.34	1.6E-01	AW281215.1	EST_HUMAN	U1-H-B12-seq1-b-06-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
6417	15814	25078	2.81	1.6E-01	LG9349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
6879	16157	25829	3.08	1.6E-01	249501.1	NT	Sorex virens chromosome X, reading frame ORF_1(R001w)
7250	16470	25962	3.11	1.8E-01	AW850893.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
7676	16875		8.9	1.8E-01	AF106064.1	NT	Plasmidium falciparum calcium-dependent protein kinase-3 (cpk3) gene, complete cds
7850	17089	26819	11.94	1.8E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
8286	18298		1.58	1.6E-01	6879466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
8406	17482	26598	3.89	1.6E-01	AV718585.1	EST_HUMAN	AV718585 GLC Homo sapiens cDNA clone GLOEMF07 5'
8854	18100		8.77	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurane synthase, complete cds
9029	17877		3.64	1.6E-01	AK024498.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
9117	17935		2.51	1.6E-01	AF287344.1	NT	Fuchsia hybrida cultivar Qiu 94-208 ribosomal protein S10 gene, partial cds, nuclear gene for mitochondrial product
9141	17947	23882	1.7	1.8E-01	9806522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
252	9528	18658	1.25	1.5E-01	BF710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
252	9528	18859	1.25	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
694	11840		1.58	1.5E-01	AV711686.1	EST_HUMAN	AV711686 DCA Homo sapiens cDNA clone DCADH06 5'
782	10032	19181	1.17	1.5E-01	AL1621284.2	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3UTR
1100	10324	19475	0.78	1.5E-01	AJ009735.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1105	10329	19479	2.27	1.5E-01	AJ251885.1	NT	Homo sapiens chromosome 21 segment HS21C084
1121	10345		1.4	1.5E-01	AV711686.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1224	10442	19597	0.77	1.5E-01	AW195516.1	EST_HUMAN	xn38d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:26960853 3'
1282	10497	18658	3.74	1.5E-01	D28535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1282	10497	18657	3.74	1.5E-01	D28535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-15)
1475	10888	19855	1.29	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1812	11079	20289	1.34	1.5E-01	AW444451.1	EST_HUMAN	U1-H-B13-akb-P-09-Q-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733841 3'
2831	12169	21301	1.28	1.5E-01	AF208068.1	NT	Marine hepatitis virus strain Penn 97-1, complete genome
2831	12169	21302	1.28	1.5E-01	AF208068.1	NT	Marine hepatitis virus strain Penn 97-1, complete genome
3326	12555	21692	4.94	1.5E-01	AA835049.1	EST_HUMAN	006805.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1671337 3' similar to gb:M11433

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 Table 4
 Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3347	12575	21715	0.77	1.5E-01	Z23104.1	NT	L_stagnalis mRNA for G protein-coupled receptor
3347	12575	21716	0.77	1.5E-01	Z23104.1	NT	L_stagnalis mRNA for G protein-coupled receptor
3738	12958	22073	1.62	1.5E-01	U09864.1	NT	Mus musculus CRISWiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3751	12970	22085	0.59	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3764	12882	22096	0.63	1.5E-01	M87982.1	NT	XNAA; Thermoanaerobacterium; XNA; 4192 base-pairs
3848	13065	22179	2.72	1.5E-01	AW685983.1	EST_HUMAN	h10f08_x1 Scores_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4027	13238	22343	0.92	1.5E-01	AW366559.1	EST_HUMAN	RC2-HT0149-191098-012-<09 HT0149 Homo sapiens cDNA
4164	13368	22467	10.65	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4484	13682	22771	0.77	1.5E-01	BE791253.1	EST_HUMAN	601583968_F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4484	13682	22772	0.77	1.5E-01	BE791253.1	EST_HUMAN	601583968_F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938345 5'
4737	13828	23032	1.55	1.5E-01	BF687685.1	EST_HUMAN	602067192_F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:40562223 5'
4762	11853	21069	2.25	1.5E-01	BF693381.1	EST_HUMAN	6020832369_F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4800	13989	23098	0.97	1.5E-01	BE1173798.1	EST_HUMAN	CIM0-HT0565-28020/245-b10 HT0565 Homo sapiens cDNA
4800	13989	23097	0.97	1.5E-01	BE1173796.1	EST_HUMAN	CIM0-HT0565-28020/245-b10 HT0565 Homo sapiens cDNA
5023	14210	23283	1.25	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5304	14536	23540	2.13	1.5E-01	F07986	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
3551	14581		7.98	1.5E-01	P15198	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5481	14687	24038	4.08	1.5E-01	AV950754.1	EST_HUMAN	IL3-C70219-160200-064-F10 CT019 Homo sapiens cDNA
5480	14707	24061	6.6	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5480	14707	24062	6.6	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFa) mRNA, complete cds
5655	14878	24287	1.86	1.5E-01	6753859	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
6656	14878	24268	1.86	1.5E-01	6753859	NT	Mus musculus DNA methyltransferase 2 (Dnm2), mRNA
5683	14803	24286	2.11	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5752	14971	24369	27.85	1.5E-01	BE727658.1	EST_HUMAN	601564322_F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
5771	14989		1.88	1.5E-01	4506395	NT	Homo sapiens RAD54 (S cerevisiae)-like (RAD54L) mRNA
5908	15025	24425	1.73	1.5E-01	AF134807.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
5976	18065	24507	2.13	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5982	15109	24520	5.01	1.5E-01	11417238	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
5899	15116	24528	1.64	1.5E-01	R48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATOR SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)

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Table 4

Single Exon Probes Expressed in HEK 293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5926	15142	24553	2.25	1.5E-01	Q28482	SWISSPROT	AMELOGENIN
5970	15185	24602	1.71	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
6078	14524	23568	5.92	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE resequences, MAGK Homo sapiens cDNA
6172	15354		2.42	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6262	15433	24872	1.72	1.5E-01	A1973157.1	EST_HUMAN	w52c08_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
6332	15513	24959	1.92	1.5E-01	AW500611.1	EST_HUMAN	UI-HFBNO-akk-d-05-o-Ut1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6332	15513	24960	1.92	1.5E-01	AW500611.1	EST_HUMAN	UI-HFBNO-akk-d-05-o-Ut1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6600	15798		19.81	1.5E-01	C16800.1	EST_HUMAN	C16800 Clonotech human acta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN:523H09 5'
6808	16003	25463	2.48	1.5E-01	NT	2a598c6_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:2868666 3' similar to	
6829	16023		3.09	1.5E-01	AV754819 TP	EST_HUMAN	PIR:S44443 S44443 RAD23 protein homolog2 - human
6895	15601	25067	7.82	1.5E-01	U00455.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
7044	16221	25696	6.88	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7044	16221	25697	6.88	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7135	16312	25783	4.58	1.5E-01	X98852.1	NT	P.leniulus mRNA for integrin beta subunit
7169	16348	25828	4.07	1.5E-01	AB114046.1	EST_HUMAN	wk53h12_x1 NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BE TA
7169	16348	25827	4.07	1.5E-01	AB114046.1	EST_HUMAN	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); wk53h12_x1 NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BE TA
7401	16614	26103	6.47	1.5E-01	AL163280.2	NT	GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C080
7401	16814	26104	6.47	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7548	16753		1.84	1.5E-01	AB042975.1	NT	Sus scrofa Cyp51 gene for lanosterol 14 alpha-demethylase, exon 1
7642	16842	26340	1.8	1.5E-01	AW841915.1	EST_HUMAN	IL5-CNP024-030300-025-D04 CNP024 Homo sapiens cDNA
7725	15433	24872	2.9	1.5E-01	A1973157.1	EST_HUMAN	wf52c08_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
8363	18157		31.79	1.6E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
8755	17698		1.5	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
8758	17699		1.22	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obliterator-1 (Dio-1)
8819	18177		6.75	1.5E-01	FB33077.1	EST_HUMAN	yp87e04_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
8916	19220		2.3	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
9027	18103	23808	6.2	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 118
9251	18020	23851	3.72	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
304	9577		1.45	1.4E-01	AF009863.1	NT	Homo sapiens T cell receptor beta locus, TCRBV2/S2A2 region
920	10155		3.95	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5')-methyltransferase, complete cds
1298	10481		2.73	1.4E-01	FB1884.1	EST_HUMAN	yd54c01_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	10592			1.43	1.4E-01	6879880 NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1723	10805	20118		1.65	1.4E-01	AE001710.1 NT	Thermogoga maritima section 22 of 138 of the complete genome
1869	11076			0.92	1.4E-01	AW135741.1 EST_HUMAN	U1-H-B11-scf-a-09-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1954	11158			10.51	1.4E-01	AA720615.1 EST_HUMAN	nt72d07.61 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:283921 3'
2745	11824	21139		4.09	1.4E-01	AI933496.1 EST_HUMAN	wm74801.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4165	13361	22461		11.2	1.4E-01	AI696094.1 EST_HUMAN	b56e02.x1 NCI CGAP_LU24 Homo sapiens cDNA clone IMAGE:2275570 3'
4165	13361	22462		11.2	1.4E-01	AI698094.1 EST_HUMAN	b56e02.x1 NCI CGAP_LU24 Homo sapiens cDNA clone IMAGE:2275570 3'
4222	13426	22518		3.52	1.4E-01	AE001710.1 NT	Thermogoga maritima section 22 of 138 of the complete genome
4680	13873	22973		0.81	1.4E-01	5453861 NT	Homo sapiens phosphodiesterase 5A, cAMP-specific (dunce (Drosophila)-Homolog phosphodiesterase E2)
5334	14585	23639		4.95	1.4E-01	T90677.1 EST_HUMAN	(PDE4A), mRNA
5352	14582	23657		4.24	1.4E-01	AB004556.1 NT	ye15c1.1s1 Stratigaea lung (#837210) Homo sapiens cDNA clone IMAGE:117812 3'
5352	14582	23658		4.24	1.4E-01	AB004556.1 NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5787	15004	24408		2.98	1.4E-01	BE326891.1 EST_HUMAN	hr87cc12.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
5885	15083	24498		4.8	1.4E-01	AU117147.1 EST_HUMAN	AU117147.1 HEMBA1 Homo sapiens cDNA clone HEMBA1000169 5'
5885	15083	24497		4.8	1.4E-01	AU117147.1 EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000169 5'
5911	15128	24537		3.7	1.4E-01	AW082786.1 EST_HUMAN	xb71d12.x1 Seares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2587751 3'
5923	15140			1.85	1.4E-01	BE266536.1 EST_HUMAN	60186523F1 NIH MGCG_7 Homo sapiens cDNA clone IMAGE:3537581 5'
5935	15151	24561		2.2	1.4E-01	BF378533.1 EST_HUMAN	CV1-LM0038-08300-103-049 UN00036 Homo sapiens cDNA
6250	15431			1.76	1.4E-01	AW015373.1 EST_HUMAN	U1-H-B10-eat-c-09-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
6749	15944	25404		7.58	1.4E-01	AA307073.1 EST_HUMAN	EST178182 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6825	16019	25484		9.29	1.4E-01	BF310959.1 EST_HUMAN	601895465F1 NIH MGCG_19 Homo sapiens cDNA clone IMAGE:4124824 5'
6867	16057	25524		2.65	1.4E-01	Y10198.1 NT	Homo sapiens PHEX gene
6867	16057	25525		2.65	1.4E-01	Y10198.1 NT	0898a03.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
7287	16516			1.91	1.4E-01	AA811480.1 EST_HUMAN	Y70c05.11 Seares breast 2N(HBSt) Homo sapiens cDNA clone IMAGE:154098 5'
7419	16631	28123		3.5	1.4E-01	FS3400.1 EST_HUMAN	C-perfringens ORF for putative membrane transport protein
7840	17032	28547		2.07	1.4E-01	X860822.1 NT	U1-H-B10-eat-c-09-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7874	15431			1.74	1.4E-01	AW015373.1 EST_HUMAN	Borreia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK).
8005	16440			2.41	1.4E-01	U287680.1 NT	Triosephosphate isomerase (TPI) genes, complete cds
8057	17192			1.63	1.4E-01	X52102.1 NT	M.musculus p18K gene for 16 kDa protein
8042	18129	23814		1.28	1.4E-01	AB000890.1 NT	Ephydias fluvialis mRNA for aldolase, partial cds
8084	17662	23846		2.39	1.4E-01	X74773.1 NT	P.saltii plastid gene secY
8708	17870			2.27	1.4E-01	11098117 NT	Rettus nonnegiculus dasmin (Des), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8753	18355		1.65	1.4E-01 BE513802.1	EST_HUMAN	601315639F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE3624329 5'	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycaminide ribonucleotide transformylase (GART) genes, complete cds
8849	17756		3.74	1.4E-01 AF083221.1	NT	NT	Synecocystis sp. PCMC6803 complete genome, 23/27, 288876/-3002865
8861	17764		2.08	1.4E-01 D84004.1	NT	NT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
8943	18374		3.7	1.4E-01 P10447	NT	NT	Mus musculus mRNA for prolidase, complete cds
9166	18178		3.78	1.4E-01 D82983.1	EST_HUMAN	MRO-HT0208-221289-204-008 HT0208 Homo sapiens cDNA	
9245	18016		1.74	1.4E-01 AW377898.1	EST_HUMAN	Hom sapiens G protein-coupled receptor 50 (GPR50) mRNA	
327	8558	18727	5.19	1.3E-01 4758467	NT	Hom sapiens G protein-coupled receptor 50 (GPR50) mRNA	
327	8558	18728	6.19	1.3E-01 4758467	NT	Hom sapiens G protein-coupled receptor 50 (GPR50) mRNA	
535	9788	18909	1.61	1.3E-01 AB013139.1	NT	Hom sapiens gene for NBS1, complete cds	
642	9888	18013	1.32	1.3E-01 AJ277608.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK	
642	9888	18014	1.32	1.3E-01 AJ277608.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK	
854	10050	18252	0.8	1.3E-01 X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4	
904	10139	19301	1.77	1.3E-01 AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds	
1034	10260	19410	1.42	1.3E-01 AL117078.1	NT	Batrachochytrium dendrobatidis strain T4 cDNA library under conditions of nitrogen deprivation	
1135	10358		2.11	1.3E-01 AL115265.1	NT	Batrachochytrium dendrobatidis strain T4 cDNA library under conditions of nitrogen deprivation	
1223	10441	19596	1.48	1.3E-01 AV712487.1	EST_HUMAN	AV712487 DCA Homo sapiens cDNA clone DCAAFF05 5'	
1445	10658		0.83	1.3E-01 AF148277.1	NT	Hom sapiens adapter protein CM/S mRNA, complete cds	
1825	11033	20228	7.72	1.3E-01 6680957	NT	Mus musculus proctolin, type XI, alpha 1 (Cet181), mRNA	
1829	11133	20328	2.16	1.3E-01 AL117078.1	NT	Batrachochytrium dendrobatidis strain T4 cDNA library under conditions of nitrogen deprivation	
2136	11334		0.97	1.3E-01 AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB7, pucA8 and pucC genes and ORF-151	
2254	11449		0.97	1.3E-01 AW812104.1	EST_HUMAN	RC4-ST0173-191098-032-012 ST0173 Homo sapiens cDNA	
2347	11540		2.94	1.3E-01 AE001018.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome	
2547	11735	20952	2.11	1.3E-01 M86918.1	NT	Cerassius eurekta keratin type I mRNA, complete cds	
3034	12270	21397	0.59	1.3E-01 AL163207.2	NT	Hom sapiens chromosome 21 segment HS21C007	
						Hom sapiens transcription factor I GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 3, and synaptophysin genes, complete cds, and L-type calcium channel α ->	
3332	12561	21689	0.63	1.3E-01 AF198779.1	NT	Bovine branched chain alpha-keto acid dihydrodiaryl transacylase mRNA, complete cds	
3428	12653	21783	1.07	1.3E-01 M21672.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287/000 nt. position (1/7)	
3702	12922	22040	0.81	1.3E-01 AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287/000 nt. position (1/7)	
3702	12922	22041	0.81	1.3E-01 AP000001.1	NT		

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Table 4

Single Exon Probes Expressed in HEK 293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3709	12929	22047	0.63	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodrol dehydrogenase 4 (AKR 1C4), exon 2
3763	12922	22040	0.68	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)
3763	12922	22041	0.68	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)
3789	13007	22122	0.89	1.3E-01	6975840	NT	Rattus norvegicus Fibroningen, gamma polypeptide (F98), mRNA
3963	13181		1.52	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4028	8898	18013	0.9	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4028	8898	19014	0.9	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NLV/Girlington/93/UK
4120	13328		1.03	1.3E-01	AF020713.1	NT	Bacteriophage SPBC2 complete genome
4140	13348		3.88	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-0B1-289-036-a03 DT0018 Homo sapiens cDNA
4148	13354	22453	2.2	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4167	13371	22470	21.57	1.3E-01	AW273741.1	EST_HUMAN	x123110.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2813995 3'
4275	13478	22575	0.84	1.3E-01	AV752278.1	EST_HUMAN	AV752278 NPD Homo sapiens cDNA clone NPDAZE02.5'
4276	13478	22576	0.94	1.3E-01	AV752279.1	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDAZE02.5'
4304	13505		1.33	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4475	13673	22763	0.68	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolyase transcriptase mRNA, complete cds
4531	13727	22824	2.2	1.3E-01	BE272339.1	EST_HUMAN	6011260986F1 NIH MGCG 9 Homo sapiens cDNA clone IMAGE:2890063 5'
5141	14320	23412	1.04	1.3E-01	AI432531.1	EST_HUMAN	th38c10.1x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5281	14452		1.03	1.3E-01	D82918.1	NT	Gallus gallus domesticus mitochondrial DNA, D-loop region, strain Ayam Kokok Belengbek
5375	14604	23713	1.94	1.3E-01	AW504417.1	EST_HUMAN	QV0-LJM0083-10040-189-a06 UMG0083 Homo sapiens cDNA
5868	15084	24498	14.91	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
5909	15126	24535	2.17	1.3E-01	X88891.1	NT	C.jacchii intron 4 of visual pigment gene (red allele)
6191	15373		1.64	1.3E-01	I48864.1	EST_HUMAN	yr33d02.1f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207075 5'
6452	15849	25117	2.19	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
6579	15775		4.84	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
6594	15790		3.41	1.3E-01	6923919	NT	Homo sapiens core histone macroH2A.2 (MACROH2A2), mRNA
7227	16448		3.33	1.3E-01	BF330999.1	EST_HUMAN	MR4-ET0358-13070-010-H08 BT0358 Homo sapiens cDNA
7442	16850	28142	1.64	1.3E-01	I01883.1	EST_HUMAN	y32609.1f1 Soares placenta Nb214P Homo sapiens cDNA clone IMAGE:150449 5'
7661	16881	28363	1.67	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
7803	16986		6.14	1.3E-01	6871745	NT	Mus musculus catlin 2, muscle (Cf2), mRNA
8123	17257	28789	4.07	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
8531	17557	23989	1.31	1.3E-01	BE616346.1	EST_HUMAN	60146274.1F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
8678	17649		3.75	1.3E-01	AJ242780.1	NT	Gallus gallus scyc1 gene for lympholeithin, exons 1-3

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9062	17891		2.08	1.3E-01	AB026829.1	NT	Ephydium fluviatile mRNA for SALK-6, complete cds
9080	17809		1.63	1.3E-01	AW001114.1	EST_HUMAN	wu24d09_x1 Scores_Dickegrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR_06287_O60287_KIAA0539 PROTEIN
388	96812	18819	10.48	1.2E-01	A1421744.1	EST_HUMAN	I89b02_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:20988539 3' similar to gb:U05760_m1
430	9265		1.32	1.2E-01	U68912.1	NT	Dicystostelium discoideum ORF DG1016 gene, partial cds
554	9804		2.91	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1383	10597	19763	2.4	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1383	10597	19764	2.4	1.2E-01	AU149148.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1390	10604		3.4	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdAAJB11 5'
1608	10821	19897	5.44	1.2E-01	Q14834	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFA13) (NFATC4) (NFAT3)
1628	10841	20018	2.84	1.2E-01	A1285402.1	EST_HUMAN	q8zj05_x1 NCI_CGAP_Es02 Homo sapiens cDNA clone IMAGE:1980553 3'
1739	10851		20.58	1.2E-01	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
1886	11093		2.95	1.2E-01	AW449368.1	EST_HUMAN	U1-H-B13-akl-e-10-0-U1_s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2148	11348	20563	2.5	1.2E-01	BF248490.1	EST_HUMAN	801821567F1 NIH MGCG_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2551	11738	20856	1.17	1.2E-01	AW896556.1	EST_HUMAN	QV3-BN0046-220300-128-110 BN0046 Homo sapiens cDNA
2795	12035	21159	1.4	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2854	12092	21222	2.39	1.2E-01	A1720470.1	EST_HUMAN	as80cd9_x1 Barley seed cDNA HPLR87 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2885	12123	21259	3.54	1.2E-01	M16834.1	NT	Human creatine kinase-B mRNA, complete cds
2864	12202	21337	0.81	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3196	12431	21587	2.17	1.2E-01	AW370568.1	EST_HUMAN	QV1-BT0259-261099-021-d05 BT0259 Homo sapiens cDNA
3224	12458		1.01	1.2E-01	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3329	12558	21698	1.01	1.2E-01	AW503374.1	EST_HUMAN	U1-HF-BN0-akw-e-10-0-U1_r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078427 5'
3454	12679		0.71	1.2E-01	Z98118.1	NT	Bacillus subtilis complete genome section 15 of 21; from 2798131 to 3013540
3484	12718	21854	0.8	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3494	12718	21855	0.8	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3584	12879		0.76	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome section 15 of 21; from 2798131 to 3013540
4163	13367	22485	2.35	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4163	13367	22468	2.35	1.2E-01	Z54256.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4300	13501	22587	0.81	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (NCAM) gene, exon 19
4343	14130	23225	15.91	1.2E-01	AF134904.1	NT	Schistoscoeca gregorii somaeplorin 2a mRNA, complete cds
5078	14258	23342	2.21	1.2E-01	EE173168.1	EST_HUMAN	MR0+T0559-24040-016-c08 HT0559 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
50778	14298	23343	2.21	1.2E-01	BE173168.1	EST_HUMAN	MRO-HIT0559-240400-016<09 HIT0559 Homo sapiens cDNA CM3-N0004-100300-111-018 NN0004 Homo sapiens cDNA clone IMAGE:3216398 5'
5284	14455	23524	0.73	1.2E-01	AW892592.1	EST_HUMAN	CM3-N0004-100300-111-018 NN0004 Homo sapiens cDNA clone IMAGE:3216398 5'
5337	14568	23642	2.63	1.2E-01	WV33035.1	EST_HUMAN	z508d22.r1 Scores_parathyroid_tumor_NbHpa Homo sapiens cDNA clone IMAGE:3216398 5'
5380	14609	23721	3.16	1.2E-01	Z98266.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5753	14972	24370	2.02	1.2E-01	BE620945.1	EST_HUMAN	601483518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5' IL0-C10031-221098-113-804 CT0031 Homo sapiens cDNA clone IMAGE:3895613 5'
5788	15005	24409	2.3	1.2E-01	AW845275.1	EST_HUMAN	wc89103.x1 NCI_CGAP_Cg3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN Q89735 MICROSONAL GLUTATHIONE S-TRANSFERASE II;
6446	15643	25110	4.78	1.2E-01	AJ913733.1	EST_HUMAN	xc49df7.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gbm13452 LAMIN A
6599	16795		4.89	1.2E-01	AW083652.1	EST_HUMAN	(HUMAN);
6606	15802		3.94	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sisn (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
6677	15872		2.87	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
6648	16106	25573	4.01	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
7075	16252	25725	2.20	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CuAAKE08 5'
7463	16671		3.61	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
7633	16834		3.64	1.2E-01	BE862324.2	EST_HUMAN	601655578R1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846283 3'
7707	16908		1.79	1.2E-01	BF314481.1	EST_HUMAN	6019801763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
7807	17000	28512	2.62	1.2E-01	AF180493.1	NT	Homo sapiens dynein intermediate chain DNA11(DNA11) gene, exon 17
8041	17177		1.98	1.2E-01	MB5109.1	NT	Rab9b glycoprotein phosphatase regulatory subunit (RG1) mRNA, complete cds
8293	17405		2.6	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
8659	17636		2.36	1.2E-01	AJ271736.1	NT	Homo sapiens Xq1 pseudoautosomal region; segment 2/2
8741	18317	23594	3.89	1.2E-01	QD04912	SWISSPROT (CDW136 ANTIGEN)	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
8833	17758		1.79	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and synapsin gene, partial cds
8955	9804		8.49	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
8969	17839		2.13	1.2E-01	X539881.1	NT	R.henleyi NF68 gene for 68kDa neurofilament
9043	18328	23601	1.55	1.2E-01	BE061418.1	EST_HUMAN	CN4-B10234-11199-03-1910 B10234 Homo sapiens cDNA clone IMAGE:1898840 3'
9066	17883	23900	8.08	1.2E-01	AI289503.1	EST_HUMAN	gn20905.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone alpha 3 subunit mRNA, partial cds
9088	17907		2.44	1.2E-01	L10187.1	NT	Xenopus laevis Integrin alpha 3 subunit mRNA, partial cds
9092	18249		5.45	1.2E-01	O98433	SWISSPROT CYCLIN T	Vibrio cholerae chromosome II, section 85 of 83 of the complete chromosome
9120	17836	23878	1.47	1.2E-01	AE04428.1	NT	Vibrio cholerae chromosome II, section 85 of 83 of the complete chromosome

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
9274	18038			1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
571	9821	18942	1.35	1.1E-01	AI581003.1	EST_HUMAN	in18q11.s1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
621	9886	18987	2.28	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_m11 HEME_OXYGENASE_1 (HUMAN);
1081	10287	19438	1.48	1.1E-01	BF697308.1	EST_HUMAN	60129847F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4286771 5'
1083	10317			1.63	1.1E-01	AL161560.2	NT
1187	11987	19540	3.89	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80 EST384112 IMAGE sequences, MAGI Homo sapiens cDNA Synecocystis sp. PCC6803 complete genome, 23/27_2888767-3002985
1256	10472	19835	3.8	1.1E-01	D84004.1	NT	Mus musculus pre T-cell antigen receptor alpha (Ptcra), mRNA
1508	10721	19883	2.15	1.1E-01	AU140363.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2280	11475			2.2	1.1E-01	6755215 NT	Interleukin-12 p35 subunit [mice, genomic; 700 nt, segment 4 of 5]
2503	11953			1.9	1.1E-01	6878376 NT	Y82g01.s1 Soares fetal liver spleen 1NFCS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
2807	12047	21168	1.04	1.1E-01	S82418.1	NT	Alu repetitive element;
2889	12235	21365	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC11R/Fc22 normalized infant brain cDNA Homo sapiens cDNA clone c-1fif2 3'
3115	12545			1.76	1.1E-01	6753231 NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caen19), mRNA
3399	12626	21757	2.28	1.1E-01	BE393186.1	EST_HUMAN	601308079F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:362/066 5'
3429	12654	21784	1.56	1.1E-01	682135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3486	12691	21828	0.7	1.1E-01	R86948.1	EST_HUMAN	Y82g01.s1 Soares fetal liver spleen 1NFCS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3559	12782	21911	0.94	1.1E-01	107695.1	NT	Alu repetitive element for transposase
3881	12902			0.78	1.1E-01	P97384	ANNEXIN XI (CALCYCILIN ASSOCIATED ANNEXIN 50) (CAP-50)
3889	12910	22029	1.91	1.1E-01	522708.1	NT	G. gallois gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4088	13297	22393	1.04	1.1E-01	AW819412.1	EST_HUMAN	MF3-S70290-280100-025-g07 ST0280 Homo sapiens cDNA
4088	13297	22394	1.04	1.1E-01	AW819412.1	EST_HUMAN	MF3-S70290-280100-025-g07 ST0280 Homo sapiens cDNA
							Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2).
4995	13303			0.68	1.1E-01	AF030001.1	CREB-RP, and tenascin X (TNX) genes, complex
4240	13443			10.22	1.1E-01	AF167066.1	Drosophila melanogaster klarsicht protein (Klar) mRNA, complete cds
4272	13475	22572	0.63	1.1E-01	AW802056.1	EST_HUMAN	IL6-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4641	13835	22824	1.09	1.1E-01	S44957.1	NT	Tapa-1= integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, genomic, 1973 nt, segment 1 of 7]
4649	14038	23131	1.24	1.1E-01	107695.1	NT	Alu/mimmersus gene for transposase
5045	13303			0.87	1.1E-01	AF030001.1	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex

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Table 4

Single Exon Probes Expressed In HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5224	14398		0.62	1.1E-01	8923317 NT		Homo sapiens hypothetical protein FLJ20342 (FLJ20342), mRNA
5588	14810	24184	1.79	1.1E-01	X68851.1 NT		S. pombe ste8 gene encoding protein kinase
5801	14825	24201	4.71	1.1E-01	M863533.1 NT		Providencia rettgeri penicillin G arylidase gene
5886	14908	24288	1.72	1.1E-01	BE789152.1 EST_HUMAN	PM3_F70024-130800-004-f12_F7024 Homo sapiens cDNA	
5996	14916	24310	7.89	1.1E-01	AW853598.1 EST_HUMAN	RC3-C70254-280999-011-a01 C70254 Homo sapiens cDNA	
5937	15153	24564	3.68	1.1E-01	OB98355 SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)	
5866	15181		2.67	1.1E-01	AF032822.1 NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	
5895	15278	24708	2.49	1.1E-01	11432372 NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA	
6305	15488	24930	7.65	1.1E-01	BF884628.1 EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'	
6305	15496	24931	7.65	1.1E-01	BF884628.1 EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'	
6361	15541	24996	1.77	1.1E-01	P41087 SWISSPROT	TRAB PROTEIN	
6375	15555	25012	2.92	1.1E-01	AA788784.1 EST_HUMAN	an3106_s1 Scores parathyroid_tumor_NbHPA_Homo sapiens cDNA clone 1240403 3' similar to gb:J03483	
6881	15777	25237	3.04	1.1E-01	AL134349.1 EST_HUMAN	CHROMOGRANIN A PRECURSOR (HUMAN); DKFZ547P194_1 r547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZ547P194 5'	
6780	15975	25432	3.04	1.1E-01	AA192153.1 EST_HUMAN	2P83b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'	
6780	15976	25433	3.04	1.1E-01	AA192153.1 EST_HUMAN	2P83b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'	
6821	16015	25480	4.18	1.1E-01	T72675.1 EST_HUMAN	YD9R03_s1 Scores fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM ATPASE BETA-2 (HUMAN);	
6910	18098		3.01	1.1E-01	BF085149.1 EST_HUMAN	MR2-CN10027-040900-005-a08 GNG0271 Homo sapiens cDNA	
7383	12235	21365	2.34	1.1E-01	FO3265.1 EST_HUMAN	7SC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'	
7496	16703		3.49	1.1E-01	AF168032.1 NT	Cerassus aureus, activin beta A precursor, mRNA, complete cds	
7614	16817	26313	3.37	1.1E-01	R23708.1 EST_HUMAN	YN3512.r1 Scores placenta Nb2:IP_Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Aliu repetitive element:contains TAR1 repetitive element;	
7620	16823	26319	1.68	1.1E-01	69811351 NT	Rattus norvegicus Phosphofuctokinase, liver, B-type (PKL), mRNA	
7636	14786	24157	1.98	1.1E-01	AL110985.1 NT	Batrachis cinerea strain T4 cDNA library under conditions of nitrogen deprivation	
7736	16933	26441	1.93	1.1E-01	X70058.1 NT	M.musculus cytokine gene	
7760	16956	26464	3.14	1.1E-01	Z11910.1 NT	Z.mobilis lgi and lig genes encoding tRNA guanine transglycosylase and DNA ligase	
7760	16958	26465	3.14	1.1E-01	Z11910.1 NT	Z.mobilis lgi and lig genes encoding tRNA guanine transglycosylase and DNA ligase	
7854	17044	26561	3.45	1.1E-01	P17437 SWISSPROT	SKIN SECRETORY PROTEIN XP22 PRECURSOR (APEG PROTEIN)	
8511	17547		2.88	1.1E-01	BE767023.1 EST_HUMAN	RC2-N70112-12080-014-f03 NT0112 Homo sapiens cDNA	
8772	18117		2.2	1.1E-01	BE874556.1 EST_HUMAN	601880551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'	
9212	17893	23865	5.88	1.1E-01	BF239753.1 EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'	
9283	18287		1.42	1.1E-01	Y08172.1 NT	R.norvegicus mRNA for 2-arylpromonyl-CoA epimerase	
1209	10428		2.64	1.0E-01	OB2855 SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1279	10484	18653		1.87	1.0E-01	A1985499.1	EST_HUMAN	w508dd01_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2498577 3' similar to contains MER7.13
1398	10610	19774		1.78	1.0E-01	AL161604.2	NT	MER7 repetitive element; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3487	12711	21847		1.08	1.0E-01	BF033891.1	EST_HUMAN	6014563201_F1 NIH MGC_66 Homo sapiens cDNA clone IMAGE:3898849 5'
3700	12820	22038		1.03	1.0E-01	BF239878.1	EST_HUMAN	601805489f1 NIH MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3930	13148	22263		2.78	1.0E-01	BF385703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4401	13601	22701		1.96	1.0E-01	AE002265.2	NT	Chlamydomonas pneumoniae AR39, section 91 of 94 of the complete genome
4552	13747			0.89	1.0E-01	A1792349.1	EST_HUMAN	an32d04_y5 Gossypium raimondii clone IMAGE:1700358 5'
4723	13914	23015		1.51	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4842	14129	23224		2.15	1.0E-01	AW952344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5181	14351	23443		0.66	1.0E-01	BE389100.1	EST_HUMAN	601288969f1 NIH MGC_44 Homo sapiens cDNA clone IMAGE:3613562 5'
5285	14495			0.83	1.0E-01	AV783960.1	EST_HUMAN	AV783960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5345	14575			9.19	1.0E-01	W86490.1	EST_HUMAN	ZB162164_s1 Scarece fetal liver spliced_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
5670	14891	24283		11.88	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
								y34hg6_r1 Scarece placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Aliu repetitive element;
6095	15285			1.97	1.0E-01	R23821.1	EST_HUMAN	
6391	15571			2.51	1.0E-01	Y12488.1	NT	Musculus whn gene
6913	16101			2.59	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7050	16227	25702		12.67	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7050	16227	25703		12.67	1.0E-01	AB046791.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7251	16471			2.48	1.0E-01	AU159127	EST_HUMAN	AU159127 ThYRO1 Homo sapiens cDNA clone THYRO1000699 3'
7600	16803	28297		3.47	1.0E-01	BF242946.1	EST_HUMAN	601877703f1 NIH MGC_55 Homo sapiens cDNA clone IMAGE:4105089 5'
7600	16803	28298		3.47	1.0E-01	BF242946.1	EST_HUMAN	601877703f1 NIH MGC_55 Homo sapiens cDNA clone IMAGE:4105089 5'
7639	17079	28606		4.68	1.0E-01	BT780543.1	EST_HUMAN	601582558f1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
8497	17897			3.22	1.0E-01	BE537719.1	EST_HUMAN	601065554f1 NIH MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
8736	17682			2.74	1.0E-01	7662765	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
8752	17695			1.76	1.0E-01	X00854.1	NT	Drosophila melanogaster fz gene
9039	18309			2.64	1.0E-01	U52691.1	NT	Corynebacterium polylestra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9070	17897			2.48	1.0E-01	BE537719.1	EST_HUMAN	601065554f1 NIH MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
9132	18280			12.74	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9194	17981			8.43	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2733	11912	21125		0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2740	11910	21133		1.16	9.9E-02	BE545554.1	EST_HUMAN	601070219f1 NIH MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2740	11919	21134	1.16	9.8E-02	BE545554.1	EST_HUMAN	60107021951 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3233	12487	21598	1.43	9.8E-02	AF098810.1	NT	Homo sapiens neuregulin III-alpha gene, partial cds
3928	13144	22281	0.79	9.8E-02	AB21637.1	EST_HUMAN	ZI45033.x5 Scores over tumor NblHOT Homo sapiens cDNA clone IMAGE:740932 3'
6074	14520	23563	8.08	9.8E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
6840	16045	25510	2.52	9.8E-02	675511.1	NT	Mus musculus phospholipid transfer protein (Plip), mRNA
570	9820		1.04	9.8E-02	X56338.1	NT	O sativa RAMy3C gene for alpha-amylase
3110	12345	21472	3.7	9.8E-02	AF184274.1	NT	Daucus carota leucanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4209	13412	22508	8.37	9.8E-02	AF257328.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4209	13412	22507	8.37	9.8E-02	AF257328.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7895	16430	25917	2.22	9.8E-02	BF037421.1	EST_HUMAN	60146078951 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:38684287 5'
8460	17518		1.34	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1359	10573	19739	1.29	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1585	10778		3.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), mRNA
2228	11422	20484	1.89	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-095-004 HT0516 Homo sapiens cDNA
3861	13176		4.12	9.7E-02	CG9765	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
6206	15387	24830	2.95	9.7E-02	ZB9119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2897771 to 3213410
6732	15927	25386	2.42	9.7E-02	AI953984.1	EST_HUMAN	Wx78bp6_x1 NCI CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gbx52851_mat1
7751	16947		2.37	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligatin (Lgtn) mRNA, partial cds
1883	11186	20395	3.52	9.6E-02	AI080721.1	EST_HUMAN	oz47d11_x1 Scores_NIHNMPr_S1 Homo sapiens cDNA clone IMAGE:1678435 3'
1883	11186	20398	3.52	9.6E-02	AI080721.1	EST_HUMAN	oz47d11_x1 Scores_NIHNMPr_S1 Homo sapiens cDNA clone IMAGE:1678435 3'
4338	13539	22630	7.92	9.6E-02	Z32986.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4695	13886	22987	0.98	9.6E-02	U37056.1	NT	Clostridium cellulovorans endo-1,4-beta glucanase Engf (engF) gene, complete cds
5025	14211	23294	0.89	9.6E-02	AW886239.1	EST_HUMAN	EST38303 MAGE sequences, MAG1 Homo sapiens cDNA
5710	14929		3.07	9.6E-02	BE910039.1	EST_HUMAN	601480888F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
7153	16330	25813	4.32	9.6E-02	F08174	SWISSPROT	COMPLEMENT DEGRADATION FACTOR PRECURSOR (CD55)
7228	16544	26033	7.1	9.6E-02	Z79102.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
8210	17341	26880	1.89	9.6E-02	AA826755.1	EST_HUMAN	ZI91901_s1 Scores_tes1s_NHT Homo sapiens cDNA clone IMAGE:745392 3'
9108	17928		1.56	9.6E-02	HH14569.1	EST_HUMAN	ym19103_s1 Scores infant brain HH1B Homo sapiens cDNA clone IMAGE:48653 3'
4079	13289	22388	2.65	9.5E-02	AW982395.1	EST_HUMAN	CM2-BN0023-050200-087-112 BN0023 Homo sapiens cDNA
6208	15389	24833	4.86	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for Phospholipase A2 inhibitor, complete cds
6321	15503	24849	8.19	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
6420	15617	25080	4.43	9.5E-02	BF-0358861.1	EST_HUMAN	601453642F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857243 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6420	15617	25081	4.43	9.5E-02	BF035881.1	EST_HUMAN	601455642F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243'5'
7271	16490	25980	4.04	9.5E-02	BF035881.1	EST_HUMAN	601455642F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243'5'
7271	16490	25981	4.04	9.5E-02	BF035881.1	EST_HUMAN	601455642F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857243'5'
1801	11010	20202	3.64	9.4E-02	BF871063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291617'5'
3981	13077	22183	5.59	9.4E-02	Z33059.1	NT	M capricolum DNA for CONTIG MG073
5081	14281	23346	0.7	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdbp), mRNA
6055	15850			2.23	9.4E-02	Z46863.1	NT
7507	15511	24957	2.62	9.4E-02	L78833.1	NT	Human BRCA1, RH07 and vav genes, complete cds, and ipf35 gene, partial cds
8345	18213			3.65	9.4E-02	U31815.1	NT
2846	12184			2.07	9.3E-02	4809280	NT
2894	12231			8.36	9.3E-02	6912625	NT
3223	12457	21591	1.85	9.3E-02	EF575511.1	EST_HUMAN	6021303086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269'5'
4134	13340	22439	4.02	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653'5'
4134	13340	22440	4.02	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653'5'
4746	13837			2.16	9.3E-02	AV732224.1	EST_HUMAN
5036	14221	23305	1	9.3E-02	AF15443.1	NT	HIV-1 isolate Br12 from Brazil gag protein (gag) gene, partial cds
5239	14413	23492	0.67	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
5239	14413	23493	0.67	9.3E-02	D16583.1	NT	Human gene for L-histidine decarboxylase, complete cds
7131	16308	25788	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7131	16308	25789	4.97	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7174	16351			4.06	9.3E-02	AW208117.1	EST_HUMAN
8619	18137			2.88	9.3E-02	AJ249850.1	NT
9003	18168			13.31	9.3E-02	AW468850.1	EST_HUMAN
9216	18212						Mus musculus major histocompatibility locus class II region: Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapashin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr->
234	9513	18639	1.48	9.3E-02	AF009586.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18640	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
234	9513	18641	8.2	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2184	11391			1.48	9.2E-02	R64156.1	EST_HUMAN
3144	12379	21510	3.99	9.2E-02	Q28831	SWISSPROT	MAJOR EPIDYMIS-SPECIFIC PROTEIN E4 (EPIDYMAL PROTEIN BE-20)
3226	12509	21639	0.88	9.2E-02	AA534354.1	EST_HUMAN	inf8001:s1 NCI CGAP_Co3 Homo sapiens cDNA clone IMAGE:9261583'3'
3583	12786			1.48	9.2E-02	6755215	NT

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4223	13426			1.12	9.2E-02 U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4285	13498			0.74	9.2E-02 BE289722.1	EST_HUMAN	600944365F1 NIH_MGCC_17 Homo sapiens cDNA clone IMAGE:2980178 5'
4640	13834	22923		1.21	9.2E-02 X86402.1	NT	G_gallus_Mla-CK gene
6518	15714	25178		2.57	9.2E-02 X85256.1	NT	H_wilgeye_xylose_isomerase gene
428	9294	18397		2.98	9.1E-02 X777685.1	NT	O_cuniculus_k12 Keratin gene
2378	11571	20791		1.02	9.1E-02 P78986	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOHEXOKINASE)
4481	13679	22769		1.85	9.1E-02 AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
6251	15432	24871		13.12	9.1E-02 AW160858.1	EST_HUMAN	au7465.y1 Schmidauer fetal brain clone IMAGE:2781968 5'
8526	18315			1.51	9.1E-02 AA179904.1	EST_HUMAN	zz38h12_s1 Strategene muscle 83720B Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN_P45378 TROponin T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
8907	17605			1.53	9.1E-02 AF052695.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
9091	18159			6.56	9.1E-02 AJ291380.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
762	8983	19137		3.57	9.0E-02 P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (F-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1611	10824	18999		6.83	9.0E-02 BE220482.1	EST_HUMAN	hg39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2755	11634	21150		3.82	9.0E-02 AF138522.1	NT	HIV-1_p46C05-08 from USA envelope glycoprotein (env) gene, partial cds
2755	11934	21151		3.82	9.0E-02 AF138522.1	NT	HIV-1_p46C05-08 from USA envelope glycoprotein (env) gene, partial cds
3310	12540	21675		0.75	9.0E-02 AF279135.1	NT	Dicytostelium discoideum coat structural protein SP65 (cotE), gene, complete cds
4671	13865	22966		1.88	9.0E-02 X85740.2	NT	Pleurodemum felicinum P-type ATPase 3 gene
5236	14410			0.98	9.0E-02 AJ132388.1	NT	Helicobacter pylori (strain P1) combB and pm1/agmA (partial) genes, and partial ORF1 and ORF2
5652	14875	24262		12.37	9.0E-02 W56037.1	EST_HUMAN	za68e12_r1 Soares_fetal_lung_NbHL16W Homo sapiens cDNA clone IMAGE:287694 5' similar to PIR:SS2171_SS2171 small G protein - human ;
8929	17811			1.35	9.0E-02 AF022238.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf2 (orf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tr), OrfU (orfU), >
1439	10853	19828		1.23	8.9E-02 BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1439	10853	19827		1.23	8.9E-02 BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
4181	13385			1.78	8.9E-02 AF228055.1	NT	Atrichum angustatum AtranFl02 protein (AtranFl02) gene, partial cds
5234	14408			0.95	8.9E-02 AB025822.1	NT	Mus musculus Gln mRNA, complete cds
5563	14817	24192		2.61	8.9E-02 AW452122.1	EST_HUMAN	U-H-BI3-alo-f-08-0-1s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5563	14817	24193		2.61	8.9E-02 AW452122.1	EST_HUMAN	U-H-BI3-alo-f-08-0-1s1 NC1_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
5568	14822	24190		3.12	8.9E-02 1143478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA

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Table 4

Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
6318	15498			2	8.9E-02 Z79021.1	NT	Homo sapiens flow-sorted chromosome 6 HindIII fragment, SC6p/20F8	
6654	15849	25308		7.54	8.9E-02 AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end	
8344	18164			1.33	8.9E-02 P19524	SWISSPROT	MYOSIN-2 ISOFORM	
8499	17540			4.1	8.9E-02 BF696918.1	EST_HUMAN	602128682F1 NIH MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'	
1380	10564	19760		1.39	8.8E-02 Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP))	
4012	13224			4.05	8.8E-02 C00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFI-135) (TAFI135) (TAFI1-130)	
4224	13427			1.03	8.8E-02 4502804	NT	Homo sapiens chromogranin A (panethyroid secretory protein 1) (CHGA) mRNA	
4288	13490			0.65	8.8E-02 4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA	
7678	16877	26382		3.02	8.8E-02 BE284455.1	EST_HUMAN	601191770F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'	
7679	16877	26383		3.02	8.8E-02 BE284455.1	EST_HUMAN	601191770F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'	
7813	17008	28519		11.51	8.8E-02 AL040129.1	EST_HUMAN	DKFZ443D1313_r1434 (synonym: htes2) Homo sapiens cDNA clone DKFZp434D1313 5'	
8577	17593	24001		1.56	8.8E-02 Z71581.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285W	
1624	10837	20014		2.52	8.7E-02 AI167281.1	EST_HUMAN	ox65b01.s1 Soares_NhHMPU_S1 Homo sapiens cDNA clone IMAGE:1661161 3'	
3672	12893	22014		5.01	8.7E-02 U82985.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	
3672	12893	22015		5.01	8.7E-02 U82985.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	
3672	12893	22015		5.01	8.7E-02 U82985.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	
4717	13908	23010		1.41	8.7E-02 AF178638.1	NT	Mus musculus JNK interacting protein-3 (Jip3) mRNA, complete cds	
5341	14571	23646		5.63	8.7E-02 AA285875.1	EST_HUMAN	z585g08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	
5341	14571	23647		5.63	8.7E-02 AA285875.1	EST_HUMAN	z585g08.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'	
7500	16519			2.75	8.7E-02 LO4758.1	NT	Oncotlegus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end	
7445	16853	28144		1.71	8.7E-02 AI823393.1	EST_HUMAN	wh59a07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384484 3'	
7859	17049	26568		2.23	8.7E-02 AJ007763.1	NT	Glucuronidase oxidans tRNA-ile and tRNA-Ala genes	
8586	17588			1.74	8.7E-02 X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease	
8771	17705			1.7	8.7E-02 6679057	NT	Mus musculus nitrogen 2 (Nid2), mRNA	
1259	10474	19838		5.5	8.6E-02 AJ1271736.1	NT	Homosapiens Xq pseudautosomal region, segment 2/2	
2208	11405	20629		2.12	8.6E-02 BE408687.1	EST_HUMAN	601304016F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:2633843 5'	
3161	12386	21518		2.48	8.6E-02 U05468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds	
3623	12844			3.32	8.6E-02 AF1533862.1	NT	Dicystostelium discoideum adenylyl cyclase (ecA) gene, complete cds	
3762	12881			0.65	8.6E-02 U20187.1	NT	Mus musculus long incubation prion protein (Pmph) and prion-like protein (Prmd) genes, complete cds	

Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5239	14442			0.7	8.6E-02 BfF570286.1	EST_HUMAN	602185718T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310259 3'
5706	14825	24319		4.11	8.6E-02 Y10826.1	NT	Homo sapiens LCN1t gene
7519	16724	26214	1.93	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product	
7519	18724	26215	1.83	8.6E-02 AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product	
7801	16984	28507	3.98	8.6E-02 BF305608.1	EST_HUMAN	601853437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'	
7801	16984	28508	3.98	8.6E-02 BF305608.1	EST_HUMAN	601853437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'	
7976	18411	25897	6.33	8.6E-02 AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome	
2361	11654	20776	2.28	8.5E-02 AE000652.1	NT	Helicobacter pylori 26605 section 130 of 134 of the complete genome	
5540	14764		1.93	8.6E-02 P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR	
5661	14884	24272	6.72	8.5E-02 AF223895.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds	
6857	15852	25311	3.4	8.5E-02	8754778 NT	Mus musculus myostatin XV (Myo15), mRNA	
7022	16198	25876	4.07	8.5E-02 BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA	
7022	16199	25877	4.07	8.5E-02 BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA	
7718	16915		12.86	8.5E-02 AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds	
7730	16928	28436	4.49	8.5E-02 AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds	
8878	18034		2.18	8.5E-02 AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor	
9158	17957		2.25	8.5E-02 AA362834.1	EST_HUMAN	EST72738 Ovary II Homo sapiens cDNA clone IMAGE:343532 5'	
2827	12022	21027	2.95	8.4E-02 WV89330.1	EST_HUMAN	zg44e11.1 Scareas_fetal_heart_NbHHH9W Homo sapiens cDNA clone IMAGE:353493 5'	
4347	13549	22641	1.01	8.4E-02 AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds	
4347	13549	22842	1.01	8.4E-02 AF257213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds	
5218	14392	23477	1.41	8.4E-02 545317 NT	Homosapiens nucleobindin 1 (NUCB1), mRNA		
5239	14568	23844	9.48	8.4E-02 BE267153.1	EST_HUMAN	601194036F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:353493 5'	
5662	15177	24594	1.78	8.4E-02 AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds	
6474	15671	25142	2.87	8.4E-02 BE095074.1	EST_HUMAN	CM3-B10780-26040-162-405 BT0180 Homo sapiens cDNA	
8482	17531	24026	1.53	8.4E-02 R79408.1	EST_HUMAN	y83h12.11 Scareas placenta Nb2hP Homo sapiens cDNA clone IMAGE:145895 5'	
3570	12783	21920	6.45	8.3E-02 F75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR	
3598	12819	21939	0.67	8.3E-02 AF438797.1	EST_HUMAN	tb82g68_x1 Scareas_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'	
3598	12819	21940	0.67	8.3E-02 AF438797.1	EST_HUMAN	tb82g68_x1 Scareas_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'	
4708	13899	22898	0.69	8.3E-02 AB038490.1	NT	Homo sapiens gene for fukutin, complete cds	
5818	15035	24436	2.53	8.3E-02 AF052883.1	NT	Homo sapiens protocadherin 43 gene, exon 1	
6456	15853	25122	3.77	8.3E-02 AF185787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds	
8582	18318		1.88	8.3E-02 BE858458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'	

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13886	10600		6.88	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for QBCAM protein gamma isoform
14886	10699	16873	1.71	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3038	12275		1.94	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
37883	13006		1.65	8.2E-02	AL161488.2	NT	Alebiddopsis thaliana DNA chromosome 4, contig fragment No. 10
3984	13198	22306	1.27	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4269	13472	22565	6.65	8.2E-02	P48860	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22568	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4269	13472	22587	6.55	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5111	14291	23378	3.05	8.2E-02	U78009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
6086	15298	24728	3.38	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
6961	16139	25609	8.44	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA 2
8589	17598	24005	4.79	8.2E-02	AE002246.2	NT	Chlamydophila pneumoniae AR39, section 73 of 94 of the complete genome
9007	18085		2.57	8.2E-02	AF275368.1	NT	Mus musculus epidermal growth factor receptor (Egr1) gene, exons 5 through 28, and complete cds, alternatively spliced
5	11957	18405	5.12	8.0E-02	AW654653.1	EST_HUMAN	EST368723 MAGE resequences, MAGE Homo sapiens cDNA
844	10177	19331	0.61	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1673	12000	20070	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1673	12000	20071	12.38	8.0E-02	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1887	11074	20265	3.81	8.0E-02	BE067219.1	EST_HUMAN	PM3-T0347-1702001-b08 BT0347 Homo sapiens cDNA
2433	11624		2.31	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_3T3/MCG-57/Homo sapiens cDNA clone IMAGE:4075619 5'
2772	10323	19474	2.25	8.0E-02	M23449.1	NT	Dicyclomium discoidatum cyclic nucleotide phosphodiesterase gene, complete cds
2852	12050	21219	0.59	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome; segment 5/5
3808	13024	22135	0.84	8.0E-02	AW966816.1	EST_HUMAN	EST378181 MAGE resequences, MAGE Homo sapiens cDNA
4829	14018		6.62	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5217	14391		1.38	8.0E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5277	10177	19331	0.75	8.0E-02	U60316.1	NT	Molluscum contagiosum virus subtype 1, complete genome
5610	14834	24209	3.45	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6156	14834	24209	1.69	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6502	15699	25165	3.28	8.0E-02	AL114983.1	NT	Bonyl's clarias strain T4 cDNA library under conditions of nitrogen deprivation
7573	16589	26078	3.74	8.0E-02	AF217786.1	NT	Homosapiens SCG10 like-protein, helicase-like protein NH ₂ , and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
8620	17616	23970	3.35	8.0E-02	AJ005375.1	NT	Drosophila arena headback region
9210	14485		1.7	8.0E-02	4903034	NT	Homo sapiens c-Maf responsive element binding protein-like 2 (CREB1L2) mRNA
2140	11338	26558	3.19	7.9E-02	BE250008.1	EST_HUMAN	600843191F1 NIH_3T3/MCG-15/Homo sapiens cDNA clone IMAGE:2956510 5'

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Table 4
Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2838	12174	21308	13.43	7.9E-02	AI582029.1	EST_HUMAN	arg98c03.x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:21738463' similar to gb:Z268876
3834	13051	22161	3.02	7.9E-02	6681044 NT		60S RIBOSOMAL PROTEIN L38 (HUMAN); Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3834	13051	22162	3.02	7.9E-02	6681044 NT		Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4826	14015		1.28	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4930	14118	23213	1.12	7.9E-02	L24757.1	NT	Human bone sialoprotein (BNSP) gene, exons 2, 3 and 4
6475	15872	25143	4.71	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Smi4-p (SMT4) gene, complete cds
7083	16280	25738	7.66	7.9E-02	A1081644.1	EST_HUMAN	gi 630551 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:16324653' similar to WP:C37A2.2
7083	16280	25737	7.66	7.9E-02	A1081644.1	EST_HUMAN	gi 630551 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:16324653' similar to WP:C37A2.2
1218	10436	19591	1.27	7.8E-02	A1783275.1	EST_HUMAN	CE08611;
1218	10436	19592	1.27	7.8E-02	A1783275.1	EST_HUMAN	CE08611;
2360	11553	20774	1.02	7.8E-02	AF221942.1	EST_HUMAN	co59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:15704675' similar to contains L1.13 L1 repetitive element;
2360	11553	20775	1.02	7.8E-02	AF221942.1	EST_HUMAN	co59d02.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:15704675' similar to contains L1.13 L1 repetitive element;
4806	13985	23103	0.59	7.8E-02	BE836331.1	EST_HUMAN	Sus scrofa telomerase RNA pseudogene
5118	12850		2.33	7.8E-02	BE836331.1	EST_HUMAN	PMS-FN0058-140700-005 FN0058 Homo sapiens cDNA
7257	16477	25983	2	7.8E-02	U2323.1	EST_HUMAN	600940555f1 NIH_MGC_5 CDNA clone IMAGE:2959693 5'
9219	17893		3.82	7.8E-02	AF096349.1	EST_HUMAN	Human interleukin-11 receptor alpha chain gene, complete cds
1403	11994	19782	1.27	7.7E-02	AF181897.1	EST_HUMAN	HIV-1 strain 97USNC30 from USA, envelope glycoprotein (env) gene, partial cds
3564	12787		2.81	7.7E-02	AJ238093.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5013	14200	23287	10.43	7.7E-02	AL161501.2	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
6428	15625	25090	3.91	7.7E-02	AA402849.1	EST_HUMAN	z153d11.11 Scores over tumor Nb10T Homo sapiens cDNA clone IMAGE:7417175' similar to TR:G1173905 G1173905 SPliceosome ASSOCIATED PROTEIN ;
7021	16198	25675	4.03	7.7E-02	F38080	SWISSPROT	PROTABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
7581	16788	26280	6.03	7.7E-02	114222757 NT		Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
8823	18172		2.35	7.7E-02	11436859 NT		Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3365	12593	21732	1.89	7.6E-02	BE514432.1	EST_HUMAN	601316428f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3386	12813	21746	1.08	7.6E-02	AA286447.1	EST_HUMAN	EST1122/14 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
3534	12757	21889	0.86	7.6E-02	AJ400877.1	EST_HUMAN	Homo sapiens ASCL3 gene, C1orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7039	16216		2.98	7.6E-02	AL159078.2	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/16

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	17309	26852	2.52	7.6E-02	AW986845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
794	10034	19183	1.35	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
784	10034	19184	1.35	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1887	11034	20284	1.13	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4509	13705	22789	0.73	7.5E-02	AB015981.1	NT	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
484	9798	18869	1.55	7.4E-02	AW983547.1	EST_HUMAN	RC5-LT054-260100-01-408 LT054-Home sapiens cDNA
3572	12785	21821	0.77	7.4E-02	AB079885.1	EST_HUMAN	WC5-LT054-260100-01-408 LT054-Home sapiens cDNA clone IMAGE:2358385 3
4715	13908	23007	1.83	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4805	13984	23102	2.72	7.4E-02	6978442	NT	Rat/tissue non-specific Activin receptor like kinase 1 (Acvr1), mRNA
4960	14147	23239	1.79	7.4E-02	6978492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchtp), mRNA
5873	15091		1.84	7.4E-02	R11747.1	EST_HUMAN	Ygt489E.71 Scores infant brain 1NIH Homo sapiens cDNA clone IMAGE:32339 5'
88541	17568		1.41	7.4E-02	11525593	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
88115	18294		3.13	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-4111 HT0243 Homo sapiens cDNA
6975	17844	23914	1.32	7.4E-02	BF036098.1	EST_HUMAN	601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:385773B 5'
9175	17968		1.77	7.4E-02	4826367	NT	Homo sapiens receptor tyrosine kinase-like orphan receptor 1 (ROR1), mRNA
475	9728	18859	1.45	7.3E-02	BE984961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3
475	9728	18860	1.45	7.3E-02	BE984961.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3
891	9834	19084	5.5	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1474	11986	18864	2.54	7.3E-02	AW980281.1	EST_HUMAN	CW4-N14004-130300-284-g08 NIH1004 Homo sapiens cDNA
1812	12003		17.52	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
50221	14208		1.28	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6280	15460	24901	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6280	15460	24902	2.17	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7770	15067	24477	2.61	7.3E-02	AA779877.1	EST_HUMAN	Z24802.s1 Scores_fetal_liver_splice_1NF1S_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gbL024265 PROTEASE SUBUNIT 4 (HUMAN);
120	9406	18538	1.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
120	9406	18539	1.42	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1470	10683	19857	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1470	10683	19858	2.33	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Descriptor	
							Top Hit Database Source	
2514	11703			2.79	7.2E-02	U14784.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
2832	12170	21303	1.39	7.2E-02	AF065133.1	NT	Drosophila melanogaster CLOCK (Cik) mRNA, complete cds	
3864	13080	22196	0.69	7.2E-02	AW298322.1	EST_HUMAN	U1-H-BW0-81-e-05-0-U.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:4251950 5'	
4339	13540	22851	4.22	7.2E-02	BF572307.1	EST_HUMAN	60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'	
4703	13884	22883	0.59	7.2E-02	11488563	NT	Rhodotorulas salina mitochondrion, complete genome	
5317	14549	23619	3	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome	
5318	14550	23620	8.39	7.2E-02	P11120	SWISSPROT	CALMODULIN	
6970	16148	25619	2.59	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone IMAGE:11111.x1 NCI_CGAP_Adrl Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340	
7074	16251	25724	2.4	7.2E-02	AW873187.1	EST_HUMAN	hd2411.x1 NCI_CGAP_Adrl Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340	
							ATYPICAL PKC SPECIFIC BINDING PROTEIN	
7181	16338	25837	2.63	7.2E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ280RF), and biglycan (BGN)	
7207	16384	25835	6.09	7.2E-02	BE585003.1	EST_HUMAN	genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds	
7213	16390		3.32	7.2E-02	BE59214.1	EST_HUMAN	6013492261 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'	
7487	16684	26178	4.78	7.2E-02	AF068874.1	NT	Reffus non virgicus bHLH transcription factor Mist1 (Mist1) gene, complete cds	
8481	17530		2.86	7.2E-02	AJ230798.1	EST_HUMAN	AJ230798 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'	
8543	17568		1.84	7.2E-02	AA584465.1	EST_HUMAN	nc005988.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:10988393 3'	
8608	17606		2.42	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATA) gene, complete cds	
8822	18141		4.54	7.2E-02	AW800362.1	EST_HUMAN	CM4N1009-2030-0116>11 NN1009 Homo sapiens cDNA	
9134	17948		1.42	7.2E-02	AA401779.1	EST_HUMAN	ZB57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5'	
1868	11075	20268	1.76	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds	
2258	11451	20670	6.31	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'	
8326	17427		6.31	7.1E-02	BE304764.1	EST_HUMAN	601149874F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'	
5334	9785	18903	0.74	7.0E-02	CD07092	SWISSPROT	COLLAGEN ALPHA 1(XVII) CHAIN PRECURSOR	
1481	10704		1.12	7.0E-02	X96877.1	NT	M. artillaria Mifcu-1 gene	
1732	10844	20127	1.13	7.0E-02	AA056343.1	EST_HUMAN	ZB5704.s1 Strategene cDNA clone (#8377204) Homo sapiens cDNA clone IMAGE:509599 3'	
2095	12232	21383	2.07	7.0E-02	AW138152.1	EST_HUMAN	U1-H-B1-acy-c-Q7-0-U.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:2116020 3'	
3875	13081	22207	0.97	7.0E-02	AA816438.1	EST_HUMAN	a165a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S	
4021	13233	22336	1.24	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);	
4121	13327		1.01	7.0E-02	AW792862.1	EST_HUMAN	QV4-BT0407-28010-090-410 BT0407 Homo sapiens cDNA CM0-LIN0001-4680300-270-812 LIN0001 Homo sapiens cDNA	

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 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4197	13401	22499	11.13	7.0E-02	AF077821.1	NT	Canis familiaris Inducible nitric oxide synthase mRNA, complete cds
4950	14137	23231	8.23	7.0E-02	BF381987.1	EST_HUMAN	60181fe29;1/F1 NIH-MGCC_58 Homo sapiens cDNA clone IMAGE:4050071 5'
6959	16137	25608	2.22	7.0E-02	K02891.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
7912	17127	26857	2.69	7.0E-02	AT24295.1	EST_HUMAN	ah98d5_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
520	9771	18894	16.86	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
520	9771	18895	16.86	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1341	10555		1.3	6.9E-02	4507868	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3775	12853	22108	1.48	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3775	12853	22109	1.48	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5182	14358		0.91	6.9E-02	AF078606.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds
8474	17527		3.36	6.9E-02	X74915.1	NT	X laevis XP02 mRNA for fork head protein
8682	17639		1.32	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
8887	17782		2.42	6.9E-02	AF198953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1847	11055	20244	1.09	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN); aa80f02_r1 Gassier Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1847	11055	20245	1.09	6.8E-02	AA498759.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
1871	11078	20268	3.81	6.8E-02	AF156873.1	NT	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds MRO+T0068-Q071098-001->05 HT0069 Homo sapiens cDNA
4850	13745		0.72	6.8E-02	EE141078.1	EST_HUMAN	Home sapiens chromosome 21 segment HS21C088
6200	15381	24822	7.45	6.8E-02	AL163268.2	NT	Pyrococcus abyssi complete genome; segment 5/8
6555	15751	26212	7.23	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
6555	15751	26213	7.23	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
8273	18341		1.75	6.8E-02	T03214.1	EST_HUMAN	FB4A8 Fetal brain, Stratagene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
8405	17481		2.35	6.8E-02	AA758014.1	EST_HUMAN	ah87f05_s1 Soares_NHT Homo sapiens cDNA clone 1320705 3'
8604	17862		2.51	6.8E-02	AW975839.1	EST_HUMAN	EST387948 MAGE resequences, MAGN Homo sapiens cDNA
9069	17898		2.42	6.8E-02	9910585	NT	Mus musculus latent TGF beta binding protein (Lgfb), mRNA
9270	18287	23685	1.75	6.8E-02	6978865	NT	Rattus norvegicus Growth factor independent-1 (Gfr1), mRNA
1514	10728		2.08	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, Onmy TAP1-01 allele, complete cds
1858	11065	20258	1.82	6.7E-02	AI220285.1	EST_HUMAN	qq78e04_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
36368	12818	22035	5.07	6.7E-02	P17278	SWISSPROT	HOMEBOX PROTEIN HOXD- (CHOX-A)
1336	10571	19736	1.07	6.6E-02	AI735509.1	EST_HUMAN	brt1269_x1 Barsitead bona HPLB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW1LM_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1377	10591	19757	1.01	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2147	11345	20582	11.31	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for captein 12, exons 1-21, three alternative transcripts
3440	12865	21789	10.35	6.6E-02	RA3086.1	EST_HUMAN	y118b10.51 Scores placenta Nb2/Homo sapiens cDNA clone IMAGE:395783
3453	12878	21813	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3453	12878	21814	2.75	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4058	13268	22389	1.94	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 3 genes, complete cds, alternatively spliced
4998	14185	23273	12.34	6.6E-02	Q611703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (II) HEAVY CHAIN H2)
4998	14185	23274	12.34	6.6E-02	Q811703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (II) HEAVY CHAIN H2)
5922	15139	24551	3.91	6.6E-02	X06411.1	NT	P vulgaris mRNA for chalcone synthase
6441	15638	25105	2.34	6.6E-02	AF052572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7534	16739	26230	7.23	6.6E-02	BF374248.1	EST_HUMAN	MRN-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
8882	17777		2.4	6.6E-02	9937091	NT	Mus musculus DIPB gene (Dipb), mRNA
9201	17888		1.32	6.6E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
589	98317	18958	1.66	6.5E-02	BF027639.1	EST_HUMAN	60167104671 NIH_3T3 MIGC_20 Homo sapiens cDNA clone IMAGE:39561785
694	10228	19382	2.86	6.5E-02	7705668	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1395	10608	19773	3.06	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1708	10920	20105	1.9	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
4887	14154	23246	3.91	6.5E-02	7661663	NT	Homo sapiens KIAA0019 gene product (KIAA0019), mRNA
5472	14698	24051	1.87	6.5E-02	AA443891.1	EST_HUMAN	ZV46112.s1 Scores ovary tumor NIH3T3 MIGC_20 Homo sapiens cDNA clone IMAGE:756743 similar to gb:M26638
7233	16454	25943	6.3	6.5E-02	AA198648.1	EST_HUMAN	Z32955.51 Scores_NHMMPu_S1 Homo sapiens cDNA clone IMAGE:68511443
8285	17408		3.32	6.5E-02	M21498.1	NT	Rabbit microsomal epoxide hydrolase
8870	17845		4.71	6.5E-02	AF102983.1	NT	Nectria haematoceca kinase related protein 2 (KRP2) gene, complete cds
582	9831	18949	2.37	6.4E-02	X94549.1	NT	A carboxylic precursor of peridinin-chlorophyll-a-protein (PCP) gene
5714	14932	24327	3.38	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gng-1) gene, complete cds
5714	14932	24328	3.38	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gng-1) gene, complete cds
6005	15287	24719	4.78	6.4E-02	BE974448.1	EST_HUMAN	601680425R2 NIH_3T3 MIGC_83 Homo sapiens cDNA clone IMAGE:39505033
6576	15772		2.71	6.4E-02	8753323	NT	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
6673	15868	25327	4.73	6.4E-02	AA083305.1	EST_HUMAN	k1419 seq_F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
6887	16175	25646	2.28	6.4E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
8198	17331	28873	2.12	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRo gene, and sodium phosphate transporter (NP73) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8199	17331	28874		2.12	6.4E-02 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, ReRe gene, and sodium phosphate transporter (NPT3) gene, complete cds
8562	18248			3.94	6.4E-02 AF07890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
8813	17610	239855		2.47	6.4E-02 AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
							Mus musculus major histocompatibility locus class III regions Hsc70l genes, partial cds; emRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
1726	10838	20121		2.34	6.3E-02 AF108905.1	NT	MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3582	12804			2.89	6.3E-02 P137092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7077	18254	25727		5.25	6.3E-02 AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS2A region), partial cds, strain: CMV-152
7303	14946	24343		3.42	6.3E-02 BF210736.1	EST_HUMAN	601873316F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE:4097499 5'
8849	17632			1.45	6.3E-02 P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGP3)
42337	13440	22532		3.53	6.2E-02 AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
4331	13532			1.31	6.2E-02 AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4581	13775			7.65	6.2E-02 Q82181	SWISSPROT	52 KDR PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SSA)) (ROS2)
7888	17104	28634		1.97	6.2E-02 AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin chy1 gene
8393	18372			6.87	6.2E-02 AE000750.1	NT	Aquifex aeolicus section 82 of 108 of the complete genome
8829	17741	23932		2.62	6.2E-02 BF112039.1	EST_HUMAN	7137n08.x1 Soay/F8_9W_OTP_S-Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR-Q8Y4S8_Q8Y4S8_HYPOTHETICAL_30_3_KD PROTEIN.[1];
260	9536	18668		5.6	6.1E-02 D16471.1	NT	Human mRNA, Xq terminal portion
3969	13184			2.44	6.1E-02 U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKC1) gene, complete cds
4557	13851	22946		0.95	6.1E-02 AF119413.1	NT	Lupinus albus 1-aminoacylpropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4557	13851	22947		0.95	6.1E-02 AF119413.1	NT	Lupinus albus 1-aminoacylpropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6549	15745	25205		4.27	6.1E-02 Q89288.1	NT	H. sapiens mRNA for B-LH DNA binding protein
7317	16535	28023		6.21	6.1E-02 BE179543.1	EST_HUMAN	II.3-HT07818-110500-136-C06 HT0618 Homo sapiens cDNA
8349	18289			7.82	6.1E-02 JX70869.1	NT	S. japonicum mRNA for serine-enzyme
9089	17608			4.49	6.1E-02 AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1289	10484	19843		1.24	6.0E-02 AE001777.1	NT	Thermolobus maritimus a section 89 of 136 of the complete genome
2835	11818	21035		1.2	6.0E-02 AW868848.1	EST_HUMAN	EST380924: MAGE resequences, MAGJ Homo sapiens cDNA
2728	11807			1.34	6.0E-02 AB031289.1	NT	Mesocestoides cord mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gin, tRNA-Pro, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2887	9390	18918		0.97	6.0E-02 AA1488730.1	EST_HUMAN	ZP78004.1 Stratagene HeLa cell 3.837216 Homo sapiens cDNA clone IMAGE:626310 5'
2887	9390	18520		0.97	6.0E-02 AA1488730.1	EST_HUMAN	ZP78004.1 Stratagene HeLa cell 3.837216 Homo sapiens cDNA clone IMAGE:626310 5'

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3195	12430	21565	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	
3195	12430	21566	1.53	6.0E-02	AA372376.1	EST_HUMAN	EST84288 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein	
3813	12834		1.01	6.0E-02	BE84443.2	EST_HUMAN	601858150R1 NIH_MIGC_68 Homo sapiens cDNA clone IMAGE:3876050 3'	
6083	14529	23553	2.83	6.0E-02	5174698 NT	Hom sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA		
6083	14529	23554	2.93	6.0E-02	5174698 NT	Hom sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA		
6160	15343	24780	2.16	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MIGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'	
6368	15548	25004	1.78	6.0E-02	A1204275.1	EST_HUMAN	qf5888.1X Seares testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'	
6878	16059	25538	3.1	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IgLV gene for immunoglobulin light chain variable region, exons 1-2	
6878	16059	25539	3.1	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IgLV gene for immunoglobulin light chain variable region, exons 1-2	
7878	17056		2.05	6.0E-02	AA128386.1	EST_HUMAN	zN87608.1X Strategene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X89181 60S RIBOSOMAL PROTEIN L31 (HUMAN);	
8612	17609	23984	1.52	6.0E-02	11431702 NT	Hom sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA		
9016	17888		2.41	6.0E-02	A1809273.1	EST_HUMAN	wf69n3.x1 SearesNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O62288	
235	9514	18642	5.1	5.9E-02	AW634719.1	EST_HUMAN	O6298 KIAA0551 PROTEIN ;	
2940	12178	21313	2.38	5.9E-02	AF180269.1	NT	RC1-DT001-286100-012-e10 DT0001 Homo sapiens cDNA	
5249	14422	23498	0.67	5.9E-02	AW028748.1	EST_HUMAN	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partially spliced	
5249	14422	23499	0.67	5.9E-02	AW028748.1	EST_HUMAN	wf34602.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386	
5249	14422	23499	0.67	5.9E-02	AW028748.1	EST_HUMAN	wf34602.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:2531450 3' similar to TR:O65386	
8660	15855	25314	2.7	5.9E-02	9055349 NT	Mus musculus Iroquois related homeobox 5 (Drosophila) (lhx5), mRNA		
7366	16592		3.4	5.9E-02	6679870 NT	Mus musculus follistatin-like (Fst), mRNA		
7590	16794	28286	2.73	5.9E-02	11433356 NT	Homo sapiens ninjine (LOC51199), mRNA		
8075	17210		1.66	5.9E-02	BF572539.1	EST_HUMAN	602076548F1 NIH_MIGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'	
8089	17224		1.97	5.9E-02	AJ240753.1	NT	Gallus gallus HKCG telomere junction	
E41	10174		6.49	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1	
3644	12885	21983	13.62	5.8E-02	AE001775.1	NT	Thermologos maritima section 87 of 136 of the complete genome	
4348	13550	22643	5.33	5.8E-02	AW051927.1	EST_HUMAN	wf24c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	
4348	13550	22644	6.33	5.8E-02	AW051927.1	EST_HUMAN	wf24c02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'	
4544	13739	22838	5.2	5.8E-02	A1247505.1	EST_HUMAN	qf5801.x1 Seares_fetal_liver_spleen_1NF1S_1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	
4544	13739	22839	5.2	5.8E-02	A1247505.1	EST_HUMAN	qf5801.x1 Seares_fetal_liver_spleen_1NF1S_1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);	
4571	13765		2.44	5.8E-02	AF098284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds	

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Table 4
Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5151	14330	23421	0.8	5.8E-02	AF275368.1	NT	<i>Mus musculus</i> epidermal growth factor receptor (Egr1) gene, exons 5 through 28, and complete cds, alternatively spliced
5151	14330	23422	0.6	5.8E-02	AF275368.1	NT	<i>Mus musculus</i> epidermal growth factor receptor (Egr1) gene, exons 5 through 28, and complete cds, alternatively spliced
5233	14407		0.94	5.8E-02	L76979.1	NT	Schizosaccharomyces pombe HMG-CoA reductase (hmg1+) gene, complete cds
6397	15547	25002	2.53	5.8E-02	MB91150.1	NT	Human polymorphic microsatellite DNA
6397	15547	25003	2.53	5.8E-02	MB91150.1	NT	Human polymorphic microsatellite DNA
8498	17539		2.41	5.8E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
8805	18369		6.22	5.8E-02	AA804289.1	EST_HUMAN	no75e1.51 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684.3'
3022	12258	21386	1.34	5.7E-02	AI081644.1	EST_HUMAN	cu63805.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465.3' similar to WP:C37A2.2 CEE8611
3036	12272	21400	1.43	5.7E-02	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3687	12808		0.93	5.7E-02	AF001282.1	NT	Chironomus thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2Beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3788	13004	22119	2.32	5.7E-02	AW986791.1	EST_HUMAN	EST378865 MAGE resequences, MAGI Homo sapiens cDNA
4691	13882		1.01	5.7E-02	MB95099.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
7743	16939	26448	4.13	5.7E-02	AT752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
7743	16939	26449	4.13	5.7E-02	AT752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH-TBC_cn18b09 random
8718	18169		7	5.7E-02	DS0320.1	NT	Pig DNA for SPaI-2, complete cds
8959	18244		2.46	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
9105	18349		4.1	5.7E-02	AF261280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
4642	13836	22925	1.34	5.6E-02	AB013100.1	NT	Lycoptisicon esculentum LE-ACS6 mRNA for 1-aminoacyclopropane-1-carboxylate synthase, complete cds
4706	13897	22936	1.32	5.6E-02	AA280588.1	EST_HUMAN	zS45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416.3'
5958	15112	24587	4.45	5.6E-02	AW172708.1	EST_HUMAN	x102c10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2656050.3' similar to TR:Q94979 Q94979 KIAA0385 PROTEIN
6140	15324	24759	3.23	5.6E-02	BE008001.1	EST_HUMAN	Q0-BN0147-280400-214-007 BN0147 Homo sapiens cDNA
6717	15912	25370	3.92	5.6E-02	BE542683.1	EST_HUMAN	60108715871 NIH_MIGC_10 Homo sapiens cDNA clone IMAGE:3453279.6'
6717	15912	25371	3.92	5.6E-02	BE542683.1	EST_HUMAN	60108715871 NIH_MIGC_10 Homo sapiens cDNA clone IMAGE:3453279.5'
8089	17233		2.72	5.6E-02	AF280225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2616	11800	21016	5.48	5.5E-02	X97869.1	NT	H.sapiens gene encoding La autoantigen
3181	12416	21551	3.98	5.5E-02	67556501	NT	Mus musculus Sh3 domain protein 1B (Sh3d1B), mRNA

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 Table 4
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Probe SEQ ID NO.	Exon ORF SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
41869	13403	22500	1.12	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5158	14337		1.07	5.5E-02	U67518.1	NT	Methanococcus jannaschii section 80 of 150 of the complete genome
5516	14741	24107	3.4	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
5871	14741	24107	4.13	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7589	16783	28285	14.31	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhad), transcriptional activator (dhAr), 1,3-propanediol dehydrogenase (dhT), glycerol dehydratase (dhB), >
1296	10511		0.6	5.4E-02	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2884	12221		1.01	5.4E-02	J277488.1	NT	Oryza sativa rbb3-1 gene for putative Bowman-Birk trypsin inhibitor
3400	14477		7.28	5.4E-02	BE073488.1	EST_HUMAN	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3889	13105	22223	0.72	5.4E-02	U85806.1	NT	Hindu medicinalis SNAP-25 homolog mRNA, complete cds
7289	16508	25898	2.68	5.4E-02	U20790.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
8598	18163		1.71	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1060	10286	19436	1.14	6.3E-02	AW381248.1	EST_HUMAN	QVO-ST0213-021289-062-e09 ST0213 Homo sapiens cDNA
1060	10286	19437	1.14	5.3E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021289-062-e09 ST0213 Homo sapiens cDNA
1498	10709	19882	11.81	5.3E-02	T94759.1	EST_HUMAN	y37f12.11 Strategene lung (#867210) Homo sapiens cDNA clone IMAGE:1186515 similar to gb:K01506
2460	11651	20872	2.39	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN)
2893	12131	21266	0.92	5.3E-02	M58417.1	NT	Pseudomonas putida tgsS gene
2893	12131	21266	0.92	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3115	12350	21478	3.95	5.3E-02	AJ276408.1	NT	Pseudomonas putida tgsS gene
5120	14289	23387	8.22	5.3E-02	M80468.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5343	14573	23649	1.95	5.3E-02	AE000527.1	NT	Helicobacter pylori 28695 section 5 of 134 of the complete genome
5343	14573	23650	1.95	5.3E-02	AE000527.1	NT	Helicobacter pylori 28695 section 5 of 134 of the complete genome
6034	15242	24663	4.21	5.3E-02	8695413	NT	Lymphocystis disease virus 1, complete genome
6236	15417		2.31	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053, n]
9242	18013	23850	1.36	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2249	11444		91.98	5.2E-02	5031908	NT	Homo sapiens integrin A, alpha 1(IgBA peptide hydrolyase) (IgBA) mRNA
3078	12314	21435	2.27	5.2E-02	AJ277661.1	NT	Homo sapiens partial LM01 gene for LIM domain only 1 protein, exon 1
3078	12314	21436	2.27	5.2E-02	AJ277661.1	NT	Homo sapiens partial LM01 gene for LIM domain only 1 protein, exon 1
3913	13129	22248	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana a putative dicarboxyle diiron protein (Crd1) mRNA, complete cds
4283	13486	22557	2.98	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nef-1 mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5199	14375	23462	0.72	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
2332	11525		1.1	5.1E-02	AL134071.1	EST_HUMAN	DKF7p547D073_11_547 (synonym: hfb1) Homo sapiens cDNA clone DKF7p547D073_5'
4186	13350	22489	0.81	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 37 of the complete genome
5080	14280	23345	1.07	5.1E-02	BE957423.2	EST_HUMAN	601653565R2_NIH_MoG_55_Homo sapiens cDNA clone IMAGE38948361_3'
5235	14409	23480	0.71	5.1E-02	P01785	SWISSPROT	IG HEAVY CHAIN V REGION MOO
6021	14511	23569	1.77	5.1E-02	BF378825.1	EST_HUMAN	QVOUM0051-250800-350-008 UM0051 Homo sapiens cDNA
7015	16192	25686	6.18	5.1E-02	AF012889.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
7406	16618	26108	2.98	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
7408	16618	26109	2.98	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
8856	17759		1.7	5.1E-02	AF082467.1	NT	Cucumis melo polygalacturonase precursor (MPC3) mRNA, complete cds
489	9742	18872	1	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1212	10430	19586	10.56	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 2); from 1 to 213080
1959	11163	20386	6.31	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) (CONTAINS: PEPTIDE P-C)
2770	10225	18381	1.08	5.0E-02	U72742.1	NT	Oryctodius cuniculus UDP-glucuronyltransferase (UGT2B13) mRNA, complete cds
3311	12541		1.45	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (JIL2), mRNA
3573	12796		0.94	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3684	12885	22006	4.54	5.0E-02	U112769.2	NT	Antherospora pectinifera period clock protein homolog mRNA, complete cds
4837	14026		0.88	5.0E-02	P40232	SWISSPROT	CASEIN KINASE 1(BETA CHAIN (CK 1))
6307	15488	24833	11.19	5.0E-02	P358618	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
8025	17162	26699	2.78	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
8360	18205		4.81	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
229	9507		34.14	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
374	9840	18774	2.22	4.9E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
374	9840	18775	2.22	4.9E-02	AF276948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2826	12065	21186	0.77	4.9E-02	U32636.1	NT	Zea mays phytocystathione synthase ('Y') gene, complete cds
3257	12490	21621	1.72	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATA ORIBRAL-PALLIDOLLYSIAN ATROPHY PROTEIN)
3545	12768		0.76	4.9E-02	AA188940.1	EST_HUMAN	zq48a12_s1 Stratagene hNT neuron (#Q317233) Homo sapiens cDNA clone IMAGE:6329265_3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3569	12792	21918	1.13	4.9E-02	AA400914.1	EST_HUMAN	Z178a03_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428_3'
3569	12792	21919	1.13	4.9E-02	AA400914.1	EST_HUMAN	Z178a03_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428_3'
4958	14048	23140	1.62	4.9E-02	AW167821.1	EST_HUMAN	xg56910_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386_3'
4958	14048	23141	1.62	4.9E-02	AW167821.1	EST_HUMAN	xg56910_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386_3'
5382	14811	23123	1.8	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 8

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5382	14611	23724	1.8	4.9E-02	U00122.1	NT	Rat elastase II gene, exon 6
7940	17050	26608	3.81	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
8777	17707		1.6	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
8056	17898		4.4	4.9E-02	M18984.1	NT	Human Gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
9119	18277		1.28	4.9E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395261 to 2613730
335	9604	18733	1.4	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
336	9604	18733	3	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
493	9748	18877	7.4	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2238	11433	20657	1.55	4.8E-02	W51983.1	EST_HUMAN	z5-49b02_s1 Soares,_senescent_fibroblasts_Nbh-HSF Homo sapiens cDNA clone IMAGE:3256113' similar to gb:M30838 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3175	12410	21546	2.47	4.8E-02	X17144.1	NT	Tetrahydromenostrolate histone H3II and histone H4II Intergenic DNA
4674	13868		1.11	4.8E-02	Z54280.1	NT	S_scrofa genes for skeletal muscle myosin receptor
5160	14339	23428	0.83	4.8E-02	U91914.1	NT	Streptococcus constellatus D-selenine ligase gene, partial cds
8847	17630		1.35	4.8E-02	9632993	NT	Streptococcus thermophilus bacteriophage Sf119, complete genome
6010	15260	24684	3.54	4.7E-02	W01153.1	EST_HUMAN	yeB7f09_r1 Soares melanocyte 2nbHM Homo sapiens cDNA clone IMAGE:2810175' similar to contains Alu repetitive element
6050	15218	24638	2.13	4.7E-02	M82752.1	NT	Rat statin-related protein (s1) gene, complete CDS
6843	15739	25200	13.64	4.7E-02	X15543.1	NT	B_taurus mRNA for Fgf-36-DNA-binding protein
6836	16030	25495	12.53	4.7E-02	X15543.1	NT	B_taurus mRNA for Fgf-36-DNA-binding protein
7339	16555	26043	1.93	4.7E-02	8754565	NT	Mus musculus ligand of numb-protein X (lrx) mRNA
8090	17225	26760	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8090	17225	26761	2.02	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
8680	18380		1.79	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
8947	18383		1.48	4.7E-02	P52951	SWISSPROT	HOMEobox PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEobox PROTEIN 2)
9189	17985		1.24	4.7E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
275	9550	18681	1.16	4.6E-02	BE153583.1	EST_HUMAN	PM0+HT0338-251199-003-005 HT0339 Homo sapiens cDNA
747	9988	19131	3.98	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1289	10514		1.09	4.6E-02	AJ014255.1	EST_HUMAN	em50302_s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1532979 3' similar to TR_P80533
1367	10581	19748	2.77	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA contains element LTR1 repetitive element; AV727059 HTC Homo sapiens cDNA clone HTCBW_C01 5'
2452	11643	20863	1.64	4.6E-02	AW236023.1	EST_HUMAN	xn24633_x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694853 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1;

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2760	9550	18681	1.53	4.8E-02	BE153583.1	EST_HUMAN	PM0-HIT0339-251199-003-905 HT0339 Homo sapiens cDNA
2669	12207	21343	0.82	4.8E-02	BE153583.1	EST_HUMAN	PM0-HIT0339-251199-003-905 HT0339 Homo sapiens cDNA
3304	12207	21343	0.6	4.8E-02	BE153583.1	EST_HUMAN	PM0-HIT0339-251199-003-905 HT0339 Homo sapiens cDNA
3471	12207	21343	0.67	4.8E-02	BE153583.1	EST_HUMAN	PM0-HIT0339-251199-003-905 HT0339 Homo sapiens cDNA
4103	13310		1.27	4.6E-02	AF220385.1	NT	Mus musculus nucleolar RNA helicase II/Gu (ddG21) gene, complete cds
5765	14984	24383	3.35	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
5765	14984	24384	3.35	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atpB) mRNA
6870	15885	25325	4.77	4.6E-02	BE154006.1	EST_HUMAN	PM0-HIT0339-08040-009-G12 HT0339 Homo sapiens cDNA
7841	17081	28609	4.08	4.6E-02	AA919328.1	EST_HUMAN	027109_s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15247373
8928	18358		1.28	4.8E-02	L11982.1	NT	Oryctodileus cuniculus macrophage scavenger receptor type II mRNA, complete cds
9163	17982		4.09	4.6E-02	X57808.1	NT	Human gammeline immunoglobulin lambda light chain gene
453	9706	18844	2.45	4.5E-02	F22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1226	10444	18599	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S_African/Johannesburg/1975/Ozolin VP35 gene, complete cds
1226	10444	18600	0.85	4.5E-02	AF005730.1	NT	Marburg virus strain M/S_African/Johannesburg/1975/Ozolin VP35 gene, complete cds
1773	10883	20174	5.37	4.5E-02	F32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2080	11280	20498	1.63	4.5E-02	AE00984.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3703	12923	22042	4.72	4.5E-02	AL168278.2	NT	Hom sapiens chromosome 21 segment HS21C078
5766	14985	24385	1.65	4.5E-02	AJ400877.1	NT	Hom sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6597	15783	25251	2.49	4.5E-02	AF036894.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
7054	16231	25706	5.35	4.5E-02	AA325216.1	EST_HUMAN	EST287_Cat cellulin II_Homo sapiens cDNA 5' end similar to sim1 to neuro-D4 protein
8576	17592	24000	2.89	4.5E-02	11418013	NT	Hom sapiens ret finger protein-like 3 (RFPL3), mRNA
8989	18250	23708	5.94	4.5E-02	AA191097.1	EST_HUMAN	zq45f11.r1 Stratego hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:8324935
224	9503		4.97	4.4E-02	BE972733.1	EST_HUMAN	601652154F1 NIH MGCG_82 Homo sapiens cDNA clone IMAGE:39353885
1032	10258	19409	0.86	4.4E-02	BE19295.1	NT	Drosophila melanogaster extradenticle (EXD) mRNA, complete cds
2068	11267		4.78	4.4E-02	P31568	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2453	11644	20564	1.05	4.4E-02	AW875475.1	EST_HUMAN	QV2-P70012-01030-070-g02 PT0012 Homo sapiens cDNA
3346	12574	21714	0.93	4.4E-02	X086212.1	NT	Chironomus tentans ecdisisone-controlled gene -18c
3619	12840	21859	1.8	4.4E-02	AF59160.1	NT	Mycooccus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4629	13823	22911	1.22	4.4E-02	AF109807.1	NT	Hom sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4629	13823	22912	1.22	4.4E-02	AF109807.1	NT	Hom sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4754	13945		2.85	4.4E-02	AJ222689.1	NT	Ornithobius CCAAT-enhancer binding protein epsilon gene

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Table 4

Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	15897	25358	3.19	4.4E-02	AA736969.1	EST_HUMAN	nw13h03.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3' Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
7639	16839	26336	5.01	4.4E-02	AF060669.1	NT	
7753	16949	28457	3.27	4.4E-02	AA498739.1	EST_HUMAN	ae33f04.r1 Geissler V/Wims tumor Homo sapiens cDNA clone IMAGE:897631 5'
8280	17403		1.83	4.4E-02	AB040828.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
8477	18373		1.48	4.4E-02	BF241245.1	EST_HUMAN	601878746F NIH_MIGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
780	10030	19179	7.71	4.3E-02	AF003249.1	NT	Marine seabird myosin heavy chain FM3A (FM3A) mRNA, complete cds
2533	11721	20838	2.39	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB_Homo sapiens cDNA clone ADBA0CH08 5'
3408	12634	21765	8.67	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3639	12860		1.05	4.3E-02	AF060568.1	NT	Homo sapiens prion/leucytic leukemia zinc finger protein (PLZF) gene, complete cds
5256	14429	23505	1.34	4.3E-02	D100061	NT	questRH03 gene, complete cds
5874	15082	24504	4.79	4.3E-02	F30427	SWISSPROT	PLECTIN
5874	15092	24505	4.79	4.3E-02	F30427	SWISSPROT	PLECTIN
8344	17569		1.41	4.3E-02	AL138077.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 4/6
832	10070	19225	2.2	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2/2000020 5'
876	10112		2.68	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2/2000020 5'
906	10141	19303	0.71	4.2E-02	AW003845.1	EST_HUMAN	wk3-q01_x1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR_Q63291 Q63291 L1 RETOPON, ORF2 mRNA ;contains L1:3 L1 L1 repetitive element ;
1095	10907		1.65	4.2E-02	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
1748	10960	20142	1.25	4.2E-02	FB23091	SWISSPROT	TRANSFORMING PROTEIN MAP
3045	12866	21984	1.56	4.2E-02	FB23091	SWISSPROT	
4098	13306	22406	1.01	4.2E-02	BE262605.1	EST_HUMAN	601150533F1 NIH_MIGC_19 Homo sapiens cDNA clone IMAGE:3503505 5'
4156	13947	23049	0.67	4.2E-02	BF342895.1	EST_HUMAN	602017105F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
6302	15483	24927	4.36	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
6721	16916	25375	5.82	4.2E-02	FO5095	SWISSPROT	ALPHA-ACTinin 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7855	17045	26562	2.53	4.2E-02	BB515822.1	EST_HUMAN	PM3-BN0174-25050-009-d10 BN0174 Homo sapiens cDNA
7855	17045	26563	2.53	4.2E-02	BB515822.1	EST_HUMAN	PM3-BN0174-25050-009-d10 BN0174 Homo sapiens cDNA
8038	17174	26714	1.97	4.2E-02	AF176458.1	NT	PRRS Isolate PRRSV36 envelope glycoprotein gene, complete cds
8561	18301		2.53	4.2E-02	AL983494.1	EST_HUMAN	wk48910x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
4468	13668		9.32	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-18040-164-08 NN0012 Homo sapiens cDNA
5152	14331		0.59	4.1E-02	XK85880.1	NT	L monocytogenes Mo 3 partial lyp gene (strain 443)
6295	15476	24918	1.84	4.1E-02	7682347	NT	Homo sapiens KIAA0887 protein (KIAA0887) mRNA

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6401	15582	25039	2.71	4.1E-02	AF028198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein SmfC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
9189	18302	23689	23.13	4.1E-02	AJ271909.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
9275	18039	23845	1.3	4.1E-02	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
3210	12444	21570	3.38	4.0E-02	AB040904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3782	13090	22115	0.97	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5153	14332	23423	0.9	4.0E-02	AB042287.1	NT	Homo sapiens PTS gene for 8-pyruvyltetrahydroxyproline synthase, complete cds
5385	14814	23727	5.43	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6372	15552	25009	5.79	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
6887	15882	25341	3.68	4.0E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8243	17372		1.71	4.0E-02	AJ001018.1	NT	Kluyveromyces lactis gene for Ca++ ATPase
8481	18114	23809	7.93	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-CoA carboxylase
1128	10352	19504	4.68	3.9E-02	BF516149.1	EST_HUMAN	U(H)-BW1-ank-h-08-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:30841343'
1352	10567	19731	1.9	3.9E-02	PA1047	SWISSPROT	FAS ANTIGEN LIGAND
1831	11135	20330	2.37	3.9E-02	AJ403386.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2865	11846		1.53	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5077	14257	23340	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5077	14257	23341	1.42	3.9E-02	U61380.1	NT	Bacillus megaterium germination protein (gerAA, gerAC, gerAB) genes, complete cds
5117	14297	23385	0.6	3.9E-02	U92882.1	NT	Mus musculus slow skeletal muscle troponin T (TmT1) gene, complete cds
5169	14348	23436	1.01	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C08 S70258 Homo sapiens cDNA
5182	14368	23454	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
5192	14368	23455	1	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163) mRNA
7948	15593	25055	1.69	3.9E-02	PA48778	SWISSPROT	ANTIGEN GOR
8317	18258		10.48	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
8996	17657					NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1, TCRBV5S1, TCRBD1, TCRBD1, TCRBJ1S2,>

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9123	18180		7.38	3.9E-02 AL049886.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxa28orf	
4896	14084	23177	4.3	3.8E-02 AF000580.1	NT	Dicytostellum discoidinum plasmid Ddp5, complete genome	
7246	18466	25957	2.32	3.8E-02 AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds	
999	10230	18305	6.13	3.7E-02 P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)	
2203	11400	20625	4.9	3.7E-02 AJ984806.1	EST_HUMAN	wr85408.xt NCI CGAP Kid11 Homo sapiens cDNA clone MAGE:2494502 3'	
3015	12251	21381	1.02	3.7E-02 P78944	SWISSPROT	EOME SODERMIN	
3017	12253	21382	5.68	3.7E-02 BF129833.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone MAGE:4125584 5'	
8358	17450	26941	4.56	3.7E-02 BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone MAGE:4024973 5'	
9060	18150	23753	12.69	3.7E-02 114158392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1). mRNA	
3834	12855	21974	0.78	3.6E-02 X73221.1	NT	H. vulgaris Sst1 gene for sucrose synthase	
3642	12863	21981	0.84	3.6E-02 AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens	
5967	15182	24597	4.28	3.6E-02 AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	
5967	15182	24598	4.29	3.6E-02 AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA	
6119	15303	24735	1.68	3.6E-02 AF205952.1	NT	Chromatium vinosum sulfur globule protein Cv2 precursor (sgp2) gene, complete cds	
6209	15390	24834	2.73	3.6E-02 AA714521.1	EST_HUMAN	nw20e05.s1 NCI CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to g6.J00314_ma2 TUBULIN BETA-1 CHAIN (HUMAN);	
6873	16064	25530	3.35	3.6E-02 U20608.1	NT	Dicytostellum discoidinum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds	
6873	16064	25531	3.35	3.6E-02 U20608.1	NT	Dicytostellum discoidinum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds	
805	10140	18302	1.14	3.5E-02 U09506.1	NT	Drosophila melanogaster tiggrin mRNA, complete cds	
1018	10245	19397	1.05	3.5E-02 AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds	
1546	10760	19933	0.91	3.5E-02 BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone MAGE:4248377 5'	
1546	10760	19934	0.81	3.5E-02 BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone MAGE:4248377 5'	
4198	13400	22498	1.84	3.5E-02 AE001773.1	NT	Thermologos maritima section 85 of 138 of the complete genome	
4206	13507	22603	1.35	3.5E-02 P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)	
5761	14980	24378	1.69	3.5E-02 J01238.1	NT	Maize actin 1 gene (MAC1), complete cds	
6862	15857	25316	3.7	3.5E-02 BE958970.1	EST_HUMAN	601644701R2 NIH_MGC_56 Homo sapiens cDNA clone MAGE:3929737 3'	
8028	17165	28702	1.89	3.6E-02 AW981641.1	EST_HUMAN	PM1-C70328-281289-002-h03 C70328 Homo sapiens cDNA	
8028	17165	28703	1.89	3.6E-02 AW981641.1	EST_HUMAN	PM1-C70328-281289-002-h03 C70328 Homo sapiens cDNA	
9054	18193	4.1	3.5E-02 BE275948.1	EST_HUMAN	6011781765F1 NIH_MGC_20 Homo sapiens cDNA clone MAGE:3543833 5'		

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
585	9834	18952	1.36	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
585	9834	18953	1.38	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
586	9834	18952	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
586	9834	18953	3.54	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1058	10284	19434	4.44	3.4E-02	AW274020.1	EST_HUMAN	XV260d7.XT Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P58801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1214	10432		8.37	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2355	11548	20769	1.57	3.4E-02	T57160.1	EST_HUMAN	y02060.11 Stratagene lung (#327210) Homo sapiens cDNA clone IMAGE:81250 5' similar to MER29 repetitive element
3409	12635	21768	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3757	12976	22991	0.78	3.4E-02	BE389514.1	EST_HUMAN	RC3-FN0165-050700-01-010 FN0155 Homo sapiens cDNA RCG-UW0015-210200-021-A10 UM0013 Homo sapiens cDNA
3897	13113	22231	3.91	3.4E-02	AW794952.1	EST_HUMAN	M_musculus S-antigen gene promoter region
4598	13782	22883	3.59	3.4E-02	X58789.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5092	14272		2.41	3.4E-02	Q26457	SWISSPROT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6108	14288	23373	1.24	3.4E-02	AJ012469.1	NT	Human lysyl oxidase-like protein gene, exon 3
6019	14509	23567	4.27	3.4E-02	U24383.1	NT	w89404.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
6548	15744		4.73	3.4E-02	AB868629.1	EST_HUMAN	z40411.s1 Stratagene muscle 637209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR.G1017425 G1017425
							IPI5GKPLPKVTKLTSRDPVKLATAKTRNFNTETTAENLTNLKESVTADAGRYEITAANSSGGTAKAFINIVVLDPG
6751	15946		6.27	3.4E-02	AA194306.1	EST_HUMAN	PPT GPV/ISDITEESVTKLWEPKYDGGSGVNYLLKRETSVAVTEVATVARTMMKVMKL ...
377	9843		13.74	3.3E-02	AA398755.1	EST_HUMAN	Z175608.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1175	10398	19548	15.21	3.3E-02	AB058867.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1616	10829	20004	1.02	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
1712	10924		1.2	3.3E-02	AE000700.1	NT	Aequifex aequipinnatus section 32 of 109 of the complete genome
2053	11254		2.44	3.3E-02	R09112.1	EST_HUMAN	Y25608.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
3337	12588	21704	0.81	3.3E-02	H02389.1	EST_HUMAN	Y355f02.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4158	10829	20004	1.9	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4463	13661	22755	2.12	3.3E-02	6755862	NT	Mus musculus tumor rejection antigen gp96 (Tnfr), mRNA
4825	14014	23114	0.65	3.3E-02	AW275696.1	EST_HUMAN	xp40604.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742709 3'
6086	14265	23352	1	3.3E-02	AW500191.1	EST_HUMAN	UI-HFB-BN0-akc-9-10-0-11 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:3076785 5'
5843	15060	24468	15.35	3.3E-02	BF245995.1	EST_HUMAN	601855910f_NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
5843	15060	24489	15.35	3.3E-02	BF245995.1	EST_HUMAN	601855910f_NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
7681	16880	26387	4.07	3.3E-02	BF691107.1	EST_HUMAN	60224717f_NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8563	17583		1.52	3.3E-02	T96545.1	EST_HUMAN	ye4911.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:1211015'
8691	17659		1.26	3.3E-02	AF289685.1	NT	Mus musculus ElF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
8722	17675		1.73	3.3E-02	MB1890.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
129	94112	18547	2.2	3.2E-02	AJ002005.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1134	10357	19508	26.12	3.2E-02	AF088275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1134	10357	19509	26.12	3.2E-02	AF086275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2089	11289		0.9	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
3089	12335	21462	13.54	3.2E-02	EST67353.1	EST_HUMAN	601442431F1 NIH_NGC_65 Homo sapiens cDNA clone IMAGE:38467275'
3695	12815	22034	1.75	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3937	13153	22269	0.66	3.2E-02	Z74103.1	NT	Saccharomyces cerevisiae chromosome IV reading frame ORF YDL055c
3937	13153	22270	0.66	3.2E-02	Z74103.1	NT	Saccharomyces cerevisiae chromosome IV reading frame ORF YDL055c
4202	13405		18.44	3.2E-02	X94768.1	NT	H_sapiens RP3 gene (XLRP gene 3)
4778	13957	23059	3.67	3.2E-02	AF114182.1	NT	Saxifraga rivularis maturease (merk) gene, chloroplast gene encoding chloroplast protein, partial cds
4844	14033	23125	4.95	3.2E-02	AF067083.1	NT	Vitisvinifera sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes
5460	14686	24036	1.85	3.2E-02	X68709.1	NT	S.griseocanatum whG-SIV gene
5460	14686	24037	1.85	3.2E-02	X68709.1	NT	S.griseocanatum whG-SIV gene
5888	15105	24510	2.33	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
5889	15106		30.79	3.2E-02	T88387.1	EST_HUMAN	yd33h12.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:1100087 3' similar to contains yd33h12.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:397151 3' similar to
5938	15154	24585	3.94	3.2E-02	AF173845.1	NT	Alu repetitive element contains LTR1 repetitive element; Segulinus oedipus tissue kallikrein gene, complete cds
6860	15756	25219	4.07	3.2E-02	6680565	NT	Mus musculus kinase family member 3c (Kif3c), mRNA
7092	16289		2.68	3.2E-02	AA719765.1	EST_HUMAN	zb54b12.s1 Soares pineal gland N31PG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1267	10482		1.86	3.1E-02	4503416	NT	gb10441 CYTOCHROME C OXIDASE POLYPEPTIDE II (HUMAN); Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1312	10528	18889	2.11	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1357	11084	20256	0.94	3.1E-02	6671564	NT	Mus musculus adaptors-related protein complex AP-3, delta subunit (Ap3d), mRNA
5373	14602		2.56	3.1E-02	AA278478.1	EST_HUMAN	zs81a05.r1 NC_ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
1600	10814		1.73	3.0E-02	AF187125.1	NT	Pityokteines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3541	12764	21895	1.22	3.0E-02	MB94176.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SS12 gene, complete cds
3633	12854	21973	2.78	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3726	12845		0.92	3.0E-02	AW820223.1	EST_HUMAN	QV2-S570286-150200-040-009 ST0286 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit Descriptor	
3924	13140		0.89	3.0E-02 AA384003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end		
4701	13892		38.75	3.0E-02 AI240467.1	EST_HUMAN	qtl0g6.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844314 3'		
5083	14283	23348	7.54	3.0E-02 AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced		
5083	14283	23349	7.54	3.0E-02 AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced		
5393	14622		3.03	3.0E-02 AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds		
5983	15276	24706	3.37	3.0E-02 AJ242906.1	EST_HUMAN	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene		
6044	15212	24631	3.32	3.0E-02 BE889848.1	EST_HUMAN	601512206f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'		
6044	15212	24632	3.32	3.0E-02 BE889848.1	EST_HUMAN	601512206f1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'		
6114	15208	24627	1.95	3.0E-02 AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds		
6114	15208	24628	1.95	3.0E-02 AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds		
7203	16380	25881	2.8	3.0E-02 AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome		
7784	16979	26492	3.51	3.0E-02 MB1357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1		
8187	17319	26862	9.3	3.0E-02 AA483216.1	EST_HUMAN	nt87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283		
8873	18351	23607	1.98	3.0E-02 R32018.1	EST_HUMAN	nt83dc4.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'		
9044	17885		7.15	3.0E-02 AW895565.1	EST_HUMAN	QV4-NN0038-27040-187-r05 NN0038 Homo sapiens cDNA		
9885	18345		3.1	3.0E-02 AF048887.1	NT	Rattus norvegicus UDP-Gal:glucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds		
2649	12187	21320	0.92	2.9E-02 BE568644.1	EST_HUMAN	601338428f1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'		
2649	12187	21321	0.82	2.8E-02 BE568644.1	EST_HUMAN	601338428f1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'		
3803	13119	22237	0.79	2.9E-02 H72805.1	EST_HUMAN	nt07e10.r1 Soares_fetal liver spleen INF1S Homo sapiens cDNA clone IMAGE:233130 5'		
5782	15000	24403	6.95	2.9E-02 BF032233.1	EST_HUMAN	6014526861f1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'		
6184	15388	24806	10.62	2.9E-02 BE271437.1	EST_HUMAN	601140729f1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'		
672	9822		0.7	2.8E-02 AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA		
3345	12573	21712	1.21	2.8E-02 AF068063.1	NT	Hom sapiens retinal fasin (FSCN2) gene, exon 2		
3345	12573	21713	1.21	2.8E-02 AF068063.1	NT	Hom sapiens retinal fasin (FSCN2) gene, exon 2		
5435	14662	23815	11.9	2.8E-02 BE741083.1	EST_HUMAN	601594078f1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:33948097 5'		
8977	17848		1.33	2.8E-02 J06322.1	NT	Yeast CN31C chromosome III RAI8s DNA (right arm transcription hot-spot)		
3410	12836	21767	2.05	2.7E-02 AL181494.2	NT	Arabidopsis thaliana DNA chromosome Multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'		
4184	13388	22486	1.81	2.7E-02 NA7258.1	EST_HUMAN	yy86h12.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:280487 5'		
4184	13389	22487	1.81	2.7E-02 NA7258.1	EST_HUMAN	yy86h03.s1 Soares_total_fetus_Nb2HF9_9w Homo sapiens cDNA clone IMAGE:1624681 3'		
6112	15208	24625	1.94	2.7E-02 AA993571.1	EST_HUMAN			
578	9827	18948	0.91	2.6E-02 AL163282.2	NT	Hom sapiens chromosome 21 segment HS21C082		

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2334	11527	20748	2.34	2.6E-02	AA490021.1	EST_HUMAN	ab02602_s1 Strategene fetal retina 3872022 Homo sapiens cDNA clone IMAGE:839505 3'
2336	11528	20750	2.19	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2336	11529	20751	2.19	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2866	12104		1.22	2.6E-02	AF109808.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G8, HSP70, HSP70, HSC70;
3917	13133		10.04	2.6E-02	AA071307.1	EST_HUMAN	Mus musculus neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:531305 3'
4278	13481		1.53	2.6E-02	Y07848.1	NT	Homo sapiens EW5, gar22, np22 and bam22 genes
4928	14114	23269	3.97	2.6E-02	L12032.1	NT	Chicken dorsofin-1 mRNA, complete cds
5098	14278	23362	1.82	2.6E-02	AE002014.1	NT	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
5124	14303	23392	1.87	2.6E-02	AW241154.1	EST_HUMAN	xa52644_x1 NCL_CGAP_Sat4 Homo sapiens cDNA clone IMAGE:2570383 3 similar to SW:Y069_HUMAN Q15041 HYPOTHETICAL PROTEIN KIAA0069;
5278	14449	23522	0.83	2.6E-02	AE000825.1	NT	Methanobacterium thermoautotrophicum from bases 340940 to 352162 (section 31 of 148) of the complete genome
5759	14978		6.88	2.6E-02	AI206030.1	EST_HUMAN	q927f11_x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
5839	15058	24483	2.12	2.6E-02	BE621748.1	EST_HUMAN	60149347311 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
6047	15215	24635	6.57	2.6E-02	6981271	NT	Rattus norvegicus Nanogrowth factor receptor, fast (Ngfr), mRNA
7826	17139		2.09	2.6E-02	AA278351.1	EST_HUMAN	z584c02_x1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
8087	17231	28770	1.76	2.6E-02	AW500547.1	EST_HUMAN	U1-H-BNO-an-e-10-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
8395	18338	23604	1.41	2.6E-02	BF43827.1	EST_HUMAN	6020115501F1_NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4150944 5'
538	9789	18912	1.61	2.5E-02	AI783130.1	EST_HUMAN	on26fb_y6_NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
538	9789	18913	1.81	2.5E-02	EE974314.1	EST_HUMAN	on26fb_y6_NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557825 5'
819	10057	19210	20.77	2.5E-02	EE974314.1	EST_HUMAN	601680305R2_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
879	10115	19277	6.14	2.5E-02	EE974314.1	EST_HUMAN	601680305R2_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2718	11897		2.76	2.5E-02	UJ12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2809	12147	21281	3.33	2.5E-02	298697.1	NT	H.cartae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1 repetitive element;
2809	12147	21282	3.33	2.5E-02	298697.1	NT	H.cartae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4022	14468	22337	0.86	2.5E-02	BE701165.1	EST_HUMAN	PM2-NIN0128-080700-001-a12_NIN0128 Homo sapiens cDNA
4022	14469	22338	0.86	2.5E-02	BE701165.1	EST_HUMAN	PM2-NIN0128-080700-001-a12_NIN0128 Homo sapiens cDNA
4188	13392	22490	5.68	2.5E-02	AW582114.1	EST_HUMAN	hf36fb8_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015 3'
5751	14970		4.59	2.5E-02	BE870128.1	EST_HUMAN	7630e09_x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1_H_L1
5756	14975		4.28	2.5E-02	BE746888.1	EST_HUMAN	PM2-NIN0128-080700-001-a12_NIN0128 Homo sapiens cDNA IMAGE:3928054 5'
7387	16601	26089	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL_46.7_KD PROTEIN C19G10.05 IN CHROMOSOME 1
7387	16601	26090	2.37	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL_46.7_KD PROTEIN C19G10.05 IN CHROMOSOME 1

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Table 4
Single Exxon Probes Extruded

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8611	17608	24007	1.27	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
8793	17720		6.39	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
8820	17737		1.23	2.4E-02	N42980.1	EST_HUMAN	YY058p08.1f Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270610_5'
8826	17740		1.35	2.4E-02	BF879477.1	EST_HUMAN	60215328TF1 NIH MGIC_83 Homo sapiens cDNA clone IMAGE:4284173_5'
9282	18378		1.22	2.4E-02	S58644.1	NT	integrin beta 5 subunit rats, NRK cells, mRNA partial, 603 nt]
1838	11046		6.31	2.3E-02	W05340.1	EST_HUMAN	zB84q08.1f Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2892284_5'
1852	11059		6.86	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
1977	11180	20388	1.04	2.3E-02	AW797355.1	EST_HUMAN	CMW0038-290400-172-b11 UMG0038 Homo sapiens cDNA
2319	11512	20733	2.33	2.3E-02	Z74293.1	NT	S cerevisiae chromosome IV reading frame ORF YDL245c
3662	12883	22034	7.23	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH_P_Human fetal Brain Whole tissue Homo sapiens cDNA
3696	12916		0.64	2.3E-02	L23428.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3' end
4131	13337	22436	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4131	13337	22437	0.87	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4412	13612	22708	1.19	2.3E-02	AW8690107.1	EST_HUMAN	CM4-N0080-290400-160-504 NNG080 Homo sapiens cDNA
4443	13643	22735	1.17	2.3E-02	BE895225.1	EST_HUMAN	CM3-MT0118-010800-318-507 MT0118 Homo sapiens cDNA
4443	13843	22736	1.17	2.3E-02	BE895225.1	EST_HUMAN	CM3-MT0118-010800-318-507 MT0118 Homo sapiens cDNA
4444	14470	22737	1.01	2.3E-02	AW583693.1	EST_HUMAN	xS25008.X1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871_3'
4444	14470	22738	1.01	2.3E-02	AW583693.1	EST_HUMAN	xS25008.X1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871_3'
4594	13783	22880	2.54	2.3E-02	BF028487.1	EST_HUMAN	6016722779f1 NIH_MIGC_20 Homo sapiens cDNA clone IMAGE:3985386_5'
4594	13788	22881	2.54	2.3E-02	BF028487.1	EST_HUMAN	6016722779f1 NIH_MIGC_20 Homo sapiens cDNA clone IMAGE:3985386_5'
5043	14221		1.06	2.3E-02	7662173.NT	Home sapiens KIAA0547 gene product (KIAA0547). mRNA	
6183	14359	23444	0.65	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5183	14359	23445	0.85	2.3E-02	AF257110.1	NT	Rattus norvegicus glutamine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5193	14369	23456	0.82	2.3E-02	AE000775.1	NT	Aquifex aeolicus section 107 of 108 of the complete genome
5283	14612	23725	3.67	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcbB) homolog gene, partial cds
5642	15158	24570	4.97	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
6119	15816	25079	6.05	2.3E-02	U83810.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7085	16262	25739	2.2	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7085	16262	25740	2.2	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
7363	16579	26070	2.17	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
8466	18123		5.76	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3546587 5'	
8014	17863	23890	2.12	2.3E-02	U3694.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds	
8072	18376		1.87	2.3E-02	U11077.1	NT	Dichotomium discoidineum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds	
745	9886	19129	3.5	2.2E-02	AF018267.1	NT	Columba livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds	
1719	10931		1.51	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA	
1882	11185	20394	1.57	2.2E-02	2B2001.1	NT	Sphingomyelinase DOPA gene and open reading frame	
2885	12024	21079	1.84	2.2E-02	AF109833.1	NT	Mus musculus ests variant protein ER81 gene, exons 1 through 4	
3413	12639		1.8	2.2E-02	AA577785.1	EST_HUMAN	nn24e04.s1 NCI CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'	
3625	12848		3.43	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain L4 VP1 gene, complete cds	
3896	13112	22230	0.63	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c	
5099	14279	23363	1.65	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c	
6183	15365	24805	3.57	2.2E-02	AV6897/21.1	EST_HUMAN	AV6897/21 GRK8 Homo sapiens cDNA clone GRENAND03 3'	
7758	16954	26462	1.7	2.2E-02	BE797601.1	EST_HUMAN	6011584309F1 NIH MGC_7 Homo sapiens cDNA clone IMAGE:3838371 5'	
8750	17683		2.84	2.2E-02	AA505553.1	EST_HUMAN	ne47h07.61 NCI CGAP_C63 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element	
425	9878		5.24	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MD5ADG01 5'	
455	9708		8.19	2.1E-02	AF029726.1	NT	Dictyostelium discoideum histidine kinase C (dhkC) mRNA, complete cds	
1270	10485	19844	8.21	2.1E-02	U72073.1	NT	Bacillus subtilis cotLM cluster, CotK (cotL), and spore coat protein CotM (cotM) genes, complete cds	
1752	10984	20147	0.89	2.1E-02	PF02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	
1752	10984	20148	0.89	2.1E-02	PF02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	
1752	10984	20149	0.89	2.1E-02	PF02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A	
2768	10028	18177	3.47	2.1E-02	N29286.1	EST_HUMAN	yx3h07.71 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284541 5'	
3360	12783	21812	1.05	2.1E-02	AA461271.1	EST_HUMAN	zg63b09.11 Soare total fetus NbHF8_9w Homo sapiens cDNA clone IMAGE:798121 5'	
4113	13320	22420	0.64	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c	
4287	13498	22694	0.77	2.1E-02	BF542665.1	EST_HUMAN	602015306F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'	
4437	13637	22730	1.76	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, espC and espD genes, complete cds, and unknown genes	
4449	13648	22744	1.73	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.x1 Soares NSF_F8 9W_O1 PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'	
4487	13695		0.63	2.1E-02	Y19213.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7	
4681	13695		1.31	2.1E-02	Y19213.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7	
4720	13911	23013	5.72	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A	
4741	13932	23036	0.63	2.1E-02	AA685737.1	EST_HUMAN	ag55g12.s1 Grossler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'	

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4834	14023	23117	0.62	2.1E-02	AI823432.1	EST_HUMAN	wh54605.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
8731	13695		8.84	2.1E-02	Y19213.1	NT	Homo sapiens putative psihthba pseudogene for hair keratin, exons 2 to 7
9173	17956	23858	3.85	2.1E-02	AF183813.1	NT	A zosophilum brasiliense major outer membrane protein OmbA precursor (omab) gene, complete cds
9286	18044		2.69	2.1E-02	BF003512.1	EST_HUMAN	CM1-TN0141-1:40800-407-408 TN0141 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1:3
18	9314	18416	0.85	2.0E-02	BF002862.1	EST_HUMAN	MER1 repetitive element;
19	9315	18417	9.16	2.0E-02	AW895585.1	EST_HUMAN	QV4-NM0036-270400-187-405 NM0038 Homo sapiens cDNA
263	95339	18683	2.89	2.0E-02	9753835	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1). mRNA
300	9573	18706	2.59	2.0E-02	AA456538.1	EST_HUMAN	aa15bi0.1 Scores_NHhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
808	10047	19198	2.09	2.0E-02	6753635	NT	Mus musculus Dmb homolog 1 (E. coli) (Dmb1). mRNA
1095	10319	18471	0.86	2.0E-02	AL086805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 11(p38.33) of Homo sapiens
1207	10423	18582	1.71	2.0E-02	8922381	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379). mRNA
1207	10428	19583	1.71	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379). mRNA
1839	11047	20238	1.93	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486). mRNA
1839	11047	20237	1.83	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486). mRNA
2751	11930		1.84	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3044	9314	18416	1.58	2.0E-02	BF002862.1	EST_HUMAN	MER1 repetitive element;
3109	12344		2.29	2.0E-02	7305474	NT	Mus musculus serata domain, transmembrane domain (TM), and cytoplasmic domain (C), (semaphorin) 6B (Sema6b). mRNA
3183	12428		1.67	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
3983	13197	22305	1.53	2.0E-02	M18085.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7031	16208		2.37	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7236	16457	25945	2.06	2.0E-02	Z73386.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 85/162
7911	17128	26858	3.17	2.0E-02	D88164.1	NT	Equus caballus DNA for 17sphne-hydroxylase/17-20-lipase, complete cds
8281	14502	23587	1.4	2.0E-02	AA456538.1	EST_HUMAN	aa15bi0.1 Scores_NHhMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
8769	11930		1.55	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9247	18148		1.53	2.0E-02	BE785595.1	EST_HUMAN	601478819F1 NIH MGC 88 Homo sapiens cDNA clone IMAGE:3884477 5'
9264	18022		5.01	2.0E-02	180037.1	EST_HUMAN	yd04c05.1 Scores_infant brain 1NB Homo sapiens cDNA clone IMAGE:24675 5'
700	9942	18076	2.49	1.9E-02	AA572764.1	EST_HUMAN	nf19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.H1 L1 repetitive element;
2006	11209	20418	2.75	1.9E-02	AL168303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2006	11209	20419		2.75	1.8E-02 AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2471	11682	20882		1.22	1.8E-02 AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2857	12095	21224		8.45	1.8E-02 AT713858.1	EST_HUMAN	mv04f05_s1 NCI_CGAP_SS51 Homo sapiens cDNA clone IMAGE:12363373'
2805	12143	21279		1.71	1.9E-02 AV848869.1	EST_HUMAN	AV848869 GLC Homo sapiens cDNA clone GLCBLH073'
3226	12460		0.63	1.9E-02 AB033611.1	NT	Urothecus laevidens mitochondrial gene for cytochrome b, complete cds	
3589	12810		1.08	1.9E-02 N52250.1	EST_HUMAN	y228p02.s1 Soares_mRNA for sclerostin, 2Nb-HMSP Homo sapiens cDNA clone IMAGE:2843313'	
3683	12904		8.88	1.9E-02 BE738098.1	EST_HUMAN	601672882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:38395645	
4024	13235	22340		1.34	1.9E-02 AF141940.1	NT	Mycobacteria initiator WhiA precursor (WhiA1) and WhiA2 precursor (WhiA2), genes, partial cds
4175	13379	22479		1.68	1.9E-02 P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4175	13379	22480		1.56	1.9E-02 P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4538	13733	22831		3.05	1.9E-02 AI452999.1	EST_HUMAN	l16d04_x1 Soares_NSF_F8_9W_QT_PA_P_S1 Homo sapiens cDNA clone IMAGE:21445613' similar to contains Alu repetitive element;
5037	11682	20892		5.49	1.9E-02 AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
8505	18128	23813		3.08	1.9E-02 AF101065.1	NT	Hirudo medicinalis Intermediate filament glialin mRNA, complete cds
9203	17988	23862		1.48	1.9E-02 X8271.1	NT	H.sapiens MUC18 gene exon 16
351	9619	18748		1.42	1.8E-02 AW771104.1	EST_HUMAN	hn52cd8_x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:30272743' similar to contains element MER28 repetitive element;
692	8935	18085		0.65	1.8E-02 BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:41389835'
1168	10389	18541		1.27	1.8E-02 X17684.1	NT	H.frankensei mRNA for myelin basic protein (MBP)
2638	11821	21037		1	1.8E-02 AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3177	12412			0.78	1.8E-02 AI005281.1	EST_HUMAN	les52a09_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:29502983'
3868	13082	22198		1.11	1.8E-02 AW878122.1	EST_HUMAN	MR1-OT0011-28030-009-504 OT0011 Homo sapiens cDNA clone MR1-OT0011-28030-009-504 OT0011 Homo sapiens cDNA
3866	13082	22199		1.11	1.8E-02 AW878122.1	EST_HUMAN	MR1-OT0011-28030-009-504 OT0011 Homo sapiens cDNA clone MR1-OT0011-28030-009-504 OT0011 Homo sapiens cDNA
4062	13272			1.4	1.8E-02 AA861446.1	EST_HUMAN	at24h04_s1 Soares_tes1s NT Homo sapiens cDNA clone IMAGE:14069353'
4422	13622	22717		1.35	1.8E-02 AW836363.1	EST_HUMAN	QV4-DT0021-301288-071-611 DT0021 Homo sapiens cDNA
4975	14162	23253		1.18	1.8E-02 O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845O24.2
6001	15283	24716		4.21	1.8E-02 F14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXIN 5' REGION
7874	16408	25894		1.87	1.8E-02 AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
7874	16408	25895		1.87	1.8E-02 AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8136	17269	26814		1.92	1.8E-02 AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 118601-1-485000 nt, position (67)
8145	17277	26821		3.39	1.8E-02 U62749.1	NT	Zebrafish acidic ribosomal protein P2a-3 (rp2a-3) mRNA, partial cds
9230	18102			1.25	1.8E-02 AF047475.1	NT	Drosophila melanogaster proprotein (proteinin) gene, partial cds
916	10151	19311		1.51	1.7E-02 BE394869.1	EST_HUMAN	601310526F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36321805'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1760	10871	20157	2.19	1.7E-02	AW573183.1	EST_HUMAN	h34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1760	10871	20158	2.19	1.7E-02	AW573183.1	EST_HUMAN	h34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1837	11045		3.2	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2083	11283		12.09	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2604	11788		1.15	1.7E-02	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homolog (RABEX5), mRNA
2955	12183	21328	1	1.7E-02	AI47615.1	EST_HUMAN	q622ae8.x1 Soares_1 Homo sapiens cDNA clone IMAGE:1696982 3'
3486	12710		4.88	1.7E-02	AW827368.1	EST_HUMAN	hm45e04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element;
3603	12824		0.6	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4151	13357		1.17	1.7E-02	AA669618.1	EST_HUMAN	act9f04.s1 Stratego ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
4182	13386		2.03	1.7E-02	RF02506.1	EST_HUMAN	y86f08.11 Soares_fetal_liver_spacer_1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4448	13647		0.65	1.7E-02	AI305279.1	EST_HUMAN	qmt8g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4725	13916	23017	1.88	1.7E-02	J00841.1	NT	Messenger RNA for anglerfish (<i>Lophius americanus</i>) somatostatin II
4828	14017		6.58	1.7E-02	AI015078.1	EST_HUMAN	ov518d2.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840856 3'
6100	14280	23364	0.67	1.7E-02	8581289	NT	Rattus norvegicus N-arginine dibasic convertase 1 (Nrd1), mRNA
5721	14939	24335	1.65	1.7E-02	AI789247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
5917	15134	24543	1.78	1.7E-02	AI038280.1	EST_HUMAN	oy85h03.x1 Soares_fetal_liver_splicein_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672861 3'
6168	15350	24788	2.17	1.7E-02	840716	NT	Homo sapiens nebulin (NEB), mRNA
6394	15574		1.93	1.7E-02	AJ010770.1	EST_HUMAN	Homo sapiens hyponet gene, exons 1-50
6687	16303	23690	2.29	1.7E-02	AW803482.1	EST_HUMAN	CMA4NN1030-040400-130-008 NN1030 Homo sapiens cDNA PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)
9177	17870		1.48	1.7E-02	QQ3211	NT	Mycobacterium tuberculosis H37RV complete genome; segment 13/162
517	9768		1.98	1.6E-02	AL021929.1	NT	SWISSPROT LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) ESTERASE-22
2213	11410	20633	1.09	1.6E-02	Q84176	NT	SWISSPROT LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) ESTERASE-22
2213	11410	20634	1.09	1.6E-02	Q84176	NT	SWISSPROT LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) ESTERASE-22
2331	11719	20936	1	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2608	11780	21010	0.89	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCI_CGAP_Ewt Homo sapiens cDNA clone IMAGE:910667
2654	11837		0.93	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
2981	12218	21353	0.83	1.6E-02	AF112282.1	NT	Lesea sp. isolate IBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product

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 Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal Value	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3480 12723	21859	5.65	1.6E-02	AW850852.1	EST_HUMAN	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA	
3832 13049	22159	1.23	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101	
4168 13362		1.49	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RaICDS-like, KE2, BING4, beta 1,3-galactosidase, RPS18 genes, complete cds; Sacm21 gene, partial>	
5157 14336	24581	0.68	1.6E-02	N80156.1	EST_HUMAN	zeb507.s1 Soares fetal liver spleen, NFLS Homo sapiens cDNA clone IMAGE:287444.3	
5952 15168	24581	2.2	1.6E-02	AB015281.1	NT	Candida albicans CatGCR3 gene, complete cds	
6520 15716		2.8	1.6E-02	X05151.1	NT	Human apoc-CII gene for preprocarboxypeptidase C-II	
7087 16284		3.13	1.6E-02	AF019784.1	NT	Human apoc-CII gene for preprocarboxypeptidase C-II	
7483 18079	26173	2.46	1.6E-02	Z84828.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds	
7765 16961	28471	2.87	1.6E-02	AL161508.2	NT	Gallus gallus microsatellite DNA (LE10250 (=T16111111))	
7765 16961	28472	2.87	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	
8044 17180	28719	2.23	1.6E-02	A373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20	
8478 11410	20633	1.65	1.6E-02	C84176	SWISSPROT	q288010.x1 Soares pregnant uterus_NbRPU Homo sapiens cDNA clone IMAGE:20424423	
8478 11410	20634	1.65	1.6E-02	C84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	
8865 17768		1.54	1.6E-02	X92751.1	NT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)	
759 10000		78.83	1.5E-02	8923734	NT	R.norvegicus gene for choline acetyltransferase, exon 1 (non coding)	
2110 11309	20522	3.85	1.5E-02	N39521.1	EST_HUMAN	Rnmpd1 transcription factor (HSA130884), mRNA	
2141 11339	20557	1.25	1.5E-02	AL161594.2	NT	Y27807.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243925.3	
3705 12925	22044	1.13	1.5E-02	BF092942.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90	
4123 13329	22427	0.8	1.5E-02	AA160987.1	EST_HUMAN	MR4-TN0115-080500-201-b12 TN0115 Homo sapiens cDNA	
6217 15398		1.63	1.5E-02	11467282	NT	Zg40910.11 Strategic HNT neuron (#83723) Homo sapiens cDNA clone IMAGE:632226.6	
6221 15618	25082	5.18	1.5E-02	11417739	NT	Cyanophora paradoxa cyanellae, complete genome	
7727 16925	26435	2.59	1.5E-02	U40609.1	NT	Xenopus laevis neurogenin related 16 (X-NGNR-16) mRNA, complete cds	
8710 18170		1.65	1.5E-02	AW750834.1	EST_HUMAN	Plasmidium falciparum (strain FCIR3) variant-specific surface protein (var-2, var-3) genes, complete cds's	
423 9876		1.46	1.4E-02	AE002230.2	NT	RC4-CN0048-740100-011-c11 CN0048 Homo sapiens cDNA	
1126 10350	19501	3.57	1.4E-02	770590	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome	
1263 10478		0.9	1.4E-02	U32800.1	NT	Hemophilus influenzae Rd section 115 of 163 of the complete genome	
1305 10521		3.25	1.4E-02	U677779.1	NT	Xenopus laevis neurogenin related 16 (X-NGNR-16) mRNA, complete cds	
3179 12414	21548	1.78	1.4E-02	AF160569.2	NT	Bifidobacterium longum Na+/H+ antipporter (nhB), cytosine deaminase, and alpha-D-galactosidase (egII) genes, complete cds; and N-acetylglucosamine-4-O-acetyltransferase (negC/NegR) gene, partial cds	
3376 12804	21739	0.96	1.4E-02	AW07421.1	EST_HUMAN	xb09009.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793.3	

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Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3459	12684	21618	6.64	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA contig fragment No. 82	
3459	12684	21619	6.64	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA contig fragment No. 82	
3493	12717	21653	0.59	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman Factor) (F12), mRNA	
3836	12857	21976	7.91	1.4E-02	6968918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA	
4486	13684	22774	8.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGE Homo sapiens cDNA	
4486	13684	22775	8.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGE resequences, MAGE Homo sapiens cDNA	
4685	13859	22958	0.96	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
4685	13859	22959	0.86	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
4893	14081	23174	7.33	1.4E-02	BE733142.1	EST_HUMAN	601587403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'	
4893	14081	23175	7.33	1.4E-02	BE733142.1	EST_HUMAN	601587403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'	
5334	15051	24457	4.63	1.4E-02	AA559030.1	EST_HUMAN	n11c04.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element;	
5834	15051	24458	4.63	1.4E-02	AA559030.1	EST_HUMAN	n11c04.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1028890 3' similar to contains Alu repetitive element;	
6877	16058	25537	2.98	1.4E-02	BE54561.1	EST_HUMAN	60107239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'	
8388	17469	28591	4.44	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon epsilon/beta receptor	
8784	17702		1.95	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J8.2 mRNA, complete cds	
9058	17889		2.17	1.4E-02	11426868	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA	
1825	11129	20323	2.04	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001	
3180	12415	21549	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'	
3180	12415	21650	2.04	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'	
3546	13162		1.42	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds	
6326	15507	24953	4.62	1.3E-02	A031583.1	EST_HUMAN	cm05g05.x1 Scares_parenthyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;	
6321	15817	25276	2.43	1.3E-02	AF156981.1	NT	Homosapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds	
7136	16313	25794	2.67	1.3E-02	ME3707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds	
7584	16769	26259	4.34	1.3E-02	AW268563.1	EST_HUMAN	x134e03.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'	
7584	16769	26260	4.34	1.3E-02	AW268563.1	EST_HUMAN	x134e03.x1 Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'	
8368	18328		2.68	1.3E-02	>X51780.1	NT	Yeast ABP1 gene for actin binding protein	
8874	17771		1.98	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome	
9063	18093		12.49	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasoressin receptor (VPR3) gene, complete cds	
9268	18364	23609	1.4	1.3E-02	AF009179.1	NT	Oryza sativa replication protein A1 (Os-RPA1) mRNA, complete cds	
350	9827	18757	4.87	1.2E-02	AA059299.1	EST_HUMAN	z65g01.r1 Scares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element;	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
459	9712	18847	2.58	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL_17.1KD PROTEIN IN PUR5_3' REGION qd6812.x1 Soares_cDNA clone IMAGE:1734670 3' similar to contains L1.t1 L1 repetitive element;
748	8987	19130	10.01	1.2E-02	A1183522.1	EST_HUMAN	
2143	11341	20359	1.48	1.2E-02	AL163213.2	NT	Human sapiens chromosome 21 segment HS21C013
2406	11598	20819	1.16	1.2E-02	AW172350.1	EST_HUMAN	XJ37605_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2446	11637	20858	1.3	1.2E-02	AL163218.2	NT	Human sapiens chromosome 21 segment HS21C018
2600	11598	20819	25.94	1.2E-02	AW172350.1	EST_HUMAN	XJ37605_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3066	12302		6.88	1.2E-02	AA075418.1	EST_HUMAN	ZN88603.1 Strategene ovarian cancer (#831219) Homo sapiens cDNA clone IMAGE:545020 5'
3266	12489	21620	2.15	1.2E-02	R62805.1	EST_HUMAN	Y11bb03.51 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3258	12491	21622	0.84	1.2E-02	A1688694.1	EST_HUMAN	ZB66907.x5 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:308532 3' similar to contains element MER22 repetitive element;
4935	14122	23217	2.68	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorC gene, and sodium phosphate transporter (NPT3) gene, complete cds
5067	14247		1.27	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CypUbiquitin mRNA, partial cds
5114	14294	23382	1.49	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5551	14775	24142	1.85	1.2E-02	D76589.1	NT	Rana rugosa mRNA for calcitonin, complete cds
6089	15280	24723	5.53	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6212	15393	24837	8.59	1.2E-02	AV732053.1	EST_HUMAN	AV732053 HTFF Homo sapiens cDNA clone HTFBG09 5'
6463	15660	25132	3.83	1.2E-02	Q11205	SWISSPROT	CMP-N-ACTYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA-2,3-ST) (GAL-NAC6S) (GA)-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL_A.2) (SIA-14-B)
6977	16155	25626	3.56	1.2E-02	AB031013.1	NT	Norwalk-like virus gene group 2 gene for capsid protein, complete cds
8442	17505	24015	1.26	1.2E-02	O15534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN FIGU) (HPER)
8877	18187		1.27	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR
9071	17893		4.48	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN:5577G06 5'
12776	10491	19650	1.91	1.1E-02	AA070384.1	EST_HUMAN	ZM68e11.1 Strategene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:5330924 3'
1681	10893	20080	1.32	1.1E-02	X75491.1	NT	H_sapiens LIPA gene, exon 4
2005	11208	20417	4.75	1.1E-02	BF345263.1	EST_HUMAN	Z0219037f NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2231	12070		4.23	1.1E-02	N98523.1	EST_HUMAN	Za40605.11 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:285040 5'
3486	12720	21857	3.07	1.1E-02	A1653508.1	EST_HUMAN	Ig95b10.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216639 3' similar to SW_XPF_HUMAN
3998	13211		63.05	1.1E-02	E5144637.1	EST_HUMAN	O92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL
							PM3-H70175-300598-001-108 HT0175 Homo sapiens cDNA

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4085	13294			0.85	1.1E-02 AW813786.1	EST_HUMAN	RC3-ST0197-120200-016-911 ST0197 Homo sapiens cDNA
4847	14038	23129		2.48	1.1E-02 AL048383.2	EST_HUMAN	DKFZp586E0924_s1_586 (synonym: hut61) Homo sapiens cDNA clone DKFZp586E0924
6331	15512	24958		2.06	1.1E-02 BE149811.1	EST_HUMAN	RC1-HT0258-100300-016-h07 HT0258 Homo sapiens cDNA
6744	15939	25400		7.88	1.1E-02 CG61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7047	16224	25699		2.79	1.1E-02 AA082578.1	EST_HUMAN	Zn248d1.r1 Strategene neuroepithelium NT2RAMI B37234 Homo sapiens cDNA clone IMAGE:548328_5'
7107	16284	25765		5.97	1.1E-02 AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
7552	18757	28251		3.86	1.1E-02 1143595 NT	EST_HUMAN	ab77111.s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005_3' similar to contains Alu repetitive element:
8327	17428			3	1.1E-02 AA688239.1	EST_HUMAN	EST10176-111098-003-610 C70176 Homo sapiens cDNA
6	8302	18406		8.12	1.0E-02 AW846120.1	EST_HUMAN	MR3-C10176.s1 NC_ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495_3'
2536	11724			0.94	1.0E-02 AA806389.1	EST_HUMAN	oc22f98.s1 NC_ CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495_3'
3055	12291	21417		3.03	1.0E-02 BE835556.1	EST_HUMAN	RCQ-FN0025-250600-021-402 FN0025 Homo sapiens cDNA
3229	12483	21595		1.34	1.0E-02 BE988999.1	EST_HUMAN	6016469867R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689_3'
3874	13090	22208		0.6	1.0E-02 AL1683302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4786	13975	23078		4.78	1.0E-02 8753321 NT		Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4861	14049	23143		5.39	1.0E-02 FR86567.1	EST_HUMAN	Y645R01.1 Seares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:119663_5'
5208	14383			1.84	1.0E-02 BE084970.1	EST_HUMAN	RC1-BT013-1304-00-016-609 BT0313 Homo sapiens cDNA
5745	14964	24363		2.8	1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0356-070101-001 BT0356 Homo sapiens cDNA
5745	14984	24364		2.8	1.0E-02 AW577113.1	EST_HUMAN	MR4-BT0356-070101-001 BT0356 Homo sapiens cDNA
6874	16065	26532		7.87	1.0E-02 BF036331.1	EST_HUMAN	601458670F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177_5'
6874	16065	26533		7.87	1.0E-02 BF036331.1	EST_HUMAN	601458670F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3863177_5'
7814	17007			2.34	1.0E-02 AF157359.1	NT	Crithidia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
7807	17122	26853		2.08	1.0E-02 AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10_5'
8407	18384			1.45	1.0E-02 Q62203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A6)
8487	18145	23751		4.31	1.0E-02 AW8355621.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
8487	18202			5.37	1.0E-02 S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
8949	18259			3.4	1.0E-02 X82854.1	NT	H.sapiens gene for M6491/CD68 antigen
9271	18034	23842		1.34	1.0E-02 AB039887.1	NT	Homo sapiens WDR4 gene for WD repeat protein, complete cds
9280	18105			20.92	1.0E-02 D17522.1	NT	Z. mitchii zlfE and zlfS genes for expression and secretion activator protein, complete cds
903	10138	18300		1.76	9.0E-03 AI796126.1	EST_HUMAN	wh4209_X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433_3' similar to contains element MER22 MER22 repetitive element
1271	10486			1.88	9.0E-03 BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346_5'

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2359	11552	20773	2.28	9.0E-03	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2368	11561	20783	1.95	8.0E-03	AF098934.1	NT	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2358	12098	21225	0.68	9.0E-03	AI251744.1	EST_HUMAN	q96f98_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone MAGE:1854281 3'
2358	12098	21226	0.68	9.0E-03	AI251744.1	EST_HUMAN	q96f98_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone MAGE:1854281 3'
3649	12870	21987	1.08	9.0E-03	J05184.1	NT	S.acidocalcarinus thermopsisin gene, complete cds
5008	14195	23284	1.11	9.0E-03	BE047949.1	EST_HUMAN	t244e10_y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone MAGE:2291468 5'
5948	15164		4.8	9.0E-03	BE745888.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone MAGE:3834752 5'
7558	16763		1.7	9.0E-03	'Y18000.1	NT	Homo sapiens NF2 gene
7583	16788	26283	1.77	9.0E-03	BS295880.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36321181 5'
8628	18385		1.56	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281269-001-609 HT0452 Homo sapiens cDNA
8846	18379		15.48	9.0E-03	BE348385.1	EST_HUMAN	hw17098_x1 NCI_CGAP_L124 Homo sapiens cDNA clone IMAGE:3183161 3'
9160	17959		14.22	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-281289-001-609 HT0452 Homo sapiens cDNA
9215	17895		1.23	9.0E-03	P16241	SWISSPROT	POU-DOMAIN PROTEIN CF-1A (CHORION FACTOR 1A) (CF1-A) (VENTRAL VEINS LACKING PROTEIN) (DRIFTER PROTEIN)
509	9760		5.44	8.0E-03	AA723007.1	EST_HUMAN	Zh30803_s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element
998	10228	19283	61.85	8.0E-03	AF06856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2125	11324	20542	1.11	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2617	11706	20919	1.37	8.0E-03	P10286	SWISSPROT	RETRONVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE)
3281	12112	21843	1.07	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-01-b08 HT0545 Homo sapiens cDNA
3334	12863	21701	0.88	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3656	12877	21986	1.48	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127/10 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3656	12877	21987	1.46	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127/10 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4244	13447	22538	1.19	8.0E-03	BE840049.1	EST_HUMAN	Q96FN0181-14700-304-910 F0161 Homo sapiens cDNA
4377	13579	22878	6.14	8.0E-03	BF363327.1	EST_HUMAN	CM44NN0118-300600-223-b05 NN0119 Homo sapiens cDNA
4723	13919	23021	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BH1F1 PROTEIN
4723	13919	23022	0.65	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BH1F1 PROTEIN
5452	14678	23838	2.83	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5980	15194	24610	4.29	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6309	15480		1.8	8.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
6748	15943	25403	4	8.0E-03	AW808862.1	EST_HUMAN	MR1-ST0111-111186-011-h05 ST0111 Homo sapiens cDNA

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7053	16230		8.75	8.0E-03	BE086509.1	EST_HUMAN	QY1-BT0677-040400-131-903 BT0677 Homo sapiens cDNA S.ceratophyllum chromosomes X reading frame ORF Y JYR152w
7557	16762		2.97	8.0E-03	Z49852.1	NT	
7820	17135	26865	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80a09_s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
7820	17135	26868	1.9	8.0E-03	AA828817.1	EST_HUMAN	cd80a09_s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
8206	17537	26877	5.58	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
8336	17434		1.97	8.0E-03	M69035.1	NT	Oryctolagus cuniculus elf-2a kinase mRNA, complete cds
8383	17468		2.41	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
701	8943	18077	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
701	8943	18078	15.31	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
884	10215	18311	9.6	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1124	19499		3.32	7.0E-03	AV731712	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTF2Z/F10 5'
1372	10586		1	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (INF3IFH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
1389	10613	19777	3.43	7.0E-03	AA688288.1	EST_HUMAN	ab7806_s1 Strategene fetal retina 337202 Homo sapiens cDNA clone IMAGE:853145 3'
1494	10707	19880	2.54	7.0E-03	AW30599.1	EST_HUMAN	x21802_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813759 3'
1715	10927	20111	1	7.0E-03	AW950556.1	EST_HUMAN	EST362628 MAGE mesequences, MAGA Homo sapiens cDNA
1715	10927	20112	1	7.0E-03	AW950556.1	EST_HUMAN	EST362628 MAGE mesequences, MAGA Homo sapiens cDNA
2222	12013	20845	1.48	7.0E-03	P04829	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3533	12756	21888	1	7.0E-03	A1150273.1	EST_HUMAN	q34h02_x1 Scores_nht Homo sapiens cDNA clone IMAGE:1751955 3'
3749	12889	22084	0.87	7.0E-03	AW444483.1	EST_HUMAN	ULH-B13-akb-c-10-0-U1_s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733891 3'
3800	13018	22131	0.81	7.0E-03	AF196344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
3995	12868	22084	0.64	7.0E-03	AW444463.1	EST_HUMAN	UI-H-B13-akb-c-10-0-U1_s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733891 3'
4332	13533		1.12	7.0E-03	U60086.1	NT	Diclostaedium discoidatum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds
4532	13728		1.04	7.0E-03	AW117711.1	EST_HUMAN	x634f09_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2609033 3' similar to TR-Q12987 Q12987
4889	13793		1.38	7.0E-03	W530988.1	EST_HUMAN	ACIDIC 82 KDA PROTEIN_1 hr8965_x1 NCI_CGAP_Gut Homo sapiens cDNA clone IMAGE:28693616 5'
5010	14197		2.53	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5113	18063		4.99	7.0E-03	AW861059.1	EST_HUMAN	RC1-CT0286-050400-018-018 CT0286 Homo sapiens cDNA
5795	15012	24416	1.73	7.0E-03	W68251.1	EST_HUMAN	z483110_x1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
5898	15113	24524	3.19	7.0E-03	AA327128.1	EST_HUMAN	EST30874 Cad1 Homo sapiens cDNA 5' end
6115	15228	24647	1.92	7.0E-03	EE928133.1	EST_HUMAN	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA

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 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
62891	15480	24923	5.21	7.0E-03	Z35838.1	NT	S_cerevisiae chromosome II reading frame ORF YBL077w
62891	15480	24924	5.21	7.0E-03	Z35838.1	NT	S_cerevisiae chromosome II reading frame ORF YBL077w
6498	15635	25159	4.1	7.0E-03	BE175687.1	EST_HUMAN	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
7403	16616	26106	3.29	7.0E-03	AB008852.1	NT	Bos taurus mRNA for NDP52, complete cds
8904	18370		1.5	7.0E-03	H94065.1	EST_HUMAN	yy15h01_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242633 3' similar to contains Alu repetitive element;
8911	17800		2.34	7.0E-03	BE263253.1	EST_HUMAN	601145154F2 NIH MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
9006	17884		1.59	7.0E-03	Y1455.1	NT	Hom sapiens LSFR2 gene, penultimate exon
9147	18367		1.41	7.0E-03	AL163300.2	NT	Hom sapiens chromosome 21 segment HS21C100
9278	18040		1.4	7.0E-03	AW868110.1	EST_HUMAN	RC0-SND052-10400-021-a04 SND052 Homo sapiens cDNA
1247	10484	19824	10.61	6.0E-03	AW511148.1	EST_HUMAN	hd22a65_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PPR_HUMAN_075469_ORPHAN NUCLEAR RECEPTOR PXR;
1247	10484	19825	10.81	6.0E-03	AW511148.1	EST_HUMAN	hd22a65_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PPR_HUMAN_075469_ORPHAN NUCLEAR RECEPTOR PXR;
2727	11908	21121	1.11	6.0E-03	AF112374.1	NT	Danio rerio odorant receptor gene cluster
2843	12082	21207	4.79	6.0E-03	AA759135.1	EST_HUMAN	ah78e11_s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
2843	12082	21208	4.79	6.0E-03	AA759135.1	EST_HUMAN	ah78e11_s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
3213	12447		2.26	6.0E-03	H75680.1	EST_HUMAN	yy77h04_x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'
3275	12508		0.7	6.0E-03	AF190338.1	NT	Natuncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3360	12588	21727	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3360	12588	21728	1.3	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3321	12745		1.25	6.0E-03	W37985.1	EST_HUMAN	zc13a11.1 Soares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:3222172 5'
3340	12861	21979	2.21	6.0E-03	BF510988.1	EST_HUMAN	ui-H-Bi4-spm-c-06-d-QU1_s1 NCI CGAP_SubHomo sapiens cDNA clone IMAGE:3087754 3'
3159	12978	22083	1.08	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
3393	13149		0.98	6.0E-03	BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858513 5'
4317	13518		0.85	6.0E-03	N58946.1	EST_HUMAN	yy62h10_s1 Soares multiple sclerosis cDNA clone IMAGE:278179 3'
4358	13560		1.94	6.0E-03	A016883.1	EST_HUMAN	ov33c11_x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4705	13896	22895	7.35	6.0E-03	AA324242.1	EST_HUMAN	EST27116 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5273	14445	23517	0.9	6.0E-03	AF050737.1	NT	Homo sapiens dopamine D2 receptor (DRD2) gene, complete cds
6413	15610	25074	13.87	6.0E-03	AK033980.1	EST_HUMAN	ow13a04_x1 Soares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10 b1 MER10 repetitive element.

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6453	15650	25118		3.3	6.0E-03 AW798337.1	EST_HUMAN	RCGUM0051-210300-302-902 UMD0051 Homo sapiens cDNA Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
6937	16081	25551		10.41	6.0E-03 D10548.1	NT	
7330	16548	26038		2.3	8.0E-03 AW962184.1	EST_HUMAN	EST374237 MAGE resequences, MAGG Homo sapiens cDNA
7388	16802			2.24	6.0E-03 11545814 NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ4011). mRNA	
7423	16653	26127		2.03	8.0E-03 A1420788.1	EST_HUMAN	leg9ic12_x1_NCI_CGAAP_Pi28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:Q000519 O000519
7423	16633	28128		2.03	8.0E-03 A1420788.1	EST_HUMAN	leg9ic12_x1_NCI_CGAAP_Pi28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:Q000519 O000519
7555	18780			4.37	8.0E-03 U14568.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
7558	18781	28254		2.64	8.0E-03 BE737895.1	EST_HUMAN	601572748F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
8262	17389	26921		1.76	8.0E-03 H70286.1	EST_HUMAN	Y95101.1 Soay sheep fetal liver spliced 1NF1S Homo sapiens cDNA clone IMAGE:213049 5' similar to SP19GD_PIG_P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING :
8449	17508			1.57	8.0E-03 AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
8559	18198			1.26	8.0E-03 BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4202212 5'
8585	18130			8.17	8.0E-03 AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 428192 to 450298 (section 39 of 148) of the complete genome
8669	18194			2.42	6.0E-03 U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
8922	17873			1.98	6.0E-03 BE798019.1	EST_HUMAN	601482821F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38853388 5'
9045	17888			1.96	6.0E-03 AJ245480.1	NT	Brassica napus ssp. nigra S-locus glycoprotein, cultivar T2
675	9920	19050		1.9	5.0E-03 L25105.1	NT	Chlamydia trachomatis partial ORF B; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpe-like protein, completed cds
675	9920	19051		1.9	5.0E-03 L25105.1	NT	Chlamydia trachomatis partial ORF B; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpe-like protein, completed cds
676	9920	19050		3.67	5.0E-03 L26105.1	NT	Chlamydia trachomatis partial ORF B; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpe-like protein, completed cds
676	9920	19051		3.67	5.0E-03 L25105.1	NT	Chlamydia trachomatis partial ORF B; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpe-like protein, completed cds
1120	10344	19495		1.63	5.0E-03 AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2041	11824	21039		1.97	5.0E-03 AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2088	12124	21257		0.79	5.0E-03 BE266057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35338789 5'
3101	12337	21465		4.54	5.0E-03 787623.1	EST_HUMAN	yc61ff98 s1 Soay sheep infant brain 1N1B Homo sapiens cDNA clone IMAGE:223953
3118	12353			2.3	5.0E-03 AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3131	12368	21498		1.13	5.0E-03 R71794.1	EST_HUMAN	Y88602 s1 Soay sheep breast 2N1HBst Homo sapiens cDNA clone IMAGE:155868 3'

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3245	12478		0.85	5.0E-03	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3677	12898	22018	4.23	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3741	12861	22076	0.74	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3848	13164		1.87	5.0E-03	AA288675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4291	13493	22591	0.84	5.0E-03	H78355.1	EST_HUMAN	yJ78g10.11 Scares fetal liver spleen INF-5 Homo sapiens cDNA clone IMAGE:2400666 5'
4293	12861	22076	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4609	13803	22893	0.84	5.0E-03	AJ131018.1	NT	Homo sapiens SCL gene locus
4731	13922	23026	1.59	5.0E-03	AT752367.1	EST_HUMAN	cN15C2X1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cN15C02 random
4854	14141	23235	0.97	5.0E-03	FI5285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5570	14795	24168	5.73	5.0E-03	F35560	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROTABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAF FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y-CHROMOSOME)
5684	14904	24297	2.82	5.0E-03	000507	SWISSPROT	
5831	15147		7.17	5.0E-03	BE300091.1	EST_HUMAN	600844584T1 NIH MGIC_17 Homo sapiens cDNA clone IMAGE:2860871 3
6016	14506	23574	6.81	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6402	16583	25040	7.06	5.0E-03	AB016816.1	NT	Homo sapiens MASL1 mRNA, complete cds
6658	15854		9.12	5.0E-03	MG1132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
7308	16526		7.45	5.0E-03	T19588.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 684 xn58g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to xccontains L1.2 L1 repetitive element;
7513	16718	26207	2.68	5.0E-03	AW170334.1	EST_HUMAN	xn58g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to xccontains L1.2 L1 repetitive element;
7513	16718	26208	2.98	5.0E-03	AW170334.1	EST_HUMAN	xn58g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to xccontains L1.2 L1 repetitive element;
7611	16814	26310	2.19	5.0E-03	T49153.1	EST_HUMAN	yb08e04.11 Stratagene placenta (#8937225) Homo sapiens cDNA clone IMAGE:70686 5'
7876	17064		3.94	5.0E-03	BE048055.1	EST_HUMAN	tz48c04.y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
8602	18332		5.41	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
8743	17688		10.59	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
8844	17753		1.75	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
8881	17776		1.3	5.0E-03	AA456397.1	EST_HUMAN	2x7803.s1 Soares ovary tumor NIH3T3 Homo sapiens cDNA clone IMAGE:809548 3' similar to SW_DXA2_MOUSE_P14585 PROTABLE DIPHENOL OXIDASE A2 COMPONENT
8912	18139		5.75	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH MGIC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
9097	17913	23869	2.68	5.0E-03	AW449109.1	EST_HUMAN	U1H-B13-ekf-f-08-0-U1.61 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
9118	18211		1.4	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							Top Hit	Database Source
238	9517	18846		3.28	4.0E-03 AW500196.1	EST_HUMAN	UI-HF-BN0-akc-h-04-0-UJ.1 NIH_MGC_50_Homo sapiens cDNA clone IMAGE:3076831 5'	
326	8597	18728		2.1	4.0E-03 R48482.1	EST_HUMAN	9851604_s1 Scores infant brain 1NIB_Homo sapiens cDNA clone IMAGE:35988 3'	
449	9702	18840	0.94	4.0E-03 P54875	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)		
610	9857	18976		2.44	4.0E-03 AA898339.1	EST_HUMAN	on75g12_s1 Scores Infant brain 1NIB_Homo sapiens cDNA clone IMAGE:35988 3'	
887	10122	18286		1.91	4.0E-03 R48482.1	EST_HUMAN	9851604_s1 Scores Infant brain 1NIB_BT0333_Homo sapiens cDNA	
821	10158			4.09	4.0E-03 AW749101.1	EST_HUMAN	281808.1 Strategene colon (#837204)_Homo sapiens cDNA clone IMAGE:5_0898 5'	
1159	10381	19533		24.84	4.0E-03 AA098777.1	EST_HUMAN	RC8-UM0014-17040-023-G01_LM0014_Homo sapiens cDNA	
1177	10398	18551		1.71	4.0E-03 AW784740.1	EST_HUMAN	RC8-UM0014-17040-023-G01_LM0014_Homo sapiens cDNA	
1310	10528	18686		0.88	4.0E-03 AA284374.1	EST_HUMAN	2259ac01_r1 NCI_CGAP_GCB1_Homo sapiens cDNA clone IMAGE:701736 5'	
1568	10779			0.95	4.0E-03 AV708305.1	EST_HUMAN	AV708305_ADC_Homo sapiens cDNA clone ADCAKB06 5'	
1717	10928	20114		2.29	4.0E-03 U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds	
1985	11188	20399		16.08	4.0E-03 AA098777.1	EST_HUMAN	281808.1 Strategene colon (#837204)_Homo sapiens cDNA clone IMAGE:5_0898 5'	
2212	11409			1.85	4.0E-03 BE410558.1	EST_HUMAN	601304161F_NIH_MGC_21_Homo sapiens cDNA clone IMAGE:3638510 5'	
2243	11438	20682		1.44	4.0E-03 AW784740.1	EST_HUMAN	RC8-UM0014-17040-023-G01_LM0014_Homo sapiens cDNA	
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >	
2537	11725	20941		1.4	4.0E-03 U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creative transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >	
							Homo sapiens polyglutamine-containing C14ORF4 gene	
2537	11725	20942		1.4	4.0E-03 U52111.2	NT	Homo sapiens polyglutamine-containing C14ORF4 gene	
2551	11834	21047		1.92	4.0E-03 AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene	
2551	11834	21048		1.92	4.0E-03 AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene	
2557	11839	21051		1.09	4.0E-03 AL163284.2	NT	Homo sapiens chromosome 21 segment 1 HS21C054	
3191	12426	21560		0.99	4.0E-03 BE164134.1	EST_HUMAN	PM1-HT0340-151289-003-h08_H10340_Homo sapiens cDNA	
3191	12426	21561		0.99	4.0E-03 BE164134.1	EST_HUMAN	PM1-HT0340-151289-003-h08_H10340_Homo sapiens cDNA	
3504	12728	21884		0.98	4.0E-03 AW188426.1	EST_HUMAN	x98f04_x1_NCI_CGAP_Cor18_Homo sapiens cDNA clone IMAGE:2865279 3'	
3504	12728	21865		0.98	4.0E-03 AW188428.1	EST_HUMAN	x98f04_x1_NCI_CGAP_Cor18_Homo sapiens cDNA clone IMAGE:2865279 3'	
3602	12823	21945		0.69	4.0E-03 Q13606	SWISSPROT	OLFACRYTO RECEPTOR 51 OLFACTORY RECEPTOR-LIKE PROTEIN OLF1	
3612	12833	21954		0.68	4.0E-03 AV646253.1	EST_HUMAN	AV646253 GLC_Homo sapiens cDNA clone GLCALDO2 3'	
3904	13120	22238		0.77	4.0E-03 AF060888.1	NT	Mus musculus tumor susceptibility protein 101 (tsg 101) gene, complete cds	
3972	13188			1.89	4.0E-03 AJ011172.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)	
4225	13428	22519		5.3	4.0E-03 AJ788727.1	EST_HUMAN	wi87ae08_x1_NCI_CGAP_Kid12_Homo sapiens cDNA clone IMAGE:2400274 3'	
5312	14344	23613		1.71	4.0E-03 AF055859.1	NT	Drosophila melanogaster anon207 (anon207) mRNA, complete cds	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	14824	23737		22.47	4.0E-03 AF169825.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5569	14784	24167		2.5	4.0E-03 P04198	SWISSPROT	(HPRG)
5702	14921			3.78	4.0E-03 U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5791	15008	24412		1.85	4.0E-03 BE548453.1	EST_HUMAN	801078015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3481054 5'
6163	15346	24783		4.05	4.0E-03 Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
6480	15877	25147		5.72	4.0E-03 AF111944.1	NT	Dicytostelium discoidinum Ax4 development protein DG1122 (DG1122) gene, partial cds
6530	15726	25191		2.26	4.0E-03 7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
6884	15878	25338		8.28	4.0E-03 AF539883.1	EST_HUMAN	1843p11.1x1 Spares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980013 3' similar to contains Ali repetitive element
6743	15638	25398		5.44	4.0E-03 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7889	16898	28395		6.92	4.0E-03 AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
8242	17371	26907		2.1	4.0E-03 AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
8569	18347			3.66	4.0E-03 BE815173.1	EST_HUMAN	PM4-BN0138-180800-002-008 BN0138 Homo sapiens cDNA
8592	17601			1.6	4.0E-03 BE298280.1	EST_HUMAN	601116184F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
8876	17848			2.3	4.0E-03 AW504273.1	EST_HUMAN	U1-HFBN0-slip-9-04-0-U1/r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
8923	17807			3.28	4.0E-03 BF224125.1	EST_HUMAN	7q74c59.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Ali repetitive element; contains element MER31 repetitive element;
8865	18253			1.91	4.0E-03 AW614586.1	EST_HUMAN	h102cd7.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
8876	17843			1.75	4.0E-03 AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
376	9842	18777		2.69	3.0E-03 AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
889	10124	19287		7.37	3.0E-03 AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1636	10850	20028		3.13	3.0E-03 AA468110.1	EST_HUMAN	nc73cd5.81 NCI_CGAP_Pt2 Homo sapiens cDNA clone IMAGE:782984 similar to contains Ali repetitive element;
2223	11419			1.08	3.0E-03 AF055068.1	NT	Homo sapiens MHC class 1 region
2257	11452			7.21	3.0E-03 Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2850	12188			0.77	3.0E-03 Y08006.1	NT	Arabidopsis thaliana ipom1 gene
3048	12284	21411		3.88	3.0E-03 BE379286.1	EST_HUMAN	601237882F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609833 5'
3114	12349	21477		2.89	3.0E-03 AW802687.1	EST_HUMAN	IL2-JUN/M0078-240300-058-D03 UM0076 Homo sapiens cDNA
3395	12622	21753		3.37	3.0E-03 U34666.1	NT	Mus musculus alpha 1(XVII) collagen (COL18A1) gene, exon 1 and 2
3405	12631			7.36	3.0E-03 Y12560.1	NT	C.elegans samdc gene
3855	13170	22285		7.39	3.0E-03 AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSC01 5'
3855	13170	22286		7.39	3.0E-03 AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSC01 5'
4014	13226	22327		1.73	3.0E-03 AI792278.1	EST_HUMAN	ph04f99.y5 Geester Wilms tumor Homo sapiens cDNA clone IMAGE:1155889 5'

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4132	133338		1.01	3.0E-03	Z32521.1	NT	S.cerevisiae (cv. Halo) mRNA for triosephosphate isomerase
4389	13580	226982	2.97	3.0E-03	AJ011432.1	NT	Rattus norvegicus grifin gene
4455	13653		0.71	3.0E-03	BE48739.1	EST_HUMAN	htsg98.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4518	13714	22808	3.35	3.0E-03	AJ58141.1	EST_HUMAN	xu8.P10.H3 connexin Homo sapiens cDNA 3'
4850	14039	23132	2.54	3.0E-03	AJ732754.1	EST_HUMAN	eb18e08.x5 Strategene lung (#897210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element;
4870	14058	23152	8.15	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5148	14327		0.68	3.0E-03	BF204380.1	EST_HUMAN	601686843F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106960 5'
5307	14538	23543	3.67	3.0E-03	8922498	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5902	15118	24530	9.51	3.0E-03	AA468701.1	EST_HUMAN	aa1310.11 Scareas_NhhNPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
6300	15481	24925	3.2	3.0E-03	AB021758.1	NT	Oryza sativa gene for bZIP protein complete cds
6763	15958		10.15	3.0E-03	AW613774.1	EST_HUMAN	hr80f10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.L1 L1 repetitive element;
6782	15977	25635	3.28	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
6793	15988	25449	9.71	3.0E-03	AJ016731.1	EST_HUMAN	0x03d12.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_maf1 HISTONE H2B.2 (HUMAN);
6994	16172		3.95	3.0E-03	IP08872	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
7121	16298	25780	5.83	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7425	16635		2.75	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HE4B), mRNA
7738	15481	24925	1.72	3.0E-03	AB021758.1	NT	Oryza sativa gene for bZIP protein, complete cds
7918	17133	26683	2.14	3.0E-03	AF089222.1	NT	Pneumocystis carinii kexin-like serine endopeptidase mRNA, partial cds
7983	16418	26905	2.09	3.0E-03	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
8015	17154	26889	3.06	3.0E-03	AF0894481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8015	17154	26890	3.06	3.0E-03	AF0894481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
8088	17223	26759	1.74	3.0E-03	P11369	SWISSPROT	RETRORVIRUS-RELATED POLYPOXYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8249	17377		1.63	3.0E-03	AW294812.1	EST_HUMAN	Ui-H-B12-ah1-4-06-Q-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726842 3'
8330	18153		3.61	3.0E-03	AI525056.1	EST_HUMAN	promtne-E.007.r bifunctional Homo sapiens cDNA 5'
8367	17454	28582	1.75	3.0E-03	AA893154.1	EST_HUMAN	ct7710.s1 Scareas_total_fetus_Nb2HF8_SW Homo sapiens cDNA clone IMAGE:1622778 3' similar to contains L1.L3 MER26 repetitive element;
8424	18286		1.79	3.0E-03	AB009688.1	NT	Homo sapiens gene for CMP-N-acetylnumeraminic acid hydroxylase, partial cds
8615	17612	239663	1.7	3.0E-03	AJ298282.1	NT	Rattus norvegicus mRNA for cameron38 (cx38 gene)
921	9772	18896	0.69	2.0E-03	CO4652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
921	9772	18897	0.69	2.0E-03	CO4652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
795	11978		11.88	2.0E-03	T70874.1	EST_HUMAN	yd15n03.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1371	10585	19752	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1374	10588	19754	1.38	2.0E-03	AA661605.1	EST_HUMAN	nu86f1.61 NCI_CGAP_Avir1 Homo sapiens cDNA clone IMAGE:1217593
1382	10586	19762	13.61	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
1481	10684	19869	0.98	2.0E-03	P48609	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1505	10718	19839	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLD) mRNA
1505	10718	19890	1.65	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLD) mRNA
1571	10784		6.81	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1741	10853	20136	1.09	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares, total_fetus_Nb2hf8_8w Homo sapiens cDNA clone IMAGE:789114 5'
1864	11168	20373	1.15	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2214	11411	20635	0.91	2.0E-03	AL183302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2643	11731		5.05	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-0-1-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3394	12621	21752	4.7	2.0E-03	AA450138.1	EST_HUMAN	zx42a10.r1 Soares, total_fetus_Nb2hf8_8w Homo sapiens cDNA clone IMAGE:789114 5'
3401	12627	21758	0.79	2.0E-03	BF568955.1	EST_HUMAN	60218396011 NIH MGCG 42 Homo sapiens cDNA clone IMAGE:4300070 3'
3647	12888	21885	5.81	2.0E-03	X87344.1	NT	H_sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING6, 9, 13 and 14 genes
4091	13289	22398	2.3	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4204	13407		9.81	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4405	13605		0.94	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4419	13619		1.04	2.0E-03	AW297380.1	EST_HUMAN	U1-H-BW0-air-g-03-0-U.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4543	13738	22836	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster short sighted class 2 (sts) mRNA, complete cds
4543	13738	22837	2.05	2.0E-03	L42512.1	NT	Drosophila melanogaster short sighted class 2 (sts) mRNA, complete cds
4721	13912		1.94	2.0E-03	R87773.1	EST_HUMAN	yo5602.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4751	13942	23044	1.3	2.0E-03	AA809468.1	EST_HUMAN	cl1405.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:15223457 3'
5044	14228	23310	0.8	2.0E-03	AF003528.1	NT	Homo sapiens X-linked arachnodactyly dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5071	14251	23334	0.71	2.0E-03	P45969	SWISSPROT	HYPOTHETICAL 37.4 KD PROTEIN TGA5.9 IN CHROMOSOME III
5245	14418		1.1	2.0E-03	BE019892.1	EST_HUMAN	bb28h05.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2961249 3'
5503	18057	24091	1.91	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0683 protein, partial cds
5541	14785	24131	2.05	2.0E-03	U63711.1	NT	Xenopus laevis xerfilin mRNA, complete cds
5712	14931	24256	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B

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 Table 4
 Single Event Phases Expressed |

Probe Seq ID No:	Exon Seq ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5712	14831	24326	3.67	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
5809	15028	24426	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2)(CA-RP II)(CA-XI)
5809	15026	24427	2.05	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2)(CA-RP II)(CA-XI)
5811	15028	24428	7.05	2.0E-03	BF308107.1	EST_HUMAN	601887434F1 NIH MGCo_17 Homo sapiens cDNA clone IMAGE:4121408 5'
5828	15043	24447	2.07	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS7) (ADAM-TS7)
5833	15050	24458	1.68	2.0E-03	X94451.1	NT	Lescutinent mRNA for lysy-tRNA synthetase (LysRS)
6068	14515	23573	1.78	2.0E-03	AB038522.1	NT	Caenorhabditis elegans mRNA for selectin LEC-11, complete cds
6117	15230	24849	2.9	2.0E-03	BE067886.1	EST_HUMAN	CM4-BT0368-061289-054-001 BT0368 Homo sapiens cDNA
6481	15878	25148	5.15	2.0E-03	AW592004.1	EST_HUMAN	hf37906.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60978
6534	15730	25183	7.85	2.0E-03	N20287.1	EST_HUMAN	Q60978 JERKY.; y42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2_L1 repetitive element;
6534	15730	25194	7.85	2.0E-03	N20287.1	EST_HUMAN	y42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:284442 3' similar to contains L1.b2_L1 repetitive element;
6841	16085	25553	3.18	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXBRAUCHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (J1) (MOTENDINICUS ANTIGEN) (GLIOMA-ASSOCIATED EXTRACELLULAR MATRIX ANTIGEN) (GP 150-255) (TENASCIN-C) (TN-C)
7088	16265		5.2	2.0E-03	AA251378.1	EST_HUMAN	z510b06.s1 NCI CGAP_GCB_1 Homo sapiens cDNA clone IMAGE:834754 3'
7585	16780		3.24	2.0E-03	MB6524.1	NT	Human dystrophin gene
8022	15522	24970	2.31	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8076	17211		2.26	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-004 BT0333 Homo sapiens cDNA
8083	17218	26753	15.54	2.0E-03	Z11740.1	NT	H.sapiens variable number tandem repeat (VNTR) locus DNA
8313	17417		2.5	2.0E-03	A1825745.1	EST_HUMAN	y65n03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW.VATG_MANSE Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G;
8329	17430	26937	2.71	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
8353	17446	26940	1.28	2.0E-03	AI084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688634 3' similar to P97535_P97535_PS_P1A1 PRECURSOR.;
8376	14500		4.25	2.0E-03	AJ245167.1	NT	Camellia sinensis L. cyp19 gene for immunoglobulin heavy chain variable region
8597	17326		2.72	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCGX015 5'
8695	17663	23947	1.54	2.0E-03	Y05088.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
8813	17733		1.56	2.0E-03	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8870	18181		1.24	2.0E-03	AI375037.1	EST_HUMAN	tae6102.x1 Soares_total_fetus_Nb2F8_9w Homo sapiens cDNA clone IMAGE:2049051 3' similar to contains Alu repetitive element;

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8995	17858			1.34	2.0E-03 AF128758.1	NT	Homo sapiens NISH55 gene, partial cds; and CLIC1, DDAH, G6b, G8c, G8d, G8e, G8f, BATS, G5b, CSKB2, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9172	18131			2.37	2.0E-03 AV697986.1	EST_HUMAN	AV697986 GK3c Homo sapiens cDNA clone GKCGX05 5'
445	9699	18836	1.13	1.0E-03	HR8471.1	EST_HUMAN	y88c08_x1 Soares_pineal gland N3HPG Homo sapiens cDNA clone IMAGE:232345'
839	10076	19235	2.02	1.0E-03	A1720283.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE;
839	10078	19236	2.02	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE;
1103	10327	18477	2.73	1.0E-03	A1865788.1	EST_HUMAN	wk865e06_x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1123	10347	18498	1.49	1.0E-03	A1854572.1	EST_HUMAN	wk83e10_x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
1174	10395	18547	3.1	1.0E-03	A1692616.1	EST_HUMAN	wd85e01_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
1897	11200	20411	4.06	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN (HMWMI)
2122	11321	20539	7.75	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2837	12175	21308	1.43	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1291 protein, partial cds
3154	12389	21521	1.49	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONIC DEHYDRATASE VI) (CA-VI) (SECRETED)
3154	12389	21522	1.49	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3221	12504	21635	0.84	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONIC DEHYDRATASE VI) (CA-VI) (SECRETED)
3646	12867		1.34	1.0E-03	AB044400.1	NT	CARBONIC ANHYDRASE (SALIVARY CARBONIC ANHYDRASE)
3908	13124	22242	0.63	1.0E-03	249849.1	NT	S.cerevisiae chromosome X reading frame ORF YR149w
4427	13627	22721	3.45	1.0E-03	BEE839162.1	EST_HUMAN	RC1-TN0128-16080-021-901 TN0128 Homo sapiens cDNA LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4471	13869	22760	5.28	1.0E-03	BE246536.1	EST_HUMAN	TCBA1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Bay1or-HGSC project=TCBA_Homo sapiens cDNA clone TCBA_P4909
4840	14029	23121	2.09	1.0E-03	A073485.1	EST_HUMAN	z344f01_x1 Soares_tes1 NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4840	14029	23122	2.09	1.0E-03	A073485.1	EST_HUMAN	ow45c04_x1 Soares_tes1 NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4841	14030		4.02	1.0E-03	BE154087.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5107	14287	23372	7.76	1.0E-03	O46409	SWISSPROT	AFOLIPROTEIN A-IV PRECURSOR (APO-AIV)
5336	14587	23641	1.91	1.0E-03	AA2290851.1	EST_HUMAN	zs44f01_x1 NCI CGCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5336	14625	23738	3.07	1.0E-03	AJ006345.1	NT	Homo sapiens KVLCQT1 gene
5422	14649	23183	1.89	1.0E-03	K03332.1	NT	Epstein-Barr virus (K876 isolate) U2-R2 domain encoding nuclear protein EBNA2, complete cds
5422	14649	23784	1.99	1.0E-03	K0332.1	NT	Epstein-Barr virus (K876 isolate) U2-R2 domain encoding nuclear protein EBNA2, complete cds

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5479	14706	24050	1.85	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5667	14839		2.54	1.0E-03	X07699.1	NT	Mouse nucleolin gene
5682	14912	24306	3.07	1.0E-03	BE963839.2	EST_HUMAN	60165519R1 NIH_M/GC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
5750	14969		9.14	1.0E-03	11526178	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6141	15326	24760	2.83	1.0E-03	D16826.1	NT	Human gene for fourth somatosatin receptor subtype
6352	15532	24984	1.65	1.0E-03	U52111.2	NT	Homo sapiens Y28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), C22+Calmodulin-dependent protein kinase (CAMKII), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
6378	15559	25015	3.58	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
6442	15639	25106	8.04	1.0E-03	AJ251973.1	NT	Homo sapiens partial stearin-1 gene
6541	15731	25199	2.89	1.0E-03	AF153980.1	NT	Homo sapiens exocystase-like protein 1 (EXT1L) gene, exons 2 through 11, and complete cds
6813	16098	25470	3	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
6813	16098	25471	3	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
6866	16144	25613	2.52	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
6868	16144	25614	2.52	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
7258	16478	25969	1.89	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-809 CT0279 Homo sapiens cDNA
7258	16478	25970	1.89	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-809 CT0279 Homo sapiens cDNA
7338	16552	26041	3.07	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220303-130-803 HT10543 Homo sapiens cDNA
7400	16613		3.38	1.0E-03	AI583847.1	EST_HUMAN	PVA1 GENE.
7468	16878	26159	1.84	1.0E-03	AW237482.1	EST_HUMAN	xm72012.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2589751 3'
7717	16916		4.02	1.0E-03	AV756949.1	EST_HUMAN	AV756949 MDS Homo sapiens cDNA clone IMAGE:2589751 5'
8507	17413	26935	5.13	1.0E-03	BE894488.1	EST_HUMAN	60143087F1 NIH_M/GC_72 Homo sapiens cDNA clone IMAGE:3916524 5'
8778	17703	23958	1.55	1.0E-03	8507208	NT	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
8803	18308		3.08	1.0E-03	AI347355.1	EST_HUMAN	tc05hn11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2083013 3' similar to contains Alu repetitive element;
8921	18330	23602	4.03	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_M/GC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5225	14389	23482	1.31	9.0E-04	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
5327	14751		1.68	9.0E-04	PR06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
4161	13365		5.68	8.0E-04	PR08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4776	13985	23068	2.33	8.0E-04	U28195.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
7705	16904		2.61	8.0E-04	AJ777084.1	EST_HUMAN	z24c10.s1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377874 3'
7843	17035		2.96	8.0E-04	AI571098.1	EST_HUMAN	In85a68.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
1785	11004	20160	1.5	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end

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Table 4

Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Host Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2363	11556	20778	0.99	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2874	11858	21071	1.13	7.0E-04	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3248	12481	21613	1.3	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
5880	15097		2.17	7.0E-04	A1769331.1	EST_HUMAN	wg36f09_x1 Scores_Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTF3 (FTF3) genes, complete cds
8100	17234		3.32	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTF3 (FTF3) genes, complete cds
8120	17254	28795	2.18	7.0E-04	Z40561.1	EST_HUMAN	CM-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA clone c-28a07 3'
8847	17755		3.68	7.0E-04	B077941.1	EST_HUMAN	CM-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA clone
9098	17912		3.4	7.0E-04	R17936.1	EST_HUMAN	CM-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA clone IMAGE:322898 5'
9125	17938		3.87	7.0E-04	6005855	NT	Homo sapiens Rat-derived POU-domain factor-1 (RPF-1), mRNA yg13cc68_r1 Scores_Infant brain [NIB] Homo sapiens cDNA clone IMAGE:4149287 5'
2656	11838		1.75	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI CGAP_Bim84_Homo sapiens cDNA clone IMAGE:4149287 5'
3936	13152	22268	1.76	6.0E-04	AB62525.1	EST_HUMAN	wf15a11.x1 NCI CGAP_Kid12_Homo sapiens cDNA clone IMAGE:2402876 3'
4065	13275	22375	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4085	13275	22376	1.44	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4166	13370	22469	3.95	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKCR8) gene, complete cds
7066	16243		5.71	6.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 S88 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
7101	16278	25758	2.59	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-25040-012-h11 BN0120 Homo sapiens cDNA clone
8019	17158	28694	2.73	6.0E-04	AJ228042.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8101	17235	26771	3.28	6.0E-04	AW013847.1	EST_HUMAN	Ui-H-Elo-ab-e-09-0-U1_s1 NCI CGAP_Sub1_Homo sapiens cDNA clone IMAGE:2708825 3'
8152	17284		2.49	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK_B) (NDK_KINASE_B) (NM23-M2) (P18)
8498	18208		2.39	6.0E-04	AV380519.1	EST_HUMAN	RC1-H-T269-26119-012-d08 HT0269 Homo sapiens cDNA
8597	8903	18029	7.85	5.0E-04	OJ0341	SWISSPROT	HYPOTHETICAL_28.3_KD PROTEIN (ORF92)
1493	10708		1.5	5.0E-04	AW851844.1	EST_HUMAN	QVO-C70225-021099-030-a07 CT0225 Homo sapiens cDNA clone
3391	12818		1.57	5.0E-04	AA548631.1	EST_HUMAN	nk27e11.s1 NCI CGAP_Co11_Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
5429	14858	23794	2.85	5.0E-04	AF248054.1	NT	Bos taurus microtide calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6847	15163	24577	4.71	5.0E-04	AA155080.1	EST_HUMAN	z033b08_r1 Stratobene colon (#931204) Homo sapiens cDNA clone IMAGE:588663 5'
6248	15427	24867	12.76	5.0E-04	M23604.1	NT	Corolla gorilla involucrin gene medium allele, complete cds
6444	15641	25107	6.01	5.0E-04	AI188382.1	EST_HUMAN	qd13fb6_x1 Scores_placenta_8tc6weeks_2NbH8ic6W Homo sapiens cDNA clone IMAGE:1723619 3'
6968	16148	25617	5.62	5.0E-04	AW270938.1	EST_HUMAN	(HUMAN):contains Alu repetitive element; xs06e02_x1 NCI CGAP_Kid11_Homo sapiens cDNA clone IMAGE:2768868 3'
7649	16764		4.31	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 S88 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8203	14656	23794	12.77	5.0E-04	AF246054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
8428	18140		2.42	5.0E-04	AA568513.1	EST_HUMAN	n15h02_s1_NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:913875
679	8923	18054	1.37	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
857	10093	19255	1.36	4.0E-04	A1720263.1	EST_HUMAN	as7088_x1_Bartsleid colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
857	10093	19256	1.36	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE;
1481	10874	19847	2.48	4.0E-04	AW753556.1	EST_HUMAN	as7088_x1_Bartsleid colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2052	11253	20467	1.21	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-f01 CT0254 Homo sapiens cDNA
2103	11303		0.9	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2590	11776	20895	2.53	4.0E-04	O98615	SWISSPROT	DKFZ443D059_1r1434 (synonym: hts3) Homo sapiens cDNA clone DKFZ443D059 5'
3128	12383	21483	1.41	4.0E-04	AF281074.1	NT	SERINC2_SILK_GUM_PROTEIN 2
3335	12584	21702	0.61	4.0E-04	AV6988624.1	EST_HUMAN	Hom sapiens neuropeptidyl (NRP2) gene, complete cds, alternatively spliced
4314	13515	22603	3.3	4.0E-04	AA576331.1	EST_HUMAN	AV85861624 GKC Homo sapiens cDNA clone GKCFH07 5'
4314	13515	22609	3.3	4.0E-04	AA576331.1	EST_HUMAN	n10a10_s1_NCI_CGAP_Co1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:MM21121 T-CELL
4534	13730	22821	2.26	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5119	14298	23386	2.98	4.0E-04	BE5606650.1	EST_HUMAN	zn61cc08_s1_Strategic muscle 837209 Homo sapiens cDNA clone IMAGE:582670 3'
5190	14386		0.88	4.0E-04	BE178880.1	EST_HUMAN	PM4-HT0506-03040-001-h11 HT0506 Homo sapiens cDNA
6837	15832	25293	2.88	4.0E-04	N25507.1	EST_HUMAN	y43e12_r1 Scarce melanocyte 2NBM Homo sapiens cDNA clone IMAGE:264142 5'
8814	18112		1.78	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
8974	18085		1.81	4.0E-04	C05880	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)
159	9441	18574	3.52	3.0E-04	AL119426.1	EST_HUMAN	DKFZ761J221_1r1761 (synonym: hnmv2) Homo sapiens cDNA clone DKFZp761J221 5'
200	9480	18613	2.15	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
890	10125	19288	2.39	3.0E-04	U83981.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1807	11016	20209	1.27	3.0E-04	A1262100.1	EST_HUMAN	q228dd3_y1_NCI_CGAP_kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1821	11029		1.12	3.0E-04	A1399674.1	EST_HUMAN	lh23a02_x1_NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3279	12511	21641	3.59	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3941	13157	22274	3.38	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4033	13243		1.73	3.0E-04	AJ271735.1	NT	Homo sapiens Xg pseudoadenosine region, segment 1/2
4069	13279		1.92	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4831	14020		5.35	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0339-180200-007-912 HT0339 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor							
4903	14091	23194	0.85	3.0E-04	AW837723.1	EST_HUMAN	QV3-DT0045-221299-048-d09 DT0045 Homo sapiens cDNA Human BRCA1, Rho7 and vati genes, complete cds, and lpf35 gene, partial cds							
5289	14450	23528	1.22	3.0E-04	L78833.1	NT	Homo sapiens chromosome 21 segment HS21C081							
5732	14951	5.43	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C078								
6008	15256	24680	1.93	3.0E-04	AL163278.2	NT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)							
6546	15742	25203	6.87	3.0E-04	P226807	SWISSPROT	q124q05_s1 Soares testis cDNA clone 1391288 3' similar to gb:M36072 60S							
7202	16379	25860	7.45	3.0E-04	AA781201.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN); nc88d4.71 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L112 L1 repetitive element;							
8380	18348	23606	2.85	3.0E-04	AA228301.1	EST_HUMAN	Home sapiens mRNA for KIAA0749 protein, partial cds							
8770	18188	23758	2.87	3.0E-04	AB016292.1	NT	DKFZ547L185_r1 547 (synonym: fibr1) Home sapiens cDNA clone DKFZp547L185 5'							
9191	17979	2.55	3.0E-04	AL134483.1	EST_HUMAN	Home sapiens SCG10 like-protein, hecatase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFPP1) genes, complete cds								
179	9459	18591	1.76	2.0E-04	AF217798.1	NT	AU146707_HMBB11_Homo sapiens cDNA clone HEMBB1001253 3'							
485	9737	18870	3.52	2.0E-04	AU146707.1	EST_HUMAN	Human dystrophin gene							
917	10152	18312	10.84	2.0E-04	NR6524.1	NT	Human dystrophin gene							
917	10152	18313	10.64	2.0E-04	NR66524.1	NT	q98e11_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;							
1187	10408		4.9	2.0E-04	AI286021.1	EST_HUMAN	1184	10414	2.28	2.0E-04	AL163203.2	NT	Home sapiens chromosome 21 segment HS21C003	
1800	11009		1.44	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene							
2160	11348		1.37	2.0E-04	AA478980.1	EST_HUMAN	z139kb5_s1 Soares ovary tumor NbOTH_Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element;							
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1P, TCRBV15S1, TCRBV15S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV35S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S2; > em5Bc09_x1 Johnstons frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3'							
2539	11727	20944	2.71	2.0E-04	U68061.1	NT	5174736 NT	Home sapiens tubulin, beta, 4 (TUBB4) mRNA						
2844	12182	21315	1.02	2.0E-04	AI124529.1	EST_HUMAN	QV2-B10636-07050-194-007 B10636 Homo sapiens cDNA repetitive element;							
3308	12538	21672	0.74	2.0E-04	5174736	NT	Human germline T-cell receptor beta chain TCRBV28S1P, TCRBV28S1P, TCRBV15S1P, TCRBV15S1, TCRBV14S1, TCRBV35S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S2; > em5Bc09_x1 Johnstons frontal cortex Homo sapiens cDNA clone IMAGE:1639760 3'							
3414	12640	21769	2.01	2.0E-04	BE082317.1	EST_HUMAN	Y01e11.11 Soares pineal gland NSHPG_Homo sapiens cDNA clone IMAGE:232556 5'							
3890	13106	22224	0.7	2.0E-04	AW878441.1	EST_HUMAN	Y01e11.11 Soares pineal gland NSHPG_Homo sapiens cDNA clone IMAGE:232556 5'							
4125	13331		6.15	2.0E-04	U01028.1	NT	4872	13866	22867	1.32	2.0E-04	U98265.1	EST_HUMAN	Y01e11.11 Soares pineal gland NSHPG_Homo sapiens cDNA clone IMAGE:232556 5'
4872	13866	22868	1.32	2.0E-04	U98265.1	EST_HUMAN	4807	13996	1.61	2.0E-04	U09226.1	NT	Gallus gallus proteosome 28 kDa subunit homolog mRNA, complete cds	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5080	14270	23354	1.31	2.0E-04	AB037897.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5470	14696	24049	1.85	2.0E-04	AB680862.1	EST_HUMAN	lq03b11_x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:22077709 3'
6178	15360		2.39	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
6343	15524		13.77	2.0E-04	P08648	SWISSPROT	LIN-E-1 REVERSE TRANSCRIPTASE HOMOLOG
7428	16638	26131	6.33	2.0E-04	AV730373	HTF Homo sapiens cDNA clone HTFAAA01 5'	EST_HUMAN
7853	17043	26560	6.26	2.0E-04	AI440282.1	EST_HUMAN	t01f11_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:21402689 3' similar to contains Alu repetitive element;
7864	17143	26676	3.15	2.0E-04	AW136740.1	EST_HUMAN	UH-B11-adm-c-04-0-U1_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
8267	17394	26924	7.66	2.0E-04	AA320338.1	EST_HUMAN	EST22678 Adipose tissue, white II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
778	10015	19163	1.88	1.0E-04	H98646.1	EST_HUMAN	y26c9_s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262884 3' similar to contains L1M L1 repetitive element;
1082	10307	19453	2.39	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1122	10343	19493	3.89	1.0E-04	AW013847.1	EST_HUMAN	UH-B10-bab-e-09-0-U1_s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1122	10348	19497	3.89	1.0E-04	AW013847.1	EST_HUMAN	UH-B10-bab-e-09-0-U1_s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1340	10554		3.92	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1605	10819	19894	3.55	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoinositolglycanimidine synthase, and LAMP (LAMP) genes, complete cds
							Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoinositolglycanimidine synthase, and LAMP (LAMP) genes, complete cds
1605	10819	19995	3.55	1.0E-04	AF148805.1	NT	
1829	11037	20233	1.75	1.0E-04	AB048342.1	NT	Equis caballus DNA, chromosome 24q14, microsatellite TKY36
2648	11831	21044	0.91	1.0E-04	BE218833.1	EST_HUMAN	hw45cc8_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
2648	11831	21045	0.91	1.0E-04	BE218833.1	EST_HUMAN	hw45cc8_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176388 3'
3352	12485	21817	0.95	1.0E-04	Q82203	SWISSPROT	SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A6B)
3716	12936	22054	0.82	1.0E-04	AI440282.1	EST_HUMAN	t01f11_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:21402689 3' similar to contains Alu repetitive element;
4037	13247	22350	2.01	1.0E-04	M14042.1	NT	Mouse alpha 1 type-V collagen mRNA
4058	13269	22371	1.16	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLOBBD04 3'
4460	13658	22752	1.09	1.0E-04	P08547	SWISSPROT	LIN-E-1 REVERSE TRANSCRIPTASE HOMOLOG
6159	16342	24778	0.99	1.0E-04	AI281980.1	EST_HUMAN	q157d10_x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
6322	15342	24779	12.88	1.0E-04	AI251980.1	EST_HUMAN	q157d10_x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
6863	16053	25521	3.89	1.0E-04	AI806220.1	EST_HUMAN	mf76e08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7128	16305			5.3	1.0E-04 P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7881	17089			2.28	1.0E-04 M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8159	17291	28832	1.93	1.0E-04 AB032988.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds	
8189	17321	28884	1.97	1.0E-04 AW289061.1	EST_HUMAN	x148912.x1 Scores NFL-T GBC S1 Homo sapiens cDNA clone IMAGE:2816518 3'	
8214	17345	28884	1.65	1.0E-04 CO3686	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	
8214	17345	28885	1.85	1.0E-04 CO3686	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)	
8649	18158			1.5	1.0E-04 BE676389.1	EST_HUMAN	7129a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.i3 L1 repetitive element;
705	8947	19083	2.76	9.0E-05 AA718933.1	EST_HUMAN	sh145c11.s1 Scores_NHT Homo sapiens cDNA clone 1292468 3'	
6805	16062		2.6	9.0E-05 D85606.1	NT	Homo sapiens gene for cholecytokinin type-A receptor, complete cds	
7697	16898	26405	2.85	9.0E-05 AW073078.1	EST_HUMAN	xe34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.i2 L1 repetitive element;	
7794	16987	26501	1.84	9.0E-05 AI287878.1	EST_HUMAN	q123f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:19882435 3' similar to contains element MIR repetitive element;	
8139	14862	24247	4.58	9.0E-05 Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	
8604	18218					Homo sapiens MSH5 gene, partial cds, and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, ALF-1, 1C7, LST-1, LTb, TNF, and LTA genes, complete cds	
8331	10069	19224	3.78	9.0E-05 AF128756.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (grs2 gene)	
874	10110		1.8	8.0E-05 AJ251648.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (grs2 gene)	
4477	13675	22764	7.89	8.0E-05 AJ251646.1	NT	WY78ed1.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'	
7710	16909	26419	0.69	8.0E-05 AW044805.1	EST_HUMAN	Homo sapiens haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds	
9229	18201		2.66	8.0E-05 M69197.1	NT	Zs88K01.s1 NCI_CGAP_GCB1_Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;	
3552	9820	18747	2.43	8.0E-05 AA278933.1	EST_HUMAN	RC3-CT0208-222099-01-E04 CT0208 Homo sapiens cDNA	
3552	9820		7.28	7.0E-05 AW847445.1	EST_HUMAN	RC3-CT0208-222099-01-E04 CT0208 Homo sapiens cDNA	
574	9824	18943	1.33	7.0E-05 L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014	
574	9824	18944	1.33	7.0E-05 L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014	
1062	10288	19439	1.12	7.0E-05 Q22949	SWISSPROT	PROTABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)	
2678	11860	21074	4.06	7.0E-05 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
3122	12357	21488	5.35	7.0E-05 AB009080.1	NT	Dichotomium discoidatum gene for TRFA, complete cds	
36179	12890		0.97	7.0E-05 AI492413.1	EST_HUMAN	Ig73cc9.x1 Scores_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:2114416 3'	
4356	13568	22684	1.5	7.0E-05 AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4440	13640	22731	0.81	7.0E-05	U60580_1	NT	Cenorhabditis elegans Skip1p homolog mRNA, complete cds
4847	14134	23228	0.85	7.0E-05	9845300	NT	Rat cytomegalovirus Maasticht, complete genome
6936	16080	25550	5.65	7.0E-05	T07096_1	EST_HUMAN	EST04884 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBED60
7720	16919		6.81	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
1996	11199	20409	1.41	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXorf6), mRNA
1986	11199	20410	1.41	8.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXorf6), mRNA
2549	11737	20855	1.06	8.0E-05	A185524_1	EST_HUMAN	wb54hs08_x1 NC_CGAP_GCS Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA TOPOISOMERASE I (HUMAN)
2768	9829	19059	2.78	8.0E-05	AF053630_1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5622	14845	24225	3.42	8.0E-05	Q12980	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5622	14845	24226	3.42	8.0E-05	C12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6614	15810	25266	3.79	8.0E-05	AW896629_1	EST_HUMAN	PM4-ND050-31030-001-110 NN050 Homo sapiens cDNA
7334	16550	26040	4.35	8.0E-05	R75639_1	EST_HUMAN	y59e08_s1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Aliu repetitive element/contains LTR7 repetitive element;
8050	17188	28725	4.17	8.0E-05	AA044015_1	EST_HUMAN	2458f02_1.1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
8822	18189	23782	8.56	8.0E-05	AW890110_1	EST_HUMAN	MRO-NT0038-25040-001-009 NT0038 Homo sapiens cDNA
1407	10620	19784	59.84	5.0E-05	AW392086_1	EST_HUMAN	QV4-ST0234-241189-04-h11 ST0234 Homo sapiens cDNA
1831	11039		1.35	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55895), mRNA
3657	13172	22287	3.89	5.0E-05	AJ251884_1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5453	14879	23839	11.84	5.0E-05	X58865_1	NT	Human MLCK emb gene for embryonic myosin alkaline light chain, 3'UTR
5651	14874	24261	3.01	5.0E-05	AV655544	EST_HUMAN	AV655544 GLC Homo sapiens cDNA clone GLCDMA06 3'
8601	17775		3.78	5.0E-05	F49163	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
8879	17775		4.46	5.0E-05	F49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2759	9511		3.93	4.0E-05	U12821_1	NT	Human renin (REN) gene, 5' flanking region
4479	13677	22766	0.73	4.0E-05	F49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4479	13677	22767	0.73	4.0E-05	F49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4892	14080		0.95	4.0E-05	AF164488_1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5042	14226	23309	0.68	4.0E-05	AF212313_1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds
6923	16116		5.98	4.0E-05	AF202635_1	NT	Homo sapiens PP1200 mRNA, complete cds
7352	16568	26058	5.03	4.0E-05	AW627946_1	EST_HUMAN	h36c07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element;
8471	17524	24025	1.47	4.0E-05	AL163252_2	NT	Homo sapiens chromosome 21 segment HS21C052
8560	17581		1.54	4.0E-05	AW117580_1	EST_HUMAN	xd92e08_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
8238	18024		1.29	4.0E-05	AA417756_1	EST_HUMAN	Z01811_51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:748252 3'

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 Table 4
 Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
687	9830	19081	0.64	3.0E-05	A1248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
1066	10292	19443	0.87	3.0E-05	AW273851.1	EST_HUMAN	x124g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1139	10362	19511	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461463f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885142 5'
1139	10362	19512	2.89	3.0E-05	BF037898.1	EST_HUMAN	601461463f1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885142 5'
3261	12494		0.87	3.0E-05	A1288919.1	EST_HUMAN	q1b191.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:OD8632
4376	13578	22676	5.19	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4376	13578	22877	5.19	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4462	13650	22753	0.9	3.0E-05	AA388679.1	EST_HUMAN	EST78986 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4462	13650	22754	0.9	3.0E-05	AA388679.1	EST_HUMAN	EST78986 Placenta Homo sapiens cDNA similar to similar to p53-associated protein
4589	13783		0.89	3.0E-05	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4821	13815	22905	0.83	3.0E-05	AF149773.1	NT	Homo sapiens NOD protein (NOD1) gene, exons 1, 2, and 3
4855	9830	19081	0.83	3.0E-05	A1248061.1	EST_HUMAN	q164c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element;contains element KER repetitive element;
5471	14697	24050	1.83	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2pl), mRNA wg38R9.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
6881	16159		4.49	3.0E-05	A17686331.1	EST_HUMAN	zq16812.r1 Strategene hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
8484	17532		1.67	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region centromeric and contains Alu repetitive element;contains element L1 repetitive element;
2292	11487	20707	2.08	2.0E-05	A1286021.1	EST_HUMAN	q198e1.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element;
2545	11733	20950	4.57	2.0E-05	MT13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds.
2673	11855		6.59	2.0E-05	AA160562.1	EST_HUMAN	zq16812.r1 Strategene hNT neuron (#37233) Homo sapiens cDNA clone IMAGE:632734 5' similar to
3102	12338	21466	1.76	2.0E-05	BE068038.1	EST_HUMAN	contains Alu repetitive element;contains element L1 repetitive element;
3322	12551	21685	0.98	2.0E-05	AF184814.1	NT	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA Homo sapiens p47-phox (NCF1) gene, complete cds
3348	12576	21717	0.93	2.0E-05	X89211.1	NT	H_sapiens DNA for endogenous retroviral like element
3469	12694		0.69	2.0E-05	X95465.1	NT	S_cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3795	13013		1.31	2.0E-05	AL039107.1	EST_HUMAN	DKFZ256681064 r1 566 (synonym: lifikd2) Homo sapiens cDNA clone DKFZp5661064 5'
4802	14090	23183	0.77	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5287	14440	23513	32.31	2.0E-05	AA084052.1	EST_HUMAN	Zn18b10.s1 Stratagene neuroepithelium NT2R-ANL 937234 Homo sapiens cDNA clone IMAGE:547579 3'
5555	14778	24147	1.75	2.0E-05	AJ011712.1	NT	similar to contains L1 L1 repetitive element;
5944	15160	24573	2.4	2.0E-05	AT714330.1	EST_HUMAN	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6042	15210	24630	1.9	2.0E-05	Y08926.1	NT	nwo5612.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
							P.falciparum mRNA for AARP1 protein, partial

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Table 4
Single Exon Probes Expressed In HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6052	15220		9.31	2.0E-05	AI897025.1	EST_HUMAN	wu35f07.x1 Scores_Dickgrafera_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6142	15326	24761	2.26	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6142	15326	24762	2.26	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7223	18400	25885	5.08	2.0E-05	NA1751.1	EST_HUMAN	wu81ad6.r1 Scores_placenta_816 weeks_2NbHP816gW Homo sapiens cDNA clone IMAGE:259570 5'
7223	18400	25886	5.08	2.0E-05	NA1751.1	EST_HUMAN	wu81ad6.r1 Scores_placenta_816 weeks_2NbHP816gW Homo sapiens cDNA clone IMAGE:259570 5'
7238	15220		2.39	2.0E-05	AI897025.1	EST_HUMAN	wu35f07.x1 Scores_Dickgrafera_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7888	18423	25910	3.15	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT10582 Homo sapiens cDNA
8610	18125		5.29	2.0E-05	BE348228.1	EST_HUMAN	hw21ad3.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR;Q12832 Q12832 GLYCOPHORIN HEP2;
8723	18286		6.07	2.0E-05	AW074604.1	EST_HUMAN	x889a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:25738622 3' similar to contains L1 b3 L1 repetitive element;
8773	18110		1.82	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8935	17818	23928	1.39	2.0E-05	AI81513.1	EST_HUMAN	AU131513 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2655	12023	21050	1.24	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3829	12850	21989	1.97	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lame120 Suppressor of Hairless (Suf(H)) gene, partial cds
3801	13019		1.02	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3944	13160	22276	11.49	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4262	13465	22556	1.56	1.0E-05	AA431119.1	EST_HUMAN	wu69g04.r1 Scores_tests_NHT_Homo sapiens cDNA clone IMAGE:781494 5'
4867	14055	23149	1.7	1.0E-05	AW410134.1	EST_HUMAN	XJ49g11.x1 NCI_CGAP_Lj34.1 Homo sapiens cDNA clone IMAGE:23565648 3'
4986	141173	23263	0.67	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046 ns19gd2.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element;
6116	15229	24648	2.6	1.0E-05	AA641846.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6118	15302	24734	12.58	1.0E-05	4505644	NT	Homo sapiens chromosome 21 segment HS21C027
6750	15945		3.79	1.0E-05	AL163227.2	NT	z35h12.s1 Scores_Total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:L02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
6789	15984	25444	2.49	1.0E-05	AA452578.1	EST_HUMAN	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6851	16040	25504	15.7	1.0E-05	AA236110.1	EST_HUMAN	z505e11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE_684332 5' similar to contains Alu repetitive element/contains element TAR1 repetitive element;
7493	16700	26185	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7493	16700	28183	2.48	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
26332	11815	21034	5.6	9.0E-06	AI583811.1	EST_HUMAN	tt73ae03.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE_2246386 3'
3081	12297	21421	5.75	9.0E-06	AI218983.1	EST_HUMAN	gg11b08.x1 Soares_placenta_8to9weeks_2NbHf8toW Homo sapiens cDNA clone IMAGE_1759191 3'
3598	12809		3.56	9.0E-06	MB1755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
56117	14840	24218	2.46	9.0E-06	L23416.1	NT	Human sapiens differentiation antigen CD20 gene, exons 5, 6
64048	15587	25046	11.37	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE_1656912 3' similar to contains Alu repetitive element;
68333	160271	25493	4.11	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
75112	16717	28206	3.57	9.0E-06	Q10364	SWISSPROT	RC3-C70283-20119-01-111 CT0283 Homo sapiens cDNA
2495	12017	20902	2.21	8.0E-06	AW362539.1	EST_HUMAN	ab90f0.31 Stratego lung (#837210) Homo sapiens cDNA clone IMAGE_854251 3' similar to contains MER20.11 MER20 repetitive element;
886	10217		2.15	7.0E-06	AA668728.1	EST_HUMAN	Home sapiens KIAA0555 gene product (KIAA0555), mRNA
1440	10654	18828	2.53	7.0E-06	7682177 NT	NT	qw18g09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE_1991286 3' similar to contains Alu repetitive element;
2825	12084		5.04	7.0E-06	A1368262.1	EST_HUMAN	EST9205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
35338	12761		0.76	7.0E-06	AA385542.1	EST_HUMAN	EST9205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
55333	14757		5.93	7.0E-06	AV883141.1	EST_HUMAN	CV2-O70082-25040-173-h01 OT70082 Homo sapiens cDNA
8333	18321	23597	2.35	7.0E-06	BF215972.1	EST_HUMAN	6018815922f1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE_4083972 5'
2898	12108	21235	1.48	6.0E-06	BE069189.1	EST_HUMAN	QV3-B70379-010530-105-d11 BT0379 Homo sapiens cDNA
4774	12130	21265	2.05	6.0E-06	QD1456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4771	13980	23081	2.03	6.0E-06	AI040098.1	EST_HUMAN	ox80e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE_1655738 3' similar to contains MER8.12 MER8 repetitive element;
70725	16202		2.62	6.0E-06	AW801912.1	EST_HUMAN	IL5-UJM0070-110400-063-902 UM0070 Homo sapiens cDNA
9220	17899	23867	2.28	6.0E-06	11418157 NT	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
5694	14914	24308	4.05	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Table 4

Single Exon Probes Expressed In HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	150222	24423	1.98	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b and putative M8604 Met protein (M8604 Met) gene, complete cds
7113	162920	25771	10.33	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9104	17926	23878	3.8	5.0E-06	A1085046.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu
663	98989	19024	6.68	4.0E-06	R16267.1	EST_HUMAN	ye48c03.11 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:25890574 3' similar to contains Alu
856	10092	19254	11.86	4.0E-06	AW103354.1	EST_HUMAN	repetitive element:contains element L1 repetitive element;
1342	10558	19721	4.4	4.0E-06	A1334928.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Eso2_Homo sapiens cDNA clone IMAGE:20561683'
1342	10558	19722	4.4	4.0E-06	A1334928.1	EST_HUMAN	tb3360B_x1 NCI_CGAP_HSC2_Homo sapiens cDNA clone IMAGE:20561683'
1469	10882	19858	5.73	4.0E-06	BF365612.1	EST_HUMAN	tb3360B_x1 NCI_CGAP_HSC2_Homo sapiens cDNA clone IMAGE:20561683'
2230	11426	20652	1.39	4.0E-06	AW105401.1	EST_HUMAN	QV2-NT0046-200600-250-h07 NT0046 Homo sapiens cDNA
3028	12264	21392	1	4.0E-06	AF198349.1	NT	UH-B10-sat-1-05-0-J1.s1 NCI_CGAP_Sub1_Homo sapiens cDNA clone IMAGE:2710425 3'
3872	13088	22204	1.34	4.0E-06	AW848295.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4821	14010	23108	1.81	4.0E-06	A188639.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
6716	15911	25369	2.61	4.0E-06	AF009650.1	NT	w94610_x1 NCI_CGAP_Bm25_Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
7985	16420	25907	4.04	4.0E-06	AB007855.1	NT	Hom sapiens T cell receptor beta locus, TCRBV12S2 region
2129	11328	20546	1.11	3.0E-06	AA700562.1	EST_HUMAN	Hom sapiens mRNA, chromosome 1 specific transcript KIAA0486
2129	11328	20547	1.11	3.0E-06	AA700562.1	EST_HUMAN	z34b08.s1 Soares_fetal_liver_spleen_1NFELs_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to
2232	11427	2.13	3.0E-06	AF202635.1	NT	z34b08.s1 Soares_fetal_liver_spleen_1NFELs_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to	
2872	12110	21238	1.04	3.0E-06	AA8868218.1	EST_HUMAN	LTR1 repetitive element;
3232	12466		2.55	3.0E-06	AB57779.1	EST_HUMAN	ak48g11.11 Soares_fetal_liver_spleen_1NFELs_S1 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains L1.L1 repetitive element;
3768	12984	22089	1.35	3.0E-06	BE047094.1	EST_HUMAN	W12265_x1 NCI_CGAP_U11_Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:OB0734_OB0734
3768	12984	22100	1.35	3.0E-06	BE047094.1	EST_HUMAN	L1E-LIKE PROTEIN:contains L1.L2_L1 repetitive element;
4860	13754	22852	3.87	3.0E-06	X54816.1	NT	hq84d12_x1 NCI_CGAP_HN13_Homo sapiens cDNA clone IMAGE:3124151 3'
6177	16359		2.52	3.0E-06	PF08548	SWISSPROT	hq64d12_x1 NCI_CGAP_HN13_Homo sapiens cDNA clone IMAGE:3124151 3'
8781	17710		7.4	3.0E-06	AW385262.1	EST_HUMAN	Homo sapiens gene for alpha-1-microglobulin-lipoprotein, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
207	9487		2.17	2.0E-06	PF54366	SWISSPROT	RC0-LT0001-261199-011-A03 LT0001 Homo sapiens cDNA
							HOMEBOX PROTEIN GOOSECOID

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Host Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1549	10763		4.53	2.0E-06	P21414	SWISSPROT	POLYPOPTROPEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
2344	11537	20761	2	2.0E-06	A1672138.1	EST_HUMAN	wg04633.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1 MER30 repetitive element;
2429	11620	20841	1.48	2.0E-06	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2532	11720	20837	1.7	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3492	12716	21852	1.07	2.0E-06	AV657555 GLC	Homo sapiens cDNA clone GLCFD805 3'	Homo sapiens cDNA clone AV657555 GLC
3744	12864	22079	1.19	2.0E-06	AA173518.1	EST_HUMAN	#02605.r1 Stratagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:595222 5'
3752	12971	22086	0.62	2.0E-06	AB450215.1	EST_HUMAN	U1H-B12-akv-g-05-U1.51 NCL_CGAP_Sub5 IMAGE:273676 3'
3758	12977	22092	1.68	2.0E-06	AB030898.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5945	15082	24470	5.38	2.0E-06	AB119424.1	EST_HUMAN	wi80504.x1 NCL_CGAP_Lyn12 Homo sapiens cDNA clone IMAGE:2410063 3'
8883	18322	23598	1.53	2.0E-06	P23249	SWISSPROT	PROTEIN MOV-10
8837	17747		2.74	2.0E-06	BE328232.1	EST_HUMAN	hs82f022.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144698 3' similar to contains L1.12 L1 repetitive element;
35	9331	18436	2.01	1.0E-06	OT68082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HGH-1 AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
663	9909	19038	1.28	1.0E-06	AF084384.1	NT	Mus musculus D8Mm5e protein (D8Mm5e) mRNA, complete cds
1452	10685	19839	1.48	1.0E-06	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1510	10724	18896	1.14	1.0E-06	AL163278.2	NT	z06812.s1 Severe_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
1552	10768	19839	0.95	1.0E-06	AA034141.1	EST_HUMAN	contains Alu repetitive element; z06812.s1 Severe_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to
1552	10768	19940	0.95	1.0E-06	AA034141.1	EST_HUMAN	contains Alu repetitive element;
1563	10777		1.12	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1863	11167	20371	10.85	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1863	11167	20372	10.85	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4263	13585	22860	13.16	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5286	14439	23512	2.15	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5288	14459		0.61	1.0E-06	U61287.1	NT	Human progesterone receptor (PGR) gene, 5' flanking region
5320	14552	23622	5.34	1.0E-06	BF335015.1	EST_HUMAN	MR1-B10800-03070-002-c06 B10800 Homo sapiens cDNA
6028	15226	24659	5.56	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHAI/ALPHA-E CHAIN PRECURSOR
6985	16163	25634	2.58	1.0E-06	U82888.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6985	16163	25635	2.58	1.0E-06	U82888.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	16189		4.28	1.0E-06	AA449257.1	EST_HUMAN	2044111_s1_Scares_total_setus_Nb2HF8_Bw Homo sapiens cDNA clone IMAGE:785483 3' similar to gb:D26120 RIBONUCLEASE_PANCREATIC PRECURSOR (HUMAN);
6158	17280		5.02	1.0E-06	AW890941.1	EST_HUMAN	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
8721	17674	23949	3.45	1.0E-06	L79810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8824	11167	20371	1.88	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
8824	11167	20372	1.86	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
365	8632	18764	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glycopin 3 (GPC3) gene, partial cds and flanking repeat regions
365	9832	18765	2.24	9.0E-07	AF003528.1	NT	Homo sapiens glycopin 3 (GPC3) gene, partial cds and flanking repeat regions
5223	14391		1.4	9.0E-07	AW971932.1	EST_HUMAN	EST384021 MAGE1 resequences, MAG1 Homo sapiens cDNA
7789	16992	26505	2.85	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
4781	13970	23072	4.52	8.0E-07	A288598.1	EST_HUMAN	q182g07_x1_Scares_NhHMPU_S1_Homo sapiens cDNA clone IMAGE:1878876 3'
4781	13970	23073	4.52	8.0E-07	A288598.1	EST_HUMAN	q182g07_x1_Scares_NhHMPU_S1_Homo sapiens cDNA clone IMAGE:1878876 3'
5608	14832		8.53	8.0E-07	PF21414	SWISSPROT	POLYPOPTERIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
6865	15662		14.81	8.0E-07	AF135418.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8142	17274		8.94	8.0E-07	T07770.1	EST_HUMAN	EST08660 Fetal brain Strategene (cat#336208) Homo sapiens cDNA clone HFEBN89
8316	17420		5.59	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1877	11084	20274	2.84	8.0E-07	AW855558.1	EST_HUMAN	CM3-CT0277-221098-024-e11 C70277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin-X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes;?
2455	11646	20867	2.48	8.0E-07	AF019413.1	NT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
3949	13165		2.04	6.0E-07	PF14179	SWISSPROT	HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
8578	18267		2.08	6.0E-07	AW903222.1	EST_HUMAN	CM4-NN1028-28030-0121-h12 NN1028 Homo sapiens cDNA
331	9801		1.48	5.0E-07	AB311893.1	EST_HUMAN	wh64f10_x1_NCI_CGAP_Kid11 Homo sapiens cDNA 5' end
1084	10280		2.65	5.0E-07	AA380830.1	EST_HUMAN	EST8815 Supt cells Homo sapiens cDNA 5' end
2897	12233		0.8	5.0E-07	AB311893.1	EST_HUMAN	wh64f10_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4647	13841	22831	1.28	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6230	15411	24852	19.2	5.0E-07	AW070885.1	EST_HUMAN	x81e02_x1_NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:25688362 3' similar to gb:X15341 CYTOCHROME C OXIDASE POLYPEPTIDE VI-LIVER (HUMAN);
7183	16360	25839	5.84	5.0E-07	AI908587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
8048	17184	26723	4.83	5.0E-07	PF1087	SWISSPROT	COLLAGEN ALPH1(1) CHAIN PRECURSOR
8110	17244		2.42	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9013	18167		2.19	5.0E-07	AW862537.1	EST_HUMAN	QV0-C70383-210400-204-b12 CT0383 Homo sapiens cDNA
3976	13190	22289	1.78	4.0E-07	AW0098602.1	EST_HUMAN	ws84h05_x1_NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504697 3'
6798	15681	25441	3.15	4.0E-07	AW419134.1	EST_HUMAN	Xy48g11_x1_NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7511	16716	28204	4.29	4.0E-07	AJ765528.1	EST_HUMAN	wi81b08_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:23989703'3'
7511	16716	28205	4.29	4.0E-07	AJ765528.1	EST_HUMAN	wi81b08_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:23989703'3'
7774	16969		2.08	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0053-030300-003-e12 BN0083 Homo sapiens cDNA
447	9701	18837	4.33	3.0E-07	U19719.1	NT	Human microfibril-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
990	9838	18957	2.19	3.0E-07	AJ271735.1	NT	Homo sapiens Xr pseudautosomal region; segment 1/2
1381	10595	19761	2.22	3.0E-07	MF89149.1	NT	Human polymorphic microsatellite DNA
1603	10817		3.12	3.0E-07	MF4857.1	NT	Human IgK subgroup, germline gene, exons 1 and 2, V-region 018 allele
2013	11215		3.54	3.0E-07	AA526763.1	EST_HUMAN	nt5699_s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1,13 L1 repetitive element;
2252	11447	20668	1.24	3.0E-07	MF89149.1	NT	Human polymorphic microsatellite DNA
2432	11623	20845	11.78	3.0E-07	BE005077.1	EST_HUMAN	MFO-EFN0115-020300-001-111 BN0115 Homo sapiens cDNA
2432	11623	20846	11.76	3.0E-07	BE005077.1	EST_HUMAN	MFO-EFN0115-020300-001-111 BN0115 Homo sapiens cDNA
3000	12236	21368	1.23	3.0E-07	MF84704.1	EST_HUMAN	YD50112_11 Scares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:111695'5'
3123	12358	21487	1.82	3.0E-07	MF8739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GLUT1-TRIM1 INTERGENIC REGION PRECURSOR
4738	13929	23033	8.7	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCCD013'
4774	13963	23065	0.78	3.0E-07	AJ787238.1	EST_HUMAN	W688b12_X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23479873'
5086	14276	22359	1.39	3.0E-07	T57890.1	EST_HUMAN	yc14h09_s1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:80705'3' similar to similar to
5098	14276	23360	1.39	3.0E-07	T57890.1	EST_HUMAN	gb:M629882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5241	14415	23495	1.06	3.0E-07	BE072335.1	EST_HUMAN	yc14h09_s1 Stratogene lung (#837210) Homo sapiens cDNA clone IMAGE:80705'3' similar to similar to
5520	14745	24113	11.02	3.0E-07	MF78950.1	EST_HUMAN	gb:M629882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5595	15180		4.7	3.0E-07	AA815175.1	EST_HUMAN	QV3-BT0537-221289-048-a07 BT0537 Homo sapiens cDNA
6293	15474	24916	3.2	3.0E-07	AW797158.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6293	18026		4.28	3.0E-07	AL132352.1	NT	gb:M629882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
30	9326	18430	2.76	2.0E-07	AF262888.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
'157	9439	18572	7.69	2.0E-07	MF7569.1	NT	Homo sapiens TRIF2-interacting tetromeric RAP1 protein (RAP1) mRNA, complete cds
'157	9439	18573	7.69	2.0E-07	MF7569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
'186	9465	18586	76.92	2.0E-07	MF8849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
'756	9997	19142	2.28	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
'756	9997	19143	2.28	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]								
768	10008		1.13	2.0E-07	P11369		SWISSPROT	
951	10184	18340	3.38	2.0E-07	AA223260.1		EST_HUMAN	zr08b7_s1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:850869 3' similar to gBL31880 GLYCOPHORIN A PRECURSOR (HUMAN); contains Ali repetitive element; ye15g04_s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80780 3' similar to contains L1 repetitive element;
952	10185	19341	12.92	2.0E-07	T63042.1		EST_HUMAN	SWISSPROT
1171	10392	19544	1.22	2.0E-07	Q28798		EST_HUMAN	l6 ALTOANTIGEN HYPOTHETICAL 72.5 KD PROTEIN C277-10 IN CHROMOSOME 1
1580	10793	19870	1.82	2.0E-07	Q09701		SWISSPROT	601818916F1 NIH MGIC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3597	12818		0.6	2.0E-07	BF131397.1		EST_HUMAN	Homo sapiens cavolin 1 (CAV1) gene, exon 3 and partial cds
3668	12889	22010	22.49	2.0E-07	AF125348.1		NT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
5292	14483	23531	9.22	2.0E-07	P23289		SWISSPROT	qg56d05_x1 Scars_testis_NT1 Homo sapiens cDNA clone IMAGE:1839177 3'
5557	15173	24583	1.77	2.0E-07	A1208715.1		EST_HUMAN	nt_00003280300-124-a016 NN0003 Homo sapiens cDNA CM4-NNN003-280300-124-a016 NN0003 Homo sapiens cDNA PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
7005	16183		2.32	2.0E-07	AL168303.2		NT	Homo sapiens chromosome 21 segment HS21C103
7157	16334	25817	8.56	2.0E-07	AW892507.1		EST_HUMAN	zr85f11_x5 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:565028 3' similar to contains THR_b2 THR repetitive element;
8269	17917		1.69	2.0E-07	BE153717.1		EST_HUMAN	EST_HUMAN
8257	18168		1.85	2.0E-07	A1732482.1		NT	Hom sapiens chromosome 21 segment HS21C082
1110	10334		1.63	1.0E-07	AL163282.2		NT	Hom sapiens chromosome 21 segment HS21C013
1840	11144	20342	0.95	1.0E-07	AL163213.2		NT	Hom sapiens chromosome 21 segment HS21C013
1840	11144	20343	0.95	1.0E-07	AL163213.2		NT	Hom sapiens chromosome 21 segment HS21C013
2416	11607	20829	0.91	1.0E-07	7549818	NT	Hom sapiens RAB, member of RAS oncogenes family-like 2A (RABL2A), transcript variant 2, mRNA	
2779	10723	18895	1.75	1.0E-07	P08256		SWISSPROT	GLYCOPROTEIN GPV
3725	10334		1.43	1.0E-07	AL163282.2		NT	Hom sapiens chromosome 21 segment HS21C082
4280	13483	22580	3.17	1.0E-07	AV718862.1		EST_HUMAN	AV718862 GLC Homo sapiens cDNA clone GLCFNF04 5'
4280	13483	22581	3.17	1.0E-07	AV718862.1		EST_HUMAN	AV718862 GLC Homo sapiens cDNA clone GLCFNF04 5'
6024	15232	24652	4.61	1.0E-07	BE047871.1		EST_HUMAN	b243dd6_y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6024	15232	24653	4.61	1.0E-07	BE047871.1		EST_HUMAN	b243dd6_y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6287	15468	24910	8.24	1.0E-07	NB5081.1		EST_HUMAN	yv3gd7_s1 Scars_fetal liver spleen 1NFL-S Homo sapiens cDNA clone IMAGE:255484 3'
6755	15950	25407	4.48	1.0E-07	AA6893376.1		EST_HUMAN	z151610_s1 Scars_fetal liver spleen_1NFL-S Homo sapiens cDNA clone IMAGE:434246 3'
7051	16228	25704	4.17	1.0E-07	BP874524.1		EST_HUMAN	602137714F1 NIH MGIC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
7204	16381		2.32	1.0E-07	AL163282.2		NT	Hom sapiens chromosome 21 segment HS21C082

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8841	18143	23750	3.09	1.0E-07	BE048770.1	EST_HUMAN	hr53c-11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:31322123' similar to TR:085722 Q95722
8784	17713		1.65	1.0E-07	X64467.1	NT	H_sapiens ALAD gene for porphobilinogen synthase
8958	17831		1.35	1.0E-07	X51755.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
7036	16213	25690	2.9	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone IMAGE:24468323' similar to contains OFR.12
7737	16934	26442	3.19	9.0E-08	A1891052.1	EST_HUMAN	wn3qad7.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:24468323' similar to contains OFR.12
8111	17303	26848	4.6	9.0E-08	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
8591	17800		3.94	9.0E-08	AJ251973.1	NT	Homo sapiens partial sterin-1 gene
613	11972		3.63	8.0E-08	A1911352.1	EST_HUMAN	wd168d5.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:23282733'
1057	10283		0.68	8.0E-08	BE785469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39439765'
3519	12743		1.84	8.0E-08	BE785469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39439765'
6895	15890	25351	4.48	8.0E-08	A1752387.1	EST_HUMAN	cn15c02x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6895	15890	25352	4.48	8.0E-08	A1752387.1	EST_HUMAN	cn15c02x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
68972	16150	25621	4.01	8.0E-08	AW970693.1	EST_HUMAN	EST382778 MAGE resequences, MAGK Homo sapiens cDNA
7797	16990		2.74	8.0E-08	AF253417.1	NT	Homo sapiens microsatellite epoxide hydrolase (EPHX1) gene, complete cds
80	9373	18503	2.46	7.0E-08	Q02387	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1369	10583	19750	36.64	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L3.1
3551	12774	21902	1.31	7.0E-08	FI5305	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
3551	12774	21903	1.31	7.0E-08	PI15305	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
7391	16605		7.93	7.0E-08	A1535743.1	EST_HUMAN	cogn3.P11.A5 econom Homo sapiens cDNA 3'
8175	17307	26850	6.73	7.0E-08	U24070.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
8075	12774	21902	3.5	7.0E-08	FI5305	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
9075	12774	21903	3.5	7.0E-08	FI5305	SWISSPROT	DYNEN HEAVY CHAIN (DYHC)
9146	17851		1.31	7.0E-08	AJ131016.1	NT	Hom sapiens SCL gene locus
8227	10065	18217	2.5	8.0E-08	AL163248.2	NT	Hom sapiens chromosome 21 segment HS21C048
E227	10065	19218	2.5	8.0E-08	AL163248.2	NT	Hom sapiens chromosome 21 segment HS21C048
2331	11524	20747	1.88	8.0E-08	EE144398.1	EST_HUMAN	MR-H10188-191199-004-gp9 H10188 Homo sapiens cDNA
3026	12262	21380	0.83	8.0E-08	7682473	NT	Hom sapiens KIAA1074 protein (KIAA1074), mRNA
4234	13437	22530	1.15	8.0E-08	AL163248.2	NT	Hom sapiens chromosome 21 segment HS21C048
7833	17092	26622	2.48	8.0E-08	FI1369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8064	17199			6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
84	9377	18507		2.87	5.0E-08	AL163303.2	NT Homo sapiens chromosome 21 segment HS21C103 nho3b9_s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element
2202	11399	20624		2.64	5.0E-08	AA463651.1	EST_HUMAN SWISSPROT COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
8318	17421			3.74	5.0E-08	P05681	EST_HUMAN Q0-C0225-131089-03-a12 CT0225 Homo sapiens cDNA
8515	17549	23986		1.29	5.0E-08	AW861878.1	EST_HUMAN SWISSPROT DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
1731	10943	20125		0.92	4.0E-08	P25723	EST_HUMAN SWISSPROT DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
1731	10943	20126		0.92	4.0E-08	P25723	EST_HUMAN SWISSPROT Homo sapiens shox gene, alternatively spliced products, complete cds
3891	13107	22225		0.72	4.0E-08	UB2688.1	NT an22d10_x1 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element;contains element MER22 repetitive element;
7185	16362	25842		2.55	4.0E-08	AI050027.1	EST_HUMAN Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
7477	16885			1.77	4.0E-08	AJ238617.1	NT b62248024F1 NIH MGCG_62 Homo sapiens cDNA clone IMAGE:4333300 5'
7656	16856	26356		4.35	4.0E-08	BF632493.1	EST_HUMAN b62248024F1 NIH MGCG_62 Homo sapiens cDNA clone IMAGE:4333300 5'
7656	16856	26357		4.35	4.0E-08	BF632493.1	EST_HUMAN b6265g03_r1 Scores_fetal_heart_NbHH10W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L111 L11 repetitive element;
8323	18300			2.4	4.0E-08	W76158.1	EST_HUMAN b95a11_x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2082076 3' similar to contains MER18_L3
8002	17861			2.01	4.0E-08	AJ343353.1	EST_HUMAN bb78e10_y1 NIH MGCG_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:QBZ158 Q9Z158
5496	14722	24080		2.66	3.0E-08	BE016348.1	EST_HUMAN SYNTAXIN_17
6075	14521	23584		3.72	3.0E-08	AI922737.1	EST_HUMAN q5f6f11_y6 NCI_CGAP_Pf28 Homo sapiens cDNA clone IMAGE:1944045 5'
6397	15578			3.43	3.0E-08	AI436352.1	EST_HUMAN b93109_x1 Scores_NSF_F8_9W_OT_PA_P_S Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
8288	17402			13.41	3.0E-08	R18420.1	EST_HUMAN bb78e14_r1 Scores_infant brain_NBII Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
211	8491			12.34	2.0E-08	AV302896.1	EST_HUMAN xb7f6_x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
233	8512			6.42	2.0E-08	AA425598.1	EST_HUMAN zw48f07_r1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains element MER15 repetitive element;
503	9755	18883		3.37	2.0E-08	AF188349.1	EST_HUMAN Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
666	99112	18040		10.21	2.0E-08	AV888438.1	EST_HUMAN MFO-O10080-240200-001-q08 O10080 Homo sapiens cDNA
668	98112	18041		10.21	2.0E-08	AV888438.1	EST_HUMAN MFO-O10080-240200-001-q08 O10080 Homo sapiens cDNA
987	10229			35.03	2.0E-08	BE280477.1	EST_HUMAN 601155321F1 NIH MGCG_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1350	10685	19730		95.22	2.0E-08	AI163247.2	NT Homo sapiens chromosome 21 segment HS21C047

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acession No.	Top Hit Database Source	Top Hit Descriptor
1714	10826			1.56	BE734871.1	EST_HUMAN	601570463f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1822	11030			4.08	2.0E-08 AW270271.1	EST_HUMAN	xp43f1.1x1 NCBI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2508	11697			1.91	2.0E-08 K00216.1	NT	Sheep His-tRNA-GUG
3174	12409	21544		6.99	2.0E-08 Q42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3174	12409	21545		6.99	2.0E-08 Q42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3842	13059			1.59	2.0E-08 AW813620.1	EST_HUMAN	RC3-ST0197-161089-012-b03 ST0197 Homo sapiens cDNA ea26c07.1r NCBI CGAP_GC81 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.2L1 repetitive element;
4399	13600			1.47	2.0E-08 AA455040.1	EST_HUMAN	he171d8-x2 NCBI CGAP_CML1 Homo sapiens cDNA clone IMAGE:28198327 3' similar to contains Alu repetitive element;
4977	14164			2.92	2.0E-08 AW572881.1	EST_HUMAN	PM2-HT0130-150989-001-f12 HT0130 Homo sapiens cDNA TCBA#D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA#P232
1745	10957	20140		1.06	1.0E-08 AF125348.1	NT	PM2-HT0130-150989-001-f12 HT0130 Homo sapiens cDNA TCBA#D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA#P232
2018	11219			2.7	1.0E-08 BE141959.1	EST_HUMAN	TCBA#D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA#P232
3155	12390	21523		1.07	1.0E-08 BE246844.1	EST_HUMAN	TCBA#D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA#P232
3155	12390	21524		1.07	1.0E-08 BE246844.1	EST_HUMAN	TCBA#D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBA#P232
5490	14716	24073		4.44	1.0E-08 AJ010770.1	NT	Homo sapiens hyponatremia gene, exons 1-50 ct35a05.1s1 Scareas testis cDNA clone IMAGE:1618736 3'
6839	15834	25298		2.75	1.0E-08 AI015304.1	EST_HUMAN	ct015304.1s1 Scareas testis cDNA clone IMAGE:1618736 3'
7862	17052	28573		4.24	1.0E-08 AF0440983.1	NT	Homo sapiens major histocompatibility locus class III region
8715	17871			2.18	1.0E-08 X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4228	13431	22524		2.66	9.0E-09 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
4228	13431	22525		2.66	9.0E-09 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
6193	15375	24815		7.03	8.0E-09 AI183560.1	EST_HUMAN	qd2e07.x1 Scareas_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:1732164 3' similar to contains MSR1.11 MSR1 repetitive element;
6464	15661	25133		3.54	8.0E-09 AW890159.1	EST_HUMAN	CMO-N1004-100300-273-906 NN1004 Homo sapiens cDNA op74d08.s1 Scareas NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
6761	15956			3.3	8.0E-09 AA8938892.1	EST_HUMAN	
3885	12808			2.2	7.0E-09 D86842.1	NT	Homo sapiens DNA for 3-ketacyt-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2; 3 y858g12.s1 Scareas fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121918 3'
7265	16484			3.06	7.0E-09 BE7890.1	EST_HUMAN	PM1-HT0527-18020-01-H05 HT0527 Homo sapiens cDNA
5000	14187	23277		6.35	6.0E-09 BE163421.1	EST_HUMAN	pm85hb8.x1 Scareas NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
5386	14675	23728		6.96	6.0E-09 AW195784.1	EST_HUMAN	
6823	16017	25482		2.71	6.0E-09 4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
7161	16338			4.91	6.0E-09 AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1419	10632	19800		3.26	5.0E-09 BE149264.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1820	11028	20223		1.02	5.0E-09 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5830	15047	24451		1.78	5.0E-09 AA359454.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
7103	16295	25768		2.57	5.0E-09 AW789867.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
9028	18224			1.24	5.0E-09 BE963272.2	EST_HUMAN	60165670TR1 NIH MIGC_67 Homo sapiens cDNA clone IMAGE:3865897 3'
527	9778			1.75	4.0E-09 AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
872	10204			2.43	4.0E-09 AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1465	10678	19851		1.81	4.0E-09 9558718	NT	Homo sapiens hypothetical protein (AF038159), mRNA
2383	11588	20804		37.61	4.0E-09 AA359878.1	EST_HUMAN	EST58355 Infant brain Homo sapiens cDNA 5' end similar to heat shock protein, 80 kDa
7841	18841	28339		3.63	4.0E-09 AB886401.1	EST_HUMAN	wm9af0.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
2320	11513	20734		4.11	3.0E-09 BE222238.1	EST_HUMAN	hu09e99.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2519	11707	20922		0.91	3.0E-09 BE222238.1	EST_HUMAN	hu09e99.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
3302	12533	21685		3.29	3.0E-09 BE222239.1	EST_HUMAN	MER18 repetitive element;
3355	12583			0.68	3.0E-09 AA442272.1	EST_HUMAN	zv54af4.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:757422 5'
4074	13284			0.69	3.0E-09 X16874.1	NT	H_sapiens PADPRP_I gene for NAD(+)-ADP-ribosyltransferase
4418	13618	22714		10.9	3.0E-09 AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A (EIF-4A) gene, partial cds
4613	13709	22802		1.53	3.0E-09 Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
751	16328	25911		2.31	3.0E-09 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7591	16795	26287		3.99	3.0E-09 BF108943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_NT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3327030 3'
7591	16795	26288		3.99	3.0E-09 BF108943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_NT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3327030 3'
822	10060			0.78	2.0E-09 X16674.1	NT	H_sapiens PADPRP_I gene for NAD(+)-ADP-ribosyltransferase
1265	10480	19841		5.78	2.0E-09 AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1634	10848			11.64	2.0E-09 AL118673.1	EST_HUMAN	DKFZp761B1710_11761 (synonym: hany2) Homo sapiens cDNA clone DKFZp761B1710 5'
2295	11490	20710		4.74	2.0E-09 Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0933)
3611	13127	22244		3.74	2.0E-09 Q80241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
							zg63h06.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:7861187 5' similar to contains
6274	15454	24895		7.44	2.0E-09 AA461430.1	EST_HUMAN	Alu repetitive element;
8283	17390			1.78	2.0E-09 AF111168.2	NT	Homo sapiens seirine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8864	10060			14.46	2.0E-09 X16874.1	NT	H_sapiens PADPRP_I gene for NAD(+)-ADP-ribosyltransferase
8839	18369			1.35	2.0E-09 AA226970.1	EST_HUMAN	nc11d22.1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1002	10233			2.24	1.0E-09	W78152.1	EST_HUMAN
1117	10341	19491	5.1	1.0E-09	5031624	NT	Homo sapiens CCAT-box-binding transcription factor (CBF2) mRNA
1117	10341	19492	5.1	1.0E-09	5031624	NT	Homo sapiens CCAT-box-binding transcription factor 2 p44 (b12p44) gene, partial cds, neuronal apoptosis inhibitory protein (nap1) and survival motor neuron protein (smn) genes, complete cds
2842	12081	21206	1.57	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b12p44) gene, partial cds, neuronal apoptosis inhibitory protein (nap1) and survival motor neuron protein (smn) genes, complete cds
2878	12114	21242	12.67	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NP11) mRNA, complete cds
2876	12114	21243	12.67	1.0E-09	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NP11) mRNA, complete cds
3003	12239	21369	0.72	1.0E-09	BE554440.1	EST_HUMAN	601058602/F1 NIH MGCG_10 Homo sapiens cDNA clone IMAGE:3445177 5'
4811	14000		6.59	1.0E-09	AA718287.1	EST_HUMAN	ZN3563 s1 Scores_pineal gland N3HPG Homo sapiens cDNA clone IMAGE:414028 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5258	14431	23508	0.88	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b12p44) gene, partial cds, neuronal apoptosis inhibitory protein (nap1) and survival motor neuron protein (smn) genes, complete cds
5733	14952	24350	3.38	1.0E-09	P26694	SWISSPROT	CIRCLIMSPOROZOITE PROTEIN PRECURSOR (CS)
7171	16348		2.4	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
8255	17382		1.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
8650	17633		2.2	1.0E-09	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8766	18310	23691	2.32	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1216	10532	18694	2.22	8.0E-10	AW887740.1	EST_HUMAN	MRU-SND040-050500-002-c07 SN0040 Homo sapiens cDNA
2787	12027	21154	7.73	9.0E-10	AI870071.1	EST_HUMAN	WE7863 s1 Scores_Dickgessere_colon_NHCD_Homo sapiens cDNA clone IMAGE:2347253 3' similar to SW_R129_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 :contains element PTR5 repetitive element;
6012	15262	24688	5.41	9.0E-10	AI452982.1	EST_HUMAN	W46809 s1 Scores_NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to TR:000372/000372/PUTATIVE_P150.;
149	9431	18585	12.37	8.0E-10	U63630.2	NT	Homo sapiens MCMA (MCMA) and DNA-PKcs (PRKDC) genes, partial cds
3316	12548	21679	0.88	8.0E-10	BE080748.1	EST_HUMAN	QV1-ET70631-150200-071-011 BTG631 Homo sapiens cDNA
4183	13387	22485	4.81	8.0E-10	AA379832.1	EST_HUMAN	EST89584 Small intestine 1 Homo sapiens cDNA 5' end
7060	16237		3	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
708	9950	18088	23.81	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51588), mRNA
708	9950	19089	23.91	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC51588), mRNA
1559	10813	18990	3.1	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1989	11192		1.2	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2625	11713		13.32	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3053	12289	21414	2.97	7.0E-10	X00856.1	NT	H sapiens DHFR gene, exon 3

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	149868	24365	3.58	7.0E-10	AA345220.1	EST_HUMAN	EST5247 Gall bladder II Homo sapiens cDNA 5' end gene
923	10158	18315	3.29	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEG31 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2837	11820	21038	1.54	8.0E-10	AJ24405.1	EST_HUMAN	fl0267.1X NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:20950213'
4750	13941		2.51	8.0E-10	AW863719.1	EST_HUMAN	RC3-C10254-031086-012-g12 CT0254 Homo sapiens cDNA
8554	17447		1.84	8.0E-10	AW971923.1	EST_HUMAN	EST384012 MAGE-like sequences, MAGL Homo sapiens cDNA
769	10009		5.57	5.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_r1434 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434N219_5'
5012	14189	23286	1.35	5.0E-10	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
6219	15400		1.71	5.0E-10	BF105159.1	EST_HUMAN	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
111	9389		1.63	4.0E-10	AJ221083.1	EST_HUMAN	qq09f09_x1 Scares_Placenta_Biosweeks_2NbHP8ic9W Homo sapiens cDNA clone IMAGE:1759049 3'
598	9838	18955	1.89	4.0E-10	AA515260.1	EST_HUMAN	similar to contains LTR8_b2 LTR8 repetitive element; nf64401_s1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:924648 3'
1966	11169	20374	1.75	4.0E-10	AW594708.1	EST_HUMAN	hg58g3.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2849844 3' similar to contains Alu repetitive element;
2538	11726	20943	4.74	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6155	15339	24776	14.13	4.0E-10	AF224669.1	NT	(UBB2D3) genes, complete cds
825	10159	18317	1.78	3.0E-10	N36113.1	EST_HUMAN	yy32f6_s1 Scares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:272983 3' similar to contains L111 L1 repetitive element;
1359	10574		4.66	3.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactitin precursor, gene, complete cds
5755	14974	24373	1.92	3.0E-10	PF20350	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
5813	15030	24431	3.41	3.0E-10	BE302870.1	EST_HUMAN	ba76d08_y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
6784	15979	25438	2.33	3.0E-10	AW850731.1	EST_HUMAN	IL3-C10219-160200-06-B06 CT0219 Homo sapiens cDNA
6784	15979	25439	2.33	3.0E-10	AW850731.1	EST_HUMAN	IL3-C10219-160200-06-B06 CT0219 Homo sapiens cDNA
7224	16401		2.23	3.0E-10	AA769294.1	EST_HUMAN	nz26g03_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:128900B3'
9041	17883	238896	2.19	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
37	9333	18438	1.24	2.0E-10	PF48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
37	9333	18439	1.24	2.0E-10	PF48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1862	11069		3.01	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b2/p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2843	12181		0.76	2.0E-10	BF678047.1	EST_HUMAN	602138840F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5574	14798		2.78	2.0E-10	Q28840	SWISSPROT	(IPRR3)

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5772	14980	24390	2.13	2.0E-10 AF280107.1	NT		Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
6247	15428	24888	5.7	2.0E-10 BE791082.1	EST_HUMAN	601588208F1 NIH MGIC_7 Homo sapiens cDNA clone IMAGE:39408245'	
1498	10711		13.84	1.0E-10 AW887767.1	EST_HUMAN	MRO-SN0038-280300-001-f01 SNO038 Homo sapiens cDNA	
1586	10758	19975	2.68	1.0E-10 AV852123.1	EST_HUMAN	AV852123 GLC Homo sapiens cDNA clone GLCCXA11 3	
2544	11732		1.68	1.0E-10 AW852001.1	EST_HUMAN	QV0-CT0225-19-188-058-e08 C10225 Homo sapiens cDNA	
3473	12697	21833	0.87	1.0E-10 AW832812.1	EST_HUMAN	QV2-TT003-161188-01-9-10 TT003 Homo sapiens cDNA	
3515	12739		0.68	1.0E-10 AL041685.1	EST_HUMAN	DKFZp434N1317_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'	
3829	12739		0.98	1.0E-10 AL041685.1	EST_HUMAN	DKFZp434N1317_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'	
3991	13205		7	1.0E-10 AF213884.1	NT		Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4109	13316	22414	8.01	1.0E-10 U52111.2	NT		Homo sapiens X28 region containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4109	13316	22415	6.01	1.0E-10 U52111.2	NT		Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CaMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
4116	13323	22424	1.91	1.0E-10 AB031069.1	NT		Homo sapiens POCX1 mRNA, for protein containing CXCC domain 1, complete cds
4152	13358		2.45	1.0E-10 M30628.1	NT		Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon w862f04.X1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2376153' similar to contains MER3.1t1 MER31 repetitive element;
5191	14367		0.99	1.0E-10 A1797745.1	EST_HUMAN		
7134	16311		8.18	1.0E-10 AA081868.1	EST_HUMAN	zr239g08_r1 Strategene neuroepithelium NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:548314 5'	
7488	16695	28179	3.77	1.0E-10 AI038280.1	EST_HUMAN	oy85n03_x1 Scores_fetal_liver_spineen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'	
8287	14504		1.53	1.0E-10 X87344.1	NT		H_sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
266	9541	18671	1.07	9.0E-11 BE145600.1	EST_HUMAN	IL2-HT0203-291099-016-d08 HT0203 Homo sapiens cDNA clone DKFZp547D225 5'	
2074	11274	20489	5.81	9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1_547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'	
2074	11274	20480	5.61	9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1_547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'	
3361	12589	21729	2.52	9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1_547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'	
3361	12589	21730	2.52	9.0E-11 AL134395.1	EST_HUMAN	DKFZp547D225_r1_547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'	
4503	13700	22794	0.94	9.0E-11 AA776985.1	EST_HUMAN	se78f01_s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:370287 3'	
5477	14704		4.92	9.0E-11 EE079780.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0627 Homo sapiens cDNA	

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8890	17658	23981	3.31	9.0E-11	C16835.1	EST_HUMAN	C16835 Clontech human aorta polya+ mRNA (#6572) Homo sapiens cDNA clone GEN_506BB08 5' yf53f11.s1 Scores adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE_172173 3' similar to contains L1 repetitive element;
3080	12316		9.13	8.0E-11	H19871.1	EST_HUMAN	
3940	13156	22273	0.61	8.0E-11	A1478617.1	EST_HUMAN	tm54cd99.x1 NC_ CGAP_Kid11 Homo sapiens cDNA clone IMAGE_2161936 3'
4020	13232	22335	5.63	8.0E-11	N23712.1	EST_HUMAN	yw4866.s1 Weismann Olfactory Epithelium Homo sapiens cDNA 5' end
1449	10682	19837	1.67	7.0E-11	AA330842.1	EST_HUMAN	EST34392 Embryo, 6 week Homo sapiens cDNA 5' end
6825	15821	25281	3.07	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
8835	17745		1.38	7.0E-11	AV701658.1	EST_HUMAN	AV701658 ADB_Homo sapiens cDNA clone ADABCBG9 5'
4118	9871	18812	8.1	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
4118	9871	18813	8.1	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6373	15553	25010	3.18	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6584	15780	25240	9.08	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC_Homo sapiens cDNA clone HTCA5C08 5'
111	9307	18409	1.36	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21CC083
3342	9307	18409	1.91	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21CC083
4213	13416	22512	1.55	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5883	15100	24511	1.84	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21CC013
6303	15484	24928	13.54	5.0E-11	11416789	NT	Homo sapiens protocadherin beta 3 (PCDHB3), mRNA
1405	10618		1.26	4.0E-11	AA435042.1	EST_HUMAN	zj01612.r1 Scores testis, NIH_NHG_71 Homo sapiens cDNA clone IMAGE_730559 5'
2743	11922	21138	7.91	4.0E-11	BE885800.1	EST_HUMAN	601507531.F1 NIH_NHG_71 Homo sapiens cDNA clone IMAGE_3908295 5'
2624	12162	21287	1.04	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21CC047
4020	13814	22804	1.18	4.0E-11	CA44866.1	EST_HUMAN	HUMSUPYD69 Human brain cDNA Homo sapiens cDNA clone 069
5860	15078	24491	3.34	4.0E-11	P20095	SWISSPROT	PRE-mRNA SPLICING FACTOR RNA HELICASE PRP2
6244	15425		3.86	4.0E-11	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8808	17797	23928	1.42	4.0E-11	11545732	NT	Hom sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1483	10698	19871	14.62	3.0E-11	6878077	NT	Mus musculus expressed in non-metastatic cells 2, protein (NM23B), (Name2), mRNA
4261	13484		1.48	3.0E-11	AA308248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
987	10200	18355	1.59	2.0E-11	AI150562.1	EST_HUMAN	QT36c04.x1 Scores testis_NHT Homo sapiens cDNA clone IMAGE_1752102 3' similar to contains MER10.13 MER10 repetitive element;
1193	10413	18568	5.2	2.0E-11	R24807.1	EST_HUMAN	yg38e12.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE_35144 5'
1193	10413	19569	5.2	2.0E-11	R24807.1	EST_HUMAN	yg38e12.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE_35144 5'
1592	10805	19980	10.06	2.0E-11	L17432.1	NT	Gallus gallus rhogoblin, beta-H globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1592	10805	19981	10.06	2.0E-11	L_17432.1	NT	Gallus gallus rho-globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein COR3beta (COR3beta) genes, complete cds
1594	10803	19884	0.95	2.0E-11	AJ126371.1	EST_HUMAN	gb:102832 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPH A (HUMAN); contains L1.1 L1 repetitive element;
2720	11899	21115	0.83	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
3160	12395	21531	4.04	2.0E-11	PI0283	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3298	12528	21680	1.62	2.0E-11	AJ478617.1	EST_HUMAN	Im5459_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936.3
3339	12588	21706	0.66	2.0E-11	Q10473	SWISSPROT	POLYPEPTIDE-N-ACETYL-GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) GALNAC-T1
4436	13638	0.85	2.0E-11	BE086537.1	EST_HUMAN	RC3-BT0316-170200-014-005 BT0316 Homo sapiens cDNA	
4806	13800	0.85	2.0E-11	AL163227.2	NT	Hom sapiens chromosome 21 segment HS21CQ27	
4855	14142	1.36	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0258-261080-014-e01 BT0258 Homo sapiens cDNA	
5029	14214	23298	3.62	2.0E-11	AL163279.2	NT	Hom sapiens chromosome 21 segment HS21CQ79
5792	15009	24413	1.68	2.0E-11	AA581028.1	EST_HUMAN	nc33hs5_r1 NCI CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433.5 similar to SW:PR16_YEAST
6834	16028		2.21	2.0E-11	AF028308.1	NT	P15638 PRE-mRNA SPlicing Factor RNA HELICASE PRP16.1
7164	16341	25820	6.37	2.0E-11	Q13606	SWISSPROT	OLFACTOORY RECEPTOR 51 (OLFACTOORY RECEPTOR-LIKE PROTEIN OLF1)
7374	16873	26377	2.64	2.0E-11	AA035369.1	EST_HUMAN	Z427902_s1 Scores pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794.3'
7674	16873	26378	2.64	2.0E-11	AA035369.1	EST_HUMAN	Z427902_s1 Scores pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794.3'
7702	16801	26409	2.16	2.0E-11	AA261958.1	EST_HUMAN	Z518504_r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:885519.5
8456	17513		2.3	2.0E-11	AW842143.1	EST_HUMAN	RC01-CN0027-21010-011-c01 CN0027 Homo sapiens cDNA
8485	17533	24027	1.65	2.0E-11	BF377859.1	EST_HUMAN	CN2-TN0140-Q70800-372-g01 TN0140 Homo sapiens cDNA
8765	17703		1.99	2.0E-11	D25217.2	NT	Hom sapiens mRNA for KIAA0027 protein, partial cds
8822	17806		1.93	2.0E-11	PF08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9248	18018		2.34	2.0E-11	11417386	NT	Hom sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
6882	8925	18056	1.26	1.0E-11	AJ131016.1	NT	Hom sapiens SCL gene locus
793	10033	19182	1.21	1.0E-11	AL163209.2	NT	Hom sapiens chromosome 21 segment HS21CQ09
1223	10443	18588	2.73	1.0E-11	AL163227.2	NT	Hom sapiens chromosome 21 segment HS21CQ19
1480	10703		1.61	1.0E-11	AF119814.1	NT	Hom sapiens PRO3078 mRNA, complete cds
2096	11286	20508	2.95	1.0E-11	AF000573.1	NT	Hom sapiens homogentisate 1,2-dioxygenase gene, complete cds
3472	12698	21832	1.08	1.0E-11	BE004315.1	EST_HUMAN	CN0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA

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4944	14131	23226	0.91	1.0E-11 A1168625.1	EST_HUMAN	ox65nb6_s1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:1681243 3'	
5354	14584	23680	13.76	1.0E-11 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
6648	15843	25304	7.4	1.0E-11 R13174.1	EST_HUMAN	Y73d08.1 Homo sapiens cDNA clone IMAGE:28166 5'	
7835	17027	26544	1.73	1.0E-11 BF880078.1	EST_HUMAN	6021548071 NIH MIGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'	
8001	18038		1.62	1.0E-11 Z20377.1	EST_HUMAN	HSAAACADHP_Human fetal Brain Whole tissue Homo sapiens cDNA SWISSPROT	
2804	12142	21278	1.11	9.0E-12 P2042	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR	
8540	17665		4.76	8.0E-12 AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2	
4684	13858	22957	1.62	7.0E-12 Q05804	SWISSPROT	34-KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)	
7889	17105	26835	12.51	7.0E-12 AA704735.1	EST_HUMAN	21239g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'	
3522	12746		0.73	6.0E-12 AV730554.1	EST_HUMAN	AV730554 HTTF Homo sapiens cDNA clone HTFAWF08 5'	
4341	13543	22634	9.71	6.0E-12 AA732516.1	EST_HUMAN	n28f11.1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;	
6903	16050		2.9	6.0E-12 AA847898.1	EST_HUMAN	cd10g11.1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER28 12	
1050	10276	18429	3.79	5.0E-12 T06573.1	EST_HUMAN	MER29 repetitive element;	
3708	12923	22046	6.27	5.0E-12 AJ271736.1	NT	EST04462 Fetal brain, Strategene (cat#36206) Homo sapiens cDNA clone HFBDV33	
5668	14890	24280	5.11	5.0E-12 AL163278.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2	
5668	14890	24281	5.11	5.0E-12 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
5871	15089	24502	10.34	5.0E-12 AW974760.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA EST	
6810	16005	25469	3.01	5.0E-12 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2	
7160	16337		6.25	5.0E-12 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
248	9525	18655	5.28	4.0E-12 AA700328.1	EST_HUMAN	274g11.1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'	
249	9525	18655	6.58	4.0E-12 AA700328.1	EST_HUMAN	274g11.1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460876 3'	
4622	13816	22906	0.88	4.0E-12 AI689984.1	EST_HUMAN	b26f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TRQ1359 Q13539 MARINER TRANSPONASE ;	
6540	15736		2.37	4.0E-12 AF106807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	
7648	16848	26348	4.08	4.0E-12 AJ228043.1	NT	Hom sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3	
8808	17730		1.89	4.0E-12 U78327.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44) and FIP3 (FTP3) genes, complete cds	
622	9867	18988	4.22	3.0E-12 AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805377 3' similar to TR.O14517 O14517 SMRP ;	
622	9867	18989	4.22	3.0E-12 AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR.O14517 O14517 SMRP ;	

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 Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7248	16468	25959	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region	
7248	16468	25960	3.45	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region	
1629	10842	20019	1.81	2.0E-12	AW802131.1	EST_HUMAN	IL5-LIN0071-120400-065-805 LIN0071 Homo sapiens cDNA	
3443	12688	21803	0.75	2.0E-12	8754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA	
4092	13300	22399	1.19	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA	
4092	13300	22400	1.19	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA	
4413	13613		2.27	2.0E-12	BE083509.1	EST_HUMAN	CMD-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA	
4919	14107	23201	0.59	2.0E-12	070308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)	
4919	14107	23202	0.59	2.0E-12	070308	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)	
5881	15079		1.87	2.0E-12	AW971857.1	EST_HUMAN	EST383948 MAGE-like sequences, MAGL Homo sapiens cDNA	
6154	15338	24775	3.16	2.0E-12	TO8169.1	EST_HUMAN	EST06080 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end	
6362	15542	24997	2.07	2.0E-12	11422229	NT	Human sapiens Ac-like transposable element (ALTE), mRNA	
7069	16246		17.59	2.0E-12	BE165980.1	EST_HUMAN	MR3-HT0487-15020-1-13-g01 HT0487 Homo sapiens cDNA	
8440	17503		2.41	2.0E-12	AL163283.2	NT	Human sapiens chromosome 21 segment HS21C083	
8654	17634		1.49	2.0E-12	11418248	NT	Human sapiens sulfotransferase-related protein (SULTX3), mRNA	
-21	9407	18540	3.27	1.0E-12	AW627674.1	EST_HUMAN	hh90ep09_X1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:297040 3' similar to contains MER18.11	
1866	11160		1.52	1.0E-12	AB71726.1	EST_HUMAN	EST18 repetitive element;	
3035	12271	21398	1.76	1.0E-12	AF000981.1	NT	wm51107_X1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1,b3 L1	
3035	12271	21399	1.78	1.0E-12	AF000981.1	NT	Hom sapiens testis-specific Testis Transcript Y2 (TTY2) mRNA, partial cds	
3895	13071	22185	41.19	1.0E-12	AU132248	EST_HUMAN	Hom sapiens testis-specific Testis Transcript Y2 (TTY2) mRNA, partial cds	
3895	13071	22188	41.19	1.0E-12	AU132248	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'	
5339	14863		1.92	1.0E-12	U82282.1	NT	Hom sapiens etaxias telangiectasia (ATM) gene, complete cds	
5881	14901		1.82	1.0E-12	QBY72G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIA0861	
6127	15311	24745	1.76	1.0E-12	AF198864.1	NT	Hom sapiens putative BPES syndrome breakpoint region protein gene, complete cds	
6139	15323	24757	9.56	1.0E-12	AI248533.1	EST_HUMAN	qh68a04_X1 Soares_fetal_liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:1849814 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);contains MER10.11 MER10	
6139	15323	24758	9.56	1.0E-12	AI248533.1	EST_HUMAN	repetitive element;	
8346	17441	26839	4.2	1.0E-12	AW862164.1	EST_HUMAN	EST374237 MAGE-like sequences, MAGL Homo sapiens cDNA	
8729	16268		1.63	1.0E-12	AI163268.2	NT	Human sapiens chromosome 21 segment HS21C088	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3922	13138	22257		0.83	9.0E-13 AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfatase, exon 1, 2, 3, 4, 5
6862	16140			2.29	9.0E-13 NM9653.1	EST_HUMAN	za26b08_s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:283651 3'
724	9988	18104		6.37	8.0E-13 U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
724	9988	19105		6.37	8.0E-13 U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1806	11015	20208		1.89	8.0E-13 U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
7123	16300			2.56	8.0E-13 U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FIP3 (FIP3) genes, complete cds
8244	17373	26908		2.52	8.0E-13 U86060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV13S2, TCRBV13S3P, TCRBV13S4P, TCRBV13S5P, TCRBV13S6A2T, TCRBV13S7P, TCRBV13S8, TCRBV13S9P, TCRBV13S10P, TCRBV13S11P, TCRBV13S12P, TCRBV23S1A2T, TCRBV12>
8838	17748			13.42	7.0E-13 BE778223.1	EST_HUMAN	601463285f_NIH_MIGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
9073	17899			19.47	7.0E-13 Q10473	SWISSPROT	POLYPEPTIDE NACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc-POLYPEPTIDE-N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T-1)
2071	11271	20486		5.65	8.0E-13 AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C07
3284	12525			0.77	5.0E-13 R78398.1	EST_HUMAN	y8204_11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3375	12603			1.63	5.0E-13 AA435773.1	EST_HUMAN	Z177a12_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
7436	16845	26137		2.89	5.0E-13 P07313	SWISSPROT	PM2-HT0224-221098-001-011 HT0224 Homo sapiens cDNA
1833	11041			8.48	4.0E-13 AW3788614.1	EST_HUMAN	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
2423	11614			3.52	4.0E-13 AF003529.1	NT	
5484	14710	24066		4.77	4.0E-13 BE169131.1	EST_HUMAN	PM3-HT0520-23020-002-c08 HT0520 Homo sapiens cDNA qn32d05_x1_NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1889945 3' similar to contains Alu repetitive element;
7080	16257	25731		3.25	4.0E-13 AF289831.1	EST_HUMAN	Z178g10_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
7728	16924	26433		2.08	4.0E-13 AA435819.1	EST_HUMAN	Z178g10_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
7728	16924	26434		2.08	4.0E-13 AA435819.1	EST_HUMAN	Homo sapiens X-linked arthiodactyl ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
'184	9483			5.11	3.0E-13 AF003528.1	NT	
875	10111			5.46	3.0E-13 AA430310.1	EST_HUMAN	zw68g08_11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
2338	11531	20754		1.62	3.0E-13 AA1271736.1	NT	Homo sapiens Xq pseudobatosomal region, segment 2/2
2441	11632			2.58	3.0E-13 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2826	11610	21026		2.58	3.0E-13 BS372662.1	EST_HUMAN	CN3-F70100-140700-242-h08 FT0100 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3150	12385		2.42	3.0E-13	AA745844.1	EST_HUMAN	ob185f2_s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
6422	15619	25083	8.11	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
7268	16487		3.69	3.0E-13	A1064768.1	EST_HUMAN	HA0538 Human fetal liver cDNA library Homo sapiens cDNA
7616	16819	26314	3.1	3.0E-13	BE0083509.1	EST_HUMAN	CM0-BT0281-031190-087-403 BT0281 Homo sapiens cDNA
8126	17260	26803	2.87	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS24(C048
152	9434	18568	2.21	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMK1), creatine transporter (CRTTR), CDM protein (CDM), adrenoleukodystrophy protein >
243	9521	18652	1.34	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1277	10492	19651	5.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
2865	12203	21338	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
2965	12203	21339	0.79	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3249	12482	21614	1.03	2.0E-13	BF431898.1	EST_HUMAN	nab76105_x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'
3481	12705	21841	1.04	2.0E-13	AF109807.1	NT	Homo sapiens S104 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4086	13285		1.92	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5270	14443		2.68	2.0E-13	BE256449.1	EST_HUMAN	60111249F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357829 5'
5718	14936	24332	4.51	2.0E-13	Q06852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6004	15288	24718	6.58	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7201	16378	25859	3.55	2.0E-13	5031986	NT	Homo sapiens mbt-21 (C. elegans)-like 1 (MAB21L1) mRNA
8521	17552		10.13	2.0E-13	AW892455.1	EST_HUMAN	CM0-NN0001-100300-274-511 NN0001 Homo sapiens cDNA
296	9569	18701	1.54	1.0E-13	S74128.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
898	10133	19295	4.82	1.0E-13	AJ007973.1	NT	Homo sapiens LGM12B gene
1344	10558	19724	1.38	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1691	11194	20404	1.95	1.0E-13	AA720574.1	EST_HUMAN	rw21902_s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR, 13 THR repetitive element;
4593	13787	22879	1.19	1.0E-13	BF340987.1	EST_HUMAN	602035008F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4185868 5'
7817	17132	26862	15.9	1.0E-13	BF108755.1	EST_HUMAN	7145e10_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29_b2 MER28 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8337	17435			1.5	1.0E-13 AW715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
9015	17887			2.04	1.0E-13 AJ271735.1	NT	Homo sapiens Xg pseudautosomal region; segment 1/2
9161	17960			1.75	1.0E-13 X87579.1	NT	H sapiens CD4 gene
338	9608	18734		3.04	9.0E-14 AA781159.1	EST_HUMAN	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.1t MER19 repetitive element;
339	9607	18735		3.14	9.0E-14 AA781159.1	EST_HUMAN	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.1t MER19 repetitive element;
2664	11655			3.37	9.0E-14 AW861577.1	EST_HUMAN	RCA-CT0322-080100-013-d09 CT0322 Homo sapiens cDNA
2710	11889	21106		6.2	9.0E-14 AB038162.1	NT	Homo sapiens testis cluster for trefail factor; complete cds
3075	12311	21432		5.07	9.0E-14 AW513286.1	EST_HUMAN	x054hf5.x1 NCI CGAP_U1 Homo sapiens cDNA clone IMAGE:2707833 3'
3204	9608	18734		1.01	9.0E-14 AA781159.1	EST_HUMAN	aj24c01.s1 Soares testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.1t MER19 repetitive element;
3760	12898	22114		7.13	9.0E-14 D14547.1	NT	Human DNA_SINE repetitive element
4768	13957	23058		1.61	9.0E-14 AJ002153.1	NT	Sequinu oedipus gene for seminal vesicle secreted protein semenogelin 1
3632	13146			3.6	8.0E-14 R76269.1	EST_HUMAN	Y72601.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
6893	15599	25065		67.72	8.0E-14 X89211.1	NT	H sapiens DNA for endogenous retroviral like element
6843	16087	25555		2.85	8.0E-14 AA219318.1	EST_HUMAN	zq17c01.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:6239970 3'
7871	17150			5.08	8.0E-14 BE062558.1	EST_HUMAN	QV2-BT0288-281083-04-a01 BT0258 Homo sapiens cDNA
8138	17684	23954		1.58	8.0E-14 AI688118.1	EST_HUMAN	wc92h08.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:2326143 3'
1606	11666			4.08	7.0E-14 AW151673.1	EST_HUMAN	xf87610.x1 NCI CGAP_G4s4 Homo sapiens cDNA clone IMAGE:26231146 3' similar to contains MER10.12 MER10 repetitive element;
372	9638	18771		11.58	6.0E-14 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7018	16195	25670		3.82	6.0E-14 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7018	16195	25871		3.82	6.0E-14 AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
624	9869	18991		4.42	5.0E-14 Q83120	SWISSPROT	Hom sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
5086	14268	23353		1.24	5.0E-14 AW703791.1	EST_HUMAN	Hom sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
5458	14684	24034		5.3	5.0E-14 P08547	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2)(CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
1131	11986			2.92	4.0E-14 P04928	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1843	11051	20242		5.65	4.0E-14 AJ007973.1	NT	S-ANTIGEN PROTEIN PRECURSOR
							Homo sapiens LGMD2B gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3734	12854		0.88	4.0E-14	AA046502.1	EST_HUMAN	z467a6.r1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858.5'
4279	13482	22579	2.22	4.0E-14	NA6328.1	EST_HUMAN	y73c12.s1 Scores_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279190.3' similar to contains L1.L1 repetitive element:
9082	18381		3.28	4.0E-14	AI886224.1	EST_HUMAN	wm08c3.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332.3' similar to contains Alu repetitive element;
957	10190	18344	0.85	3.0E-14	X95486.1	NT	R_norvegicus mRNA for CPG2 protein
7788	14498	23585	9.98	3.0E-14	AW285354.1	EST_HUMAN	xp45f12.x1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343.3' similar to contains Alu repetitive element; contains element MER9 repetitive element;
8692	18243		1.51	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
395	9650	18785	3.21	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
395	8650	18786	3.21	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
697	11974	18072	8.95	2.0E-14	AL16303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2351	11544		1.78	2.0E-14	AW372888.1	EST_HUMAN	RC5-BT0377-091-299-031-D12-BT0377 Homo sapiens cDNA
2427	11618		1.48	2.0E-14	7657529	NT	Homo sapiens thyroid tumor deletion region protein 1 (RTDR1) mRNA
2492	11682	20898	2.43	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
					hw80g10.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180738.3' similar to contains Alu repetitive element; contains OFR_M OFR repetitive element;		
2805	11683		1.08	2.0E-14	BE222432.1	EST_HUMAN	Human beta globin region on chromosome 11
5543	14767	24133	3.24	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6282	15473	24914	20.84	2.0E-14	EE158761.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
6292	15473	24915	20.64	2.0E-14	EE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7381	16577	26068	5.36	2.0E-14	AW139860.1	EST_HUMAN	U1-H-B1-8dw-e-10-0-U1-s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234.3'
8033	14767	24133	1.67	2.0E-14	U01317.1	NT	Human beta globin region on chromosomes 11
1074	10289	19449	1.33	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1410	10623	19787	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
1410	10823	19788	5.94	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1970	11174	20380	12.87	1.0E-14	L44140.1	NT	Hom sapiens chromosome X region from flamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2151	11349	20565	5.32	1.0E-14	AF001689.1	NT	Homo sapiens chromosome 21 segment HS21C103
2372	11565	20788	32.19	1.0E-14		NT	Hom sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2385	12133	21269	1.12	1.0E-14	PR05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CONE_PFHFR-1)
3132	12367	21497	5.58	1.0E-14	BF733227.1	EST_HUMAN	RC2-CT0422-310700-013-a09_1 CT0432 Homo sapiens cDNA
3132	12367	21498	5.56	1.0E-14	BF5335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3865	13081	22197	2.03	1.0E-14	AA682994.1	EST_HUMAN	ee89c12.61 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971350.3'
4469	13667	22758	2.01	1.0E-14	AW275852.1	EST_HUMAN	xq39h10x1 NCI CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059.3'

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Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5576	14800	24173	2.32	1.0E-14	AF126145.1	NT	Bos taurus xerobiotic/medium-chain fatty acid:CoA ligase form X-L-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
5859	18087	24591	10.71	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
5959	18067	24592	10.71	1.0E-14	11437150	NT	Homo sapiens protein prominin (mouse)-like 1 (PROML1), mRNA
1555	10769	18841	1.52	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
							Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel α2
2139	11337			1.35	9.0E-15	AF1986779.1	NT
5002	14189	23219	1.12	9.0E-15	BF35227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
6289	15470	24911	3.85	9.0E-15	P21416	SWISSPROT	GAG POLYPROTEIN (CONTAINS: CORE PROTEINS P15, P12, P30, P10)
2763	9739			0.96	8.0E-15	BE261442.1	EST_HUMAN
							601148632F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
							xn77d02.x1 Seares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700463 3' similar to contains
7180	16367			3.7	7.0E-15	AW241958.1	EST_HUMAN
1001	10232	18387	8.38	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
7850	18391			1.99	6.0E-15	AWB38843.1	EST_HUMAN
416	9658	18809	8.63	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, ROR gene, and sodium phosphate transporter (NPT3) gene, complete cds
3445	12670	21112	2.62	5.0E-15	U91328.1	NT	U1-BW0-ajb-g-10-cJ1-s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731219 3'
7287	16486			1.05	5.0E-15	AW288817.1	EST_HUMAN
433	9298	18400	1.87	5.0E-15	AV73056.1	EST_HUMAN	AV73056 HTF Homo sapiens cDNA clone HTFAVE06 5'
7628	15592	25053	3.42	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7628	15592	25054	2.78	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
							Homo sapiens mRNA for transcription factor LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
4200	13404			7.67	3.0E-15	N89452.1	EST_HUMAN
4948	14135			5.47	3.0E-15	P92485	SWISSPROT
5054	14236	23323	4.65	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5054	14236	23324	4.65	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6199	15380	24820	3.53	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6199	15380	24821	3.53	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7046	16223			2.34	3.0E-15	AA807128.1	EST_HUMAN
							oc36a07_s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19 1 repetitive element;

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7374	16590	26079		3.8	3.0E-15 AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
8746	18275			1.51	3.0E-15 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
254	9550	18661		5.23	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	8639	18772		4.08	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
373	8639	18773		4.08	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1515	10729			1.55	2.0E-15 8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3483	12707	21843		0.82	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3483	12707	21844		0.82	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4625	13819			2.81	2.0E-15 A1806335.1	EST_HUMAN	W07108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR_Q61043 Q61043 NINEIN::
6197	15378	24819		2.21	2.0E-15 AA704185.1	EST_HUMAN	277803.61 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
6253	16434	24873		4.9	2.0E-15 W05064.1	EST_HUMAN	2878d10.11 Soares_fetal_lung_NBL1L19W Homo sapiens cDNA clone IMAGE:288875 5' similar to WP:44F4.8 CE0227 TRANSPPOSEASE;
6747	15942	25402		3.39	2.0E-15 D14547.1	NT	Human DNA, SINE repetitive element
7415	16627			3.67	2.0E-15 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9109	12707	21843		2.56	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9109	12707	21844		2.58	2.0E-15 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2730	11909			4.02	1.0E-15 A1689884.1	EST_HUMAN	b28h105.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR_Q13539 Q13539 MARINER TRANSPOSEASE::
2874	12211	21349		1.58	1.0E-15 BE043584.1	EST_HUMAN	hk40ed2.y1 NCI CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2888162 5'
3107	12342	21470		1.11	1.0E-15 P08847	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4353	13555	22651		0.89	1.0E-15 BE182696.1	EST_HUMAN	RC3-HT0649-100500-022-b05 HT1049 Homo sapiens cDNA clone IMAGE:120234 3' similar to contains y4061.s1 Soares_fetal_liver_spleen INFSL Homo sapiens cDNA clone IMAGE:2888162 5' MER6 repetitive element;
5822	15039	24441		1.78	1.0E-15 T95763.1	EST_HUMAN	QV3-BT0569-270100-074-g05 BT0569 Homo sapiens cDNA
6091	15282			1.87	1.0E-15 BE074217.1	EST_HUMAN	qf68h06.x1 Soares_nht Homo sapiens cDNA clone IMAGE:1755227 3'
6607	15803	25256		3.75	1.0E-15 AI200976.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
8807	15803	25259	3.75	1.0E-15	A1200978.1	EST_HUMAN	qf68h06.x1 Soares testis_NH7 Homo sapiens cDNA clone IMAGE:17552273'	
6779	15974	25481	2.94	1.0E-15	4507208 NT	Hom sapiens spermidine synthase (SRM) mRNA		
7395	16609	26100	6.95	1.0E-15	AF044083.1	NT	Hom sapiens major histocompatibility locus class III region	
9182	18089	23806	5.74	1.0E-15	A1783844.1	EST_HUMAN	fr31cd5.x1 NCI CGAP_Ov23 Homo sapiens cDNA clone IMAGE:22169123' similar to contains Alu repetitive element.	
4507	13703	22797	1.15	8.0E-16	4503168 NT	Hom sapiens cut (Drosophila)-like 1 (CCAAAT displacement protein) (CUTL1) mRNA		
7565	16770	26281	2.85	9.0E-16	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105	
9130	18186			9.02	7.0E-16	T94149.1	EST_HUMAN	ye28c12.r1 Strategene lung (#807210) Homo sapiens cDNA clone IMAGE:1190625'
2109	11308			7.46	6.0E-16	AW972611.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1484	10697	19872	0.88	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37D pseudogene of80c04.s1 Soares total fetus_NBHF8_9w Homo sapiens cDNA clone IMAGE:16230783 similar to contains element L1 repetitive element.	
2640	11823	21038	2.42	5.0E-16	AA892178.1	EST_HUMAN		
8052	17188	28728	3.64	5.0E-16	BF217368.1	EST_HUMAN	601885734F1 NIH MGIC_57 Homo sapiens cDNA clone IMAGE:41041285'	
9225	18003			12.84	5.0E-16	11418127 NT	Hom sapiens GTP binding protein 1 (GTPBP1). mRNA	
2346	11539	20762	0.86	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-203030-115-802 UM0036 Homo sapiens cDNA	
2346	11539	20763	0.88	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-203030-115-802 UM0036 Homo sapiens cDNA	
3434	12639	21790	5.03	4.0E-16	Q18653	SWISSPROT	MYELIN-OIL/GODEN/DRYOCYTE GLYCOPROTEIN PRECURSOR	
4124	13330	22428	5.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0850-010400-002-909 BT0650 Homo sapiens cDNA	
4124	13330	22429	5.95	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0850-010400-002-909 BT0650 Homo sapiens cDNA	
6380	15560	25016	35.49	4.0E-16	AL163284.2	NT	Hom sapiens chromosome 21 segment HS21C084	
7772	16987	26480	1.68	4.0E-16	AV730030.1	EST_HUMAN	AV730030 HTF Homo sapiens cDNA clone HTTFWAD35'	
8421	17483			1.39	4.0E-16	P08548	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
8514	17548			6.29	4.0E-16	C05847.1	EST_HUMAN	C05847 Human pancreatic islet Homo sapiens cDNA clone hbc5365
8525	17555	23988	2.97	4.0E-16	6912459 NT	Hom sapiens Grb2-associated binder 2 (KIAA0571). mRNA		
8808	17728			1.45	4.0E-16	R18891.1	EST_HUMAN	yf86b11.1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:304895'
130	9413	18548	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Monton Fetal Cochlea Homo sapiens cDNA clone IMAGE:24863765'	
130	9413	18549	1.45	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Monton Fetal Cochlea Homo sapiens cDNA clone IMAGE:24863765'	
472	9725			2.3	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P0375'
482	9734			1.72	3.0E-16	AF135448.1	NT	Hom sapiens TSX/TSX' pseudogene, exon 5
1453	10666	19840	1.97	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR	
2830	12168	21300	4.29	3.0E-16	P03200	SWISSPROT	ENVLOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]	
3907	13123	22241	0.78	3.0E-16	TO8169.1	EST_HUMAN	EST06050 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA135' and	

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4961	14148	23240	1.01	3.0E-16	AV661393.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains em98h05_s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3'
6671	15986	26326	3.01	3.0E-16	AI002836.1	EST_HUMAN	THR.62 THR repetitive element;
7118	16285	25777	6.55	3.0E-16	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ATP-2) gene, complete cds
979	10211		1.32	2.0E-16	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
2850	11833		1.1	2.0E-16	JQ3061.1	NT	Human SSAV-related endogenous retroviral LTR-like element
4159	13363	22463	1.66	2.0E-16	XKB211.1	NT	H sapiens DNA for endogenous retroviral like element
8450	15847	25115	2.24	2.0E-16	A1732837.1	EST_HUMAN	n24706.65 NCI_CGAP_P112 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849
7502	16709	26186	3.45	2.0E-16	5902145.1	NT	HYPOTHETICAL 42.9 KD PROTEIN_N24706.65 contains MER7_11 MER7 repetitive element;
189	9488	18587	2.2	1.0E-16	AF200719.1	EST_HUMAN	Homo sapiens ubiquitin carrier protein E2-C (UBCH10).mRNA
387	9881		32.18	1.0E-16	AA628592.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds af39g11.1f Soares_total_fatso_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12_OFRR repetitive element;
1941	11145	20344	2.89	1.0E-16	BF327942.1	EST_HUMAN	QVO-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5844	15081		25.88	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
5913	15130	24539	3.2	1.0E-16	Q02779	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
6314	15061		7.17	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
3719	12839	22056	2.63	9.0E-17	AW900048.1	EST_HUMAN	CIM1-N1003-200300-153-a01 NN1003 Homo sapiens cDNA
5974	15188		1.89	9.0E-17	A1392984.1	EST_HUMAN	Iq22c11_x1 NCI_CGAP_Cll1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28
6496	15693		3.18	9.0E-17	AW150257.1	EST_HUMAN	Ig49g12_x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2830950 3' similar to contains OFR.12_OFRR
7142	16319		2.25	9.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds repetitive element;
1025	10251		1.34	8.0E-17	AW880701.1	EST_HUMAN	QVO-OT0032-080300-165-d01 OT0032 Homo sapiens cDNA
3870	13086		1.01	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5482	18058	24084	3.83	8.0E-17	BE172081.1	EST_HUMAN	MRO-HT0559-060300-003-e04 HT0559 Homo sapiens cDNA
6108	15319		1.82	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
1457	10870		4.26	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (Apobec-2), mRNA
5347	14577		3.44	7.0E-17	AF216630.1	NT	Homo sapiens putative MTA1 (MTAP) mRNA, partial cds, alternatively spliced
5960	15175	24593	7.8	7.0E-17	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
208	9488	18622	8.24	6.0E-17 AW983980.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA hiBitd04,x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878895 3' similar to contains L1,12	
5784	15011	24415	1.71	6.0E-17 AW662772.1	EST_HUMAN	L1 repetitive element;	
427	92822	18394	4.13	5.0E-17 T84110.1	EST_HUMAN	ye05n08_r1 Strategene lung (#8371210) Homo sapiens cDNA clone IMAGE:78839 5'	
6328	15509	24955	1.75	5.0E-17 T81043.1	EST_HUMAN	xd28d04,r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:105827 5'	
3614	12835	21965	0.66	4.0E-17 AA643697.1	EST_HUMAN	ni8805,s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058528 3'	
8026	17163	26700	2.43	4.0E-17 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
8435	17601		2.34	4.0E-17 A1073546.1	EST_HUMAN	016530 PMS3 mRNA ,contains MER1012 MER10 repetitive element;	
2068	11268	20482	1.45	3.0E-17 AW119123.1	EST_HUMAN	x089c09,x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'	
3157	12392		1.06	3.0E-17 P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG	
3621	12842	21961	1.16	3.0E-17 BE328522.1	EST_HUMAN	hw05b04,x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3181989 3'	
3621	12842	21962	1.16	3.0E-17 BE328522.1	EST_HUMAN	hw05b04,x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3181989 3'	
6692	18170	25642	5.16	3.0E-17 AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)	
8398	17476		3.23	3.0E-17 11417066 NT	Hom sapiens SEC14 (S_cerevisiae)-like 2 (SEC14L2), mRNA		
358	9628	18758	4.54	2.0E-17 A1270080.1	EST_HUMAN	qf63ad6,x1 NCI_CGAP_Es62 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Aliu repetitive element;	
359	9628	18758	2.24	2.0E-17 A1270080.1	EST_HUMAN	qf63ad6,x1 NCI_CGAP_Es62 Homo sapiens cDNA clone IMAGE:1958922 3' similar to contains Aliu repetitive element;	
995	10227		1.92	2.0E-17 A1722832.1	EST_HUMAN	zg81d14,s1 Soares_fetal_heart_NBTH19W Homo sapiens cDNA clone IMAGE:3599751 3'	
2410	11602	20822	2.54	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	
2410	11602	20823	2.54	2.0E-17 Q28983	SWISSPROT	ZONADHESIN PRECURSOR	
2680	12118	21249	6.89	2.0E-17 F12038	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 kDa NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)	
5378	14607	23717	1.9	2.0E-17 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds	
5378	14607	23718	1.9	2.0E-17 M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds	
5774	14982		1.81	2.0E-17 AF055066.1	NT	Homo sapiens MHC class I region	
7029	16208	25683	2.43	2.0E-17 BE289888.1	EST_HUMAN	600544890F1 NIH MGIC_17 Homo sapiens cDNA clone IMAGE:2860815 5'	
7042	16219	25694	3.53	2.0E-17 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
7042	16219	25685	3.53	2.0E-17 AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
7154	16331	25614	6.53	2.0E-17 D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)	
758	8999	19446	3.33	1.0E-17 P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1683	10895			1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudosomal region; segment 2/2
1738	10950	20133		5.89	1.0E-17 AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2086	11288	20499		1.89	1.0E-17 F02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2304	11498	20718		3.54	1.0E-17 U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3543	12768			0.83	1.0E-17 AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4119	13325			8.44	1.0E-17 R098942.1	EST_HUMAN	y30507.1x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
7055	17094	26825		1.98	1.0E-17 Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) (CONTAINS: TELOKIN)
2324	11625	20847		1.79	9.0E-18 AA174078.1	EST_HUMAN	zp18g12.s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:6098862 3'
3169	12987	22103		1.31	8.0E-18 475897 NT	Hom sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN51) mRNA	
354	9622	18750		49.6	7.0E-18 AW316976.1	EST_HUMAN	xx10504.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
354	9622	18751		49.6	7.0E-18 AW316976.1	EST_HUMAN	xx10504.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
8336	9622	18750		4.04	7.0E-18 AW316976.1	EST_HUMAN	xx10504.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
8336	9622	18751		4.04	7.0E-18 AW316976.1	EST_HUMAN	xx10504.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gbl20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3264	12487	21627		1.38	6.0E-18 X71781.2	NT	Rattus norvegicus partial GdnPn-1 gene for glue-derived nexin-1 protease nexin-1 enhancer region
4759	13950			3.42	6.0E-18 F52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
6542	15738			3.47	6.0E-18 11428155 NT	mRNA,	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63448), mRNA,
7094	16893	26402		2.2	6.0E-18 AL163246.2	NT	Hom sapiens chromosome 21 segment HS21C046
7873	17062	26586		1.86	6.0E-18 X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
8231	17360			2.73	6.0E-18 11428385 NT	Hom sapiens similar to ribosomal protein L12 (H. sapiens) (LCG63091), mRNA	
8671	17648	23977		1.73	6.0E-18 U87929.1	NT	Human acornitata hydrolase (ACO2) gene, exon 4
1158	10378	19530		17.47	5.0E-18 AI2B0214.1	EST_HUMAN	qm65g11.x1 Soares_Placental_Bloeweeks_2NbHP8t9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element;
4503	13504	22601		1.26	5.0E-18 10946365 NT	Mus musculus dasdeamin (Gsdm), mRNA	
5311	14542	23611		1.95	5.0E-18 AF087813.1	NT	Human endogenous retrovirus HERV-P-T47D
7551	16756	26249		4.21	5.0E-18 10242378 NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA	
7551	16756	26250		4.21	5.0E-18 10242378 NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA	

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 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (TcP) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8890 17725			5.65	5.0E-18 AW867182.1	EST_HUMAN	MR1-SN0035-0604-00-001-911 SN0035 Homo sapiens cDNA	
9151 17854			14.87	5.0E-18 AV850547.1	EST_HUMAN	AV850547 GLC_Homo sapiens cDNA clone GLCGA02 3'	
123 9408	18541		1.78	4.0E-18 BE044078.1	EST_HUMAN	h036h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:30395113' similar to contains MER29.b3	MER29 repetitive element;
123 9408	18542		1.78	4.0E-18 BE044078.1	EST_HUMAN	h036h04_x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:30395113' similar to contains MER29.b3	MER29 repetitive element;
1891 10803	20090		18.8	4.0E-18 AA621814.1	EST_HUMAN	ng24f1_s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326	KERATIN, TYPE I CYTOSKELETON 18 (HUMAN);
1854 11061			1.02	4.0E-18 A738592.1	EST_HUMAN	w33n08_x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2392095 3'	N-ACTYLGLUCOSAMINYLTRANSFERASE (N-
2187 11365	20584		1.64	4.0E-18 Q06430	SWISSPROT	ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME) (INT)	N-ACTYLLACTOSAMINIDE BETA-1,6-NACETYLLGLUCOSAMINYLTRANSFERASE (N-
2187 11365	20585		1.84	4.0E-18 Q06430	SWISSPROT	ACETYLGLUCOSAMINYLTRANSFERASE (I-BRANCHING ENZYME) (INT)	Acetylglucosaminyltransferase (I-BRANCHING ENZYME) (INT)
3774 12892	22107		0.61	4.0E-18 AI591586.1	EST_HUMAN	ars3b06_x1 Barstead clone HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Ali	
5376 14605	23714		2.33	4.0E-18 AI017585.1	EST_HUMAN	cu23e06_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'	
5376 14605	23715		2.33	4.0E-18 AI017585.1	EST_HUMAN	cu23e06_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'	
7575 16780	26275		7.21	4.0E-18 AA371807.1	EST_HUMAN	EST8c633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat	
859 10095	19258		9.09	3.0E-18 AA814198.1	EST_HUMAN	ob23h11_s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN	
838 10171	19327		3.12	3.0E-18 BE086634.1	EST_HUMAN	P46782_40S RIBOSOMAL PROTEIN S5.	
3827 13143	22260		1.29	3.0E-18 AL163247.2	NT	CM0-B70690_B70690 Homo sapiens cDNA	
8009 15259	24683		5.18	3.0E-18 BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047	
8941 17819			5.72	3.0E-18 AW022015.1	EST_HUMAN	PM0-EN0081-10030-001-008 BN0081 Homo sapiens cDNA	
255 9531	18862		3.74	2.0E-18 AW836820.1	EST_HUMAN	d31h12_y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'	
1161 10383			130.1	2.0E-18 BE256097.1	EST_HUMAN	CV1-LT0036-1502030-070-#07 LT0036 Homo sapiens cDNA	
3087 12323	21445		0.97	2.0E-18 Q39575	SWISSPROT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'	Dynein GAMMA CHAIN, FLAGELLAR OUTER ARM
5400 14628			2.82	2.0E-18 AA868610.1	EST_HUMAN	bk53807_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1409852 3' similar to TR:O14577	
5442 14668	23824		3.16	2.0E-18 D14547.1	NT	O14577 BAC CLONE RG114406 FROM 7Q31, COMPLETE SEQUENCE.	
5442 14668	23825		3.16	2.0E-18 D14547.1	NT	Human DNA, SINE repetitive element	
5796 15013	24417		3.75	2.0E-18 AW665853.1	EST_HUMAN	h94g01_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975984 3' similar to contains MER19.12 MER19 repetitive element;	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7546	16751	26245	5.35	2.0E-18	AW470791.1	EST_HUMAN	ha33d6.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
8223	17353	26890	6.03	2.0E-18	AW151289.1	EST_HUMAN	THR repetitive element; xg7609.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
8600	10383		6.58	2.0E-18	BE256097.1	EST_HUMAN	MER8 repetitive element; 60114352/F1 NIH MGIC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
4409	13609		0.91	1.0E-18	T95406.1	EST_HUMAN	ye3905.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains L1 repetitive element;
4614	13808		0.94	1.0E-18	Y10196.1	NT	Homo sapiens PHX2 gene
5369	14599	23677	2.61	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLC0KE113'
5475	14702	24057	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit; complete cds
5475	14702	24058	3.08	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit; complete cds
7040	16217	25692	6.86	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RorC gene, and sodium phosphate transporter (NP73) gene, complete cds
8548	17572	23993	2.92	1.0E-18	AF035298.1	NT	Homo sapiens glyican 3 (GPC3) gene, partial cds and flanking repeat regions
552	9803	18930	5.11	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.b2
553	9803	18930	4	9.0E-19	AA281961.1	EST_HUMAN	MER19 repetitive element; z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.b2
6412	15609		3.42	9.0E-19	FB8888.1	EST_HUMAN	HSC23f051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f051
6676	15871	25330	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
6676	15871	25331	3.24	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
7687	16886	28394	4.7	9.0E-19	AB032693.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
8303	9803	18930	10.58	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.b2
1055	10281		1.04	8.0E-19	AW974902.1	EST_HUMAN	MER19 repetitive element; EST337007 IMAGE resequences, MAGN Homo sapiens cDNA
2210	11407	20631	1.9	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
5651	15069	24479	2.02	7.0E-19	AF092090.1	NT	Rattus norvegicus cp151 mRNA, partial cds
8443	18362		2.85	7.0E-19	AA705684.1	EST_HUMAN	z80001.s1 Soares_fetal_liver_splice_1NF-S_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3761	12880		1.41	8.0E-19	AW862930.1	EST_HUMAN	PMD-C70248-131098-001-g01 C70248 Homo sapiens cDNA
4458	13656	22750	1.47	8.0E-19	PR34986	SWISSPROT	OLFACTOORY RECEPTOR 6 (M50)
4458	13656	22751	1.47	8.0E-19	PR34986	SWISSPROT	OLFACTOORY RECEPTOR 6 (M50)
4813	14002		1.34	8.0E-19	AJ271735.1	NT	Homo sapiens Xq11 pseudautosomal region; segment 1/2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5050	142322	23317	1.01	6.0E-19	AL120817.1	EST_HUMAN	DKFZp762F192_1'762 (synonym_hmef2) Homo sapiens cDNA clone DKFZp762F192 5'
5584	14818	24194	5.29	5.0E-19	Q001983	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
8070	17205	28738	7.83	5.0E-19	AV183725.1	EST_HUMAN	x87502_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171 3' similar to contains element MSR1 repetitive element :
561	98111	18934	1.19	4.0E-18	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2642	11825	21040	1.28	4.0E-19	BF697382.1	EST_HUMAN	6021309_0F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
3836	13053	22165	1	3.0E-19	Q2B897	SWISSPROT	BETA2 ADRENERGIC RECEPTOR
3836	13053	22166	*	1	3.0E-19	Q2B897	BETA2 ADRENERGIC RECEPTOR
4271	13474	22570	0.6	3.0E-19	Q43800	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4271	13474	22571	0.8	3.0E-19	Q43800	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4441	13641	22732	1.37	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
6249	15430		2.23	3.0E-19	1_1432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC83222), mRNA
8097	17685		14.35	3.0E-19	AF166520.1	NT	Homo sapiens phorbolin I protein (FPI) mRNA, complete cds
2326	11714	20831	42.82	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4439	13639		1.65	2.0E-19	AI311783.1	EST_HUMAN	q831622_x1 NC1 CGAP_Kids Homo sapiens cDNA clone IMAGE:19158983 similar to TR:Q699388 Q693866 POLYENV GENE :
6572	15788	25231	5.48	2.0E-19	AA012854.1	EST_HUMAN	zg34c58_11 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:360980 5'
8280	17387	26919	1.88	2.0E-19	EF3308867.1	EST_HUMAN	RC3_BT0333_250800_114-f04 BT0333 Homo sapiens cDNA
8280	17387	26920	1.88	2.0E-19	EF3308867.1	EST_HUMAN	RC3_BT0333_250800_114-f04 BT0333 Homo sapiens cDNA
488	9741		1.85	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2130	11329	20548	1.23	1.0E-19	H30795.1	EST_HUMAN	y078607_r1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element :
2677	11859		1.79	1.0E-19	D38044.1	NT	Human gene for A1-receptor, exon 7-9
2800	12040		6.21	1.0E-19	4758677	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN5) mRNA
3379	12608	21740	1.3	1.0E-19	AA834967.1	EST_HUMAN	g149b12_s1 Scores_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element :
5700	14919	24313	2.41	1.0E-19	U12186.1	NT	Oryctolagus cuniculus sodium dicarboxylate cotransporter mRNA, partial cds
6696	15891		3.46	1.0E-19	T98820.1	EST_HUMAN	y72602_r1 Scores fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains OFR repetitive element :
7129	16308	25786	49.35	1.0E-19	AW812259.1	EST_HUMAN	RC0-ST0174-191089-031-b05 ST0174 Homo sapiens cDNA
7133	16310	25792	2.68	1.0E-19	N144631.1	EST_HUMAN	y31609_r1 Scores melanocyte 2NIHM Homo sapiens cDNA clone IMAGE:272872 5'

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 Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8233	17382	26900	1.82	1.0E-19	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
5954	15170	24584	2.54	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 8-1 (Krtaps9-1), mRNA
5954	15170	24585	2.64	8.0E-20	7657286	NT	Mus musculus keratin-associated protein 8-1 (Krtaps9-1), mRNA
3243	12478	21609	0.6	7.0E-20	BF326455.1	EST_HUMAN	PM4-AN0986-050900-003-004 AN00986 Homo sapiens cDNA DKFZp547D092_5'
6088	14532	23556	8.05	7.0E-20	AL138120.1	EST_HUMAN	DKFZp547D092_5' (synonym: hibr1) Homo sapiens cDNA clone n14604_s1 NCI_CGAP_Pt4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29_b2
6824	15820	25279	10.96	7.0E-20	AA557657.1	EST_HUMAN	MER29 repetitive element; n14604_s1 NCI_CGAP_Pt4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29_b2
6824	15820	25280	10.98	7.0E-20	AA557657.1	EST_HUMAN	MER29 repetitive element;
8205	17386		9.91	7.0E-20	6912833	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3530	12753	21886	3.7	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4258	13481	22653	3.37	6.0E-20	BE822434.1	EST_HUMAN	60144231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231_5'
4595	13789		1.15	5.0E-20	AV775123.1	EST_HUMAN	AV775123 HTC Homo sapiens cDNA clone HTCBTA01_5'
6440	15637	25103	6.78	5.0E-20	WV80525.1	EST_HUMAN	zh78d08_s1 Soares_fetal_liver_spliced_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191_3' similar to contains MER30_11 MER30 repetitive element;
6440	15637	25104	5.79	5.0E-20	WV90525.1	EST_HUMAN	zh78d08_s1 Soares_fetal_liver_spliced_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191_3' similar to contains MER30_11 MER30 repetitive element;
1597	10811	19889	1.55	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6435	15632		6.61	4.0E-20	AB74352.1	EST_HUMAN	lz84q03_x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2283398_3'
2108	11307	20521	0.91	3.0E-20	U03888.1	NT	Human BXp21 gene
4192	13396	22496	1.29	3.0E-20	F23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4627	13821	22910	0.81	3.0E-20	AA037618.1	EST_HUMAN	z336b12_s1 Soares_pregnant_uteris_NbHPU Homo sapiens cDNA clone IMAGE:484895_3' similar to
6753	15948		3.21	3.0E-20	D14547.1	NT	contains L1.3 L1 repetitive element;
7256	16476		2.1	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8459	17515	24021	17.57	3.0E-20	BE888422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:2761098_3' similar to SW:RS5_MOUSE
840	10077		13.56	2.0E-20	AW303898.1	EST_HUMAN	xr24e10_x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:3915522_5'
1119	10343	18493	3.84	2.0E-20	AA516335.1	EST_HUMAN	P97461_405 RIBOSOMAL PROTEIN S5_;
1119	10343	18494	3.84	2.0E-20	AA516335.1	EST_HUMAN	ng69h09_s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone FUNCTION UNKNOWN;
							g1224068 ORF2; FUNCTION UNKNOWN;
							ng69h08_s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone FUNCTION UNKNOWN;
							G1224068 ORF2; FUNCTION UNKNOWN;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2769	10077			10.39	2.0E-20 AW303686.1	EST_HUMAN	xr24610.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
4885	14152	23243		4.5	2.0E-20 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4885	14152	23244		4.5	2.0E-20 Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5176	14354			2.31	2.0E-20 5174538	NT	Homo sapiens malate dehydrogenase 1, NAD (soluble)(MDH1) mRNA
6826	16020	25485		8.64	2.0E-20 D10083.1	NT	Homo sapiens RGH gene, retrovirus-like element
6826	16020	25486		8.64	2.0E-20 D10083.1	NT	Homo sapiens RGH 1 gene, retrovirus-like element
8862	18088	23802		2.03	2.0E-20 I55371.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
1881	11949	20393		4.81	1.0E-20 AA281961.1	EST_HUMAN	z11606.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
4431	13631	22726		1.25	1.0E-20 BF115158.1	EST_HUMAN	MER19 repetitive element;
6820	16014	25479		2.76	1.0E-20 11418491	NT	hr8466.x1 NCI_CGAP_Pri1 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1 repetitive element;
8886	17221	28757		3.06	1.0E-20 AF223391.1	NT	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
8886	17603			2.02	1.0E-20 AA204453.1	EST_HUMAN	nc8098.r1 NCI_CGAP_Pri1 Homo sapiens cDNA clone alpha1E subunit (CACNA1E) gene, exons 7-19, and partial cds, alternatively spliced
8806	17412			2.65	8.0E-21 AW888189.1	EST_HUMAN	RC3-NN068-09050-021-803 NN0068 Homo sapiens cDNA
8671	17206	28739		4.47	8.0E-21 AA809411.1	EST_HUMAN	ob71f6.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
8473	17526			2.75	8.0E-21 Q21330	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2036	11237	20444		2.12	7.0E-21 F15800	SWISSPROT	LAMININ BETA-2-CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
2036	11237	20445		2.12	7.0E-21 F15800	SWISSPROT	LAMININ BETA-2-CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4242	13445			6.6	7.0E-21 AA048502.1	EST_HUMAN	z67808.r1 Seares_pregnant uterus_NIH3T3 Homo sapiens cDNA clone IMAGE:487858 5'
6874	15889	25328		7.23	7.0E-21 D14718.1	NT	Human chromosomal protein HMG-1 related gene
7286	16505	25986		3.34	7.0E-21 AA723404.1	EST_HUMAN	zg73d03.s1 Seares_fetal_heart_NkH19W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR;3 OFR repetitive element;
7817	17010	28523		2.14	7.0E-21 7706868	NT	Homo sapiens PTD013 protein (PTD013), mRNA
4081	13291	22390		0.95	8.0E-21 BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
933	10166	16323		0.75	5.0E-21 5802031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4557	13559	22854		3.53	5.0E-21 BE968839.1	EST_HUMAN	601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3938880 5'
4815	14004	23106		7.11	5.0E-21 4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
8889	17470			1.84	5.0E-21 AA383574.1	EST_HUMAN	z172504.r1 Seares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1707	10919	20104	1.53	4.0E-21	AA870713.1	EST_HUMAN	aa86e08_s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 mRNA ;contains OFR_11 OFR repetitive element ;
6027	15235	24658	3.09	4.0E-21	AB019576.1	NT	Ratius nonvegicus mRNA for TTM, complete cds
1805	11014	20207	4.17	3.0E-21	AA218891.1	EST_HUMAN	za15dd6_s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:629771 3'
2239	11434	20658	1.89	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3045	12281	21408	3.89	3.0E-21	AJ007973.1	NT	Homo sapiens LGM2B gene
5744	14963		2.05	3.0E-21	BF184739.1	EST_HUMAN	60184465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084945 5'
6113	15207	24626	6.92	3.0E-21	BF381092.1	EST_HUMAN	RC1-0T0083-100800-019-008 OT0083 Homo sapiens cDNA
6889	16167	25639	14.95	3.0E-21	AW897760.1	EST_HUMAN	CM1-N0063-28040-203-n08 NN0063 Homo sapiens cDNA
8881	18292	23688	5.77	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
148	9430		16.59	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-912 HT0458 Homo sapiens cDNA
943	10176	19329	0.75	2.0E-21	AB001857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
943	10176	19330	0.75	2.0E-21	AB001857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1222	10440		2.48	2.0E-21	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
2602	11786	21006	2.67	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2602	11786	21007	2.67	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
4888	14076		0.85	2.0E-21	AW151673.1	EST_HUMAN	xI67610_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12
6383	15779	25239	2.42	2.0E-21	BE141785.1	EST_HUMAN	MER10 repetitive element ;
6726	15921	25380	4.85	2.0E-21	AU136779.1	EST_HUMAN	CN0-H10103-091198-050-g11 HT10103 Homo sapiens cDNA AU136779 PLACE100552 5'
7825	16827		2.09	2.0E-21	BE350127.1	EST_HUMAN	hi09e01_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_b3
7866	17056	26576	2.39	2.0E-21	BE973829.1	EST_HUMAN	601680536F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
7866	17056	26577	2.39	2.0E-21	BE973829.1	EST_HUMAN	601680536F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
8706	17669		8.43	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyglutamine DNA glycosylase gene, complete cds
1262	10477	19639	1.38	1.0E-21	AA557657.1	EST_HUMAN	n146c04_s1 NCI_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043778 similar to contains MER29_b2
1406	10619		2.37	1.0E-21	AL601264.1	EST_HUMAN	MER29 repetitive element ;
5869	15087		2.67	1.0E-21	AL079752.1	EST_HUMAN	ar88d12_x1 Barstead colon HPLRB7 Homo sapiens cDNA clone DKFZp4340830_r1_434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp4340830 5'
6162	15345	24782	4.61	1.0E-21	AI223104.1	EST_HUMAN	qq4f05_x1 Soares testis_NH1 Homo sapiens cDNA clone IMAGE:1808336 3' similar to gb:M64241 QM
9107	17927		1.29	1.0E-21	AF046133.1	NT	Homo sapiens chromosome Xp22.410-8
9281	18042	23828	2.66	1.0E-21	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4404	13604	22704	6.07	9.0E-22	AI702438.1	EST_HUMAN	Iz04603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
7372	16588	28077	5.14	9.0E-22	AV761874.1	EST_HUMAN	NEUTRAL PROTEASE LARGE SUBUNIT :
8198	17330	26872	3.42	9.0E-22	AU140358.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDSCCCG05 5'
9556	10189		3.77	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000334 5'
871	9916	18045	7.04	7.0E-22	AL163246.2	NT	Cm0-h10178-28109-078-h05 H10719 Homo sapiens cDNA
4268	13471	22584	2.28	7.0E-22	QB1838	SWISSPROT	Hom sapiens chromosome 21 segment HS21C046
5063	14243	23330	1	7.0E-22	AB008681.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M1)
6729	15924	25383	5.03	7.0E-22	M78559.1	EST_HUMAN	Home sapiens gene for activin receptor type II B, complete cds EST00738 Fetal brain, Stratagene (cat#862008) Homo sapiens cDNA clone HFBCF07
6863	16141	25610	3.07	7.0E-22	AF008660.1	NT	Home sapiens T cell receptor beta locus, TCRBV12S2 region
6639	16735		2.7	6.0E-22	AW029123.1	EST_HUMAN	wx05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
5684	15101	24512	3.17	5.0E-22	AL163303.2	NT	Home sapiens chromosome 21 segment HS21C103
7173	16350	25828	5.76	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
8642	17820		2.41	5.0E-22	BF476511.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:3255888 3' similar to contains Aliu repetitive element;
36115	12836		0.97	4.0E-22	AJ271735.1	NT	Home sapiens Xq13 pseudautosomal region; segment 1/2
7310	16528	26019	2.62	4.0E-22	BF218030.1	EST_HUMAN	801882813F NIH MGCC 57 Homo sapiens cDNA clone IMAGE:4065434 5'
9113	17931		1.88	4.0E-22	AL163209.2	NT	Home sapiens chromosome 21 segment HS21C009
966	10189		1	3.0E-22	AI469879.1	EST_HUMAN	Im14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbl19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1.M1.L1 repetitive element;
2634	11722	20839	3.24	3.0E-22	AI859038.1	EST_HUMAN	wf66b4.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429839 3' similar to SW:RU21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21.;
3853	12874		1.38	3.0E-22	D14718.1	NT	Human chromosomal protein HM1 related gene
4814	14003	23105	2.9	3.0E-22	AI080125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to qb28c07.x1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
1023	11127		3.44	2.0E-22	N24942.1	EST_HUMAN	yx73d05.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:267369 3'
2489	11679	20896	1.17	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3398	12625	21756	3.85	2.0E-22	8394043	NT	Home sapiens protein kinase, AMF -activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4211	13414	22509	1.48	2.0E-22	AV817784.1	EST_HUMAN	PM1-ST0262-2611199-001-d12_S71262 Homo sapiens cDNA
6142	14861	24361	3.5	2.0E-22	Bf092116.1	EST_HUMAN	RC0-TN0078-15090-025-h12 TN0079 Homo sapiens cDNA
6893	16171	25643	2.51	2.0E-22	AI276522.1	EST_HUMAN	qj76h06.x1 Soares_NhHPu_S1 Homo sapiens cDNA clone IMAGE:1878289 3' similar to contains MER29 13 MER29 repetitive element;
8234	17363	26801	2.32	2.0E-22	AW418860.1	EST_HUMAN	ha24r04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
8271	17919	23872	1.45	2.0E-22	AL163280.2	NT	Home sapiens chromosome 21 segment HS21C050

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
1844	11052	20243	1.57	1.0E-22 AW865517.1	EST_HUMAN	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA Human familial Alzheimer's disease (STM2) gene, complete cds		
2546	11734	20951	1.88	1.0E-22 U50671.1	NT			
3388	12615	21748	1.63	1.0E-22 D14547.1	NT	Human DNA, SINE repetitive element		
9162	17881		6.27	9.0E-23 AW802801.1	EST_HUMAN	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA Gallus gallus Dach2 protein (Dach2) mRNA, complete cds		
3546	12769	21897	0.65	8.0E-23 AF198348.1	NT			
3282	12513		2.13	7.0E-23 AF647248.1	EST_HUMAN	AV647248 GLC Homo sapiens cDNA clones GLCAW C07.3 Homo sapiens Not56 (D_melanogaster)-like protein (NOT56), mRNA		
7609	16812	26308	4.68	7.0E-23 5031652	NT			
3412	12639		1.55	6.0E-23 AF198333.1	NT	Reittius novergicus RIM1B (Rim1B) mRNA, complete cds		
4254	13457	22549	1.11	6.0E-23 AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C049		
8412	17486	24008	2.85	6.0E-23 AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds		
8412	17486	24009	2.85	6.0E-23 AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds		
8617	17614	23987	4.22	6.0E-23 AI209130.1	EST_HUMAN	q8g9cd3_x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639460_3' similar to SW:MV10_MOUSE_P23249 PROTEIN MOV-10 :		
						Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), calactin (CALT), NAD(P)H dehydrogenase-like protein (NSDH), and L1>		
5414	14842	23774	4.25	5.0E-23 U82871.2	NT	Pango pygmaeus olfactory receptor (PPY116) gene, partial cds		
5769	18084	24388	4.03	5.0E-23 AF179818.1	NT	Pango pygmaeus olfactory receptor (PPY116) gene, partial cds		
6267	18084	24389	3.15	5.0E-23 AF179818.1	NT	z35e08_r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968_5' similar to contains MER29.12 MER29 repetitive element :		
6410	15607	25073	3.27	3.0E-23 AA130165.1	EST_HUMAN	Human endogenous retroviral element HC2		
6839	16044	25508	4.41	3.0E-23 Z70584.1	NT	Human endogenous retroviral element HC2		
6839	16044	25509	4.41	3.0E-23 Z70584.1	NT	RC3-NN0066-270400-011-h01 NN0066 Homo sapiens cDNA		
7172	16349		2.65	3.0E-23 AW897927.1	EST_HUMAN			
672	9917	18048	6.01	2.0E-23 AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene		
1151	11944		2.89	2.0E-23 M65270.1	NT	Human matrix Gla protein (MGP) gene, complete cds		
2748	11927	21141	1.06	2.0E-23 P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXBRACTION-LIKE)		
2748	11927	21142	1.06	2.0E-23 P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXBRACTION-LIKE)		
3350	12578		1.34	2.0E-23 AI201458.1	EST_HUMAN	q8f3f1_x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:1943757_3 similar to TRQ13537 Q13537		
3697	12917		4.49	2.0E-23 BE165980.1	EST_HUMAN	MER37 TRANSPOSSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;		
3654	13169	22283	3.05	2.0E-23 I598931.1	EST_HUMAN	MR3-H170487-150200-113-g01 HT0487 Homo sapiens cDNA		
3654	13169	22284	3.05	2.0E-23 I598931.1	EST_HUMAN	Y16a022_r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418_5'		

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8418	15815			8.05	2.0E-23 AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 6 (CYP3A5) gene, partial cds
8395	17474			4.45	2.0E-23 M32858.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
8951	17625			1.87	2.0E-23 AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV1232 region
8079	18295			1.78	2.0E-23 AU133931.1	EST_HUMAN	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4527	13723	22819		1.69	1.0E-23 AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4777	13986			4.93	1.0E-23 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5973	15187			2.6	1.0E-23 BE378471.1	EST_HUMAN	601236455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36088653 5'
6582	15778	25238		2.4	1.0E-23 AA448097.1	EST_HUMAN	ZW8266.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7822698 5' similar to contains PTR5 12 PTR5 repetitive element;
559	9809			1.82	9.0E-24 AA863213.1	EST_HUMAN	ab75ab8.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to TRE19822 E19822 CA PROTEIN 1
4649	13843	22833		1.08	8.0E-24 P23289	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN 13
4649	13843	22834		1.06	8.0E-24 P23289	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN 13
3853	13089			1.26	7.0E-24 AW937954.1	EST_HUMAN	QVO-DT0047-170201-122-606 DT0047 Homo sapiens cDNA clone XR17f03.x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Ali repetitive element; contains MER1912 MER19 repetitive element;
7234	18455			2.37	7.0E-24 AW303317.1	EST_HUMAN	Macaca fasciata mRNA for Testis-Specific Protein Y (TSPY), complete cds
713	9955			2.33	6.0E-24 AB001421.1	NT	
848	10086	19244		16.07	8.0E-24 AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
3947	13163	22278		8.91	5.0E-24 AJ228043.1	NT	Homo sapiens 59 kb contig between ANL1 and CBR1 on chromosome 21q22, segment 3/3
5628	14852	24235		3.4	4.0E-24 AA594178.1	EST_HUMAN	nn31h05.61 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:3464498 5'
7735	16932	28440		2.1	4.0E-24 BE5444822.1	EST_HUMAN	P31795 POL POLYPROTEIN
8194	17721	23982		2.81	4.0E-24 AB029016.1	NT	Homo sapiens mRNA for KIAA093 protein, partial cds
9053	17924	23875		1.67	4.0E-24 11418318 NT		Homologous G-2 and S-phase expressed 1 (GSTSE1), mRNA
6901	16058	28526		2.35	3.0E-24 AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8876	17773	23942		2.46	3.0E-24 BF1217762.1	EST_HUMAN	601810449F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053396 5'
2315	11509	20730		2.19	2.0E-24 AA167539.1	EST_HUMAN	ZP11ff98.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161 5'
3781	12899			0.88	2.0E-24 AW889189.1	EST_HUMAN	RC3-NN0068-080500-021-603 NN0068 Homo sapiens cDNA
8714	18339			9.69	2.0E-24 M28877.1	NT	Human O family dispersed repeat element
1871	10884	20068		2.13	1.0E-24 7706340 NT		Homo sapiens CG1-127 protein (LOC51846), mRNA
2633	11816			1.53	1.0E-24 AW820194.1	EST_HUMAN	Q10-S10294-10040-185-c10 ST0294 Homo sapiens cDNA
2985	12222	21355		1.19	1.0E-24 D88423.1	NT	Mus musculus mRNA for HGT keratin, partial cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4256	13459			2.16	1.0E-24 AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2
6312	15493	24939		3.94	1.0E-24 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6439	15638	25102		3.19	1.0E-24 AW801164.1	EST_HUMAN	CMD-N1010-130300-281-007 NN1010 Homo sapiens cDNA
9288	18048			1.24	1.0E-24 BE677411.1	EST_HUMAN	7683h3_x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279805 3' similar to contains MER10.3 MER10 repetitive element;
8194	17326	26883		1.83	9.0E-25	7706707 NT	Homo sapiens putative secreted protein (SG11). mRNA
5020	14207	23292		3.45	7.0E-25 AA4683944.1	EST_HUMAN	ne82610.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains MER1.b2 THR MER1 repetitive element;
6535	15731	25195		4.4	7.0E-25 AA468346.1	EST_HUMAN	ne6609.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST repetitive element;
8195	17327	28889		10.9	7.0E-25 AA583540.1	EST_HUMAN	nf25h6.s1 NCI_CGAP_ProB605 RIBOSOMAL PROTEIN L14EA. ;
6885	14531			4.79	8.0E-25 WV87623.1	EST_HUMAN	nf65h07.r1 Scarecs_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416889 5'
6384	15564	25021		10.69	8.0E-25	7305660 NT	Mus musculus globin (Oglob), mRNA
7863	17053	26574		4.51	5.0E-25 AW879107.1	EST_HUMAN	EST381217 MAGE resequences. MAGP Homo sapiens cDNA
1448	10661	19839		3.01	4.0E-25 T98107.1	EST_HUMAN	ye68f04.r1 Scarecs_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3380	12607			2.94	4.0E-25 AW887671.1	EST_HUMAN	PM3-070093-280200-001-007 O70093 Homo sapiens cDNA
4307	13508			3.15	4.0E-25 BE170957.1	EST_HUMAN	QV3-H1T0543-140-00-149-e11 HT0543 Homo sapiens cDNA
3292	12523	21654		3.43	3.0E-25	8923321 NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3282	12523	21655		3.43	3.0E-25	8923321 NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
4916	14104	23197		0.71	3.0E-25 P29622	SWISSPROT	KALLIKREIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
5255	14428	23504		0.97	3.0E-25 H52187.1	EST_HUMAN	y60511.r1 Scarecs_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:209861 5' similar to contains KALLIKREIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6577	157731	25234		4.44	3.0E-25 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C10
7601	16804	26289		2.11	3.0E-25 AA579013.1	EST_HUMAN	nt30h10.s1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.L1.L1
1555	10570	19735		3.68	2.0E-25	5032158 NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2274	11469	20690		8.59	2.0E-25 BE883016.1	EST_HUMAN	601511530FT1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2784	11696	20914		6.4	2.0E-25 P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4172	13376	22475		1.92	2.0E-25 P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S18
4172	13376	22476		1.92	2.0E-25 P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
7006	16184	25656		3.35	2.0E-25 AL449573.1	EST_HUMAN	AL449573 Homo sapiens cDNA
369	9835	18768		1.02	1.0E-25 AL040229.1	EST_HUMAN	DKFZp434H0313_r1
1255	10471			3.27	1.0E-25	9835487 NT	Human endogenous retrovirus, complete genome

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2398	11591	20809	2.1	1.0E-25	Q08055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4875	14063	23158	3.1	1.0E-25	BE_162737.1	EST_HUMAN	PMI-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
5996	18070	24709	2.88	1.0E-25	AA582690.1	EST_HUMAN	mn541n1 s1 NCI CGAP Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
6429	15626	25091	5.51	1.0E-25	AA709078.1	EST_HUMAN	zB86p4_s1 Scars_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1384822 3' similar to contains PTR5.13 PTR5 repetitive element
7541	16748	28240	3.92	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
8409	17484	28597	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
8409	17484	28598	1.54	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
9234	18008		1.31	1.0E-25	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germinal)
2445	11636	20857	1.4	9.0E-26	AL_163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
8272	18107		2.48	9.0E-26	AL_163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5532	14758		1.92	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1556	10770	19942	2.5	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3958	13173	22288	1.42	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4141	13347	22448	2.19	7.0E-26	AW340153.1	EST_HUMAN	hd02612x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2808366 3'
8172	17304		9.62	7.0E-26	AA115895.1	EST_HUMAN	zr30dd8_r1 Strategene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548943 5'
8999	17859		1.79	7.0E-26	AW9654559.1	EST_HUMAN	gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); EST368629 MAGE resequences, MAGC Homo sapiens cDNA
2192	11389	20612	2.57	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3320	12549	21683	1.57	6.0E-26	AA208131.1	EST_HUMAN	zq52R64_r1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:845271 5'
8180	17312	26854	6.07	6.0E-26	AL_163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1185	10406	19560	3.11	5.0E-26	A1708235.1	EST_HUMAN	as38h08_x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319510 3' similar to WP:F49C12.11 CE03371;
1185	10406	18561	3.11	5.0E-26	A1708235.1	EST_HUMAN	as38h08_x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319510 3' similar to WP:F49C12.11 CE03371;
6883	18074		3.97	4.0E-28	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
7253	16473	25985	4.16	4.0E-28	BE268187.1	EST_HUMAN	601919345F NIH_3T3G_7 Homo sapiens cDNA clone IMAGE:25535210 5'
7869	17059	26580	1.85	4.0E-28	AL_163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
1730	10942	20124	1.37	3.0E-28	D14547.1	NT	Human DNA, SINE repetitive element
1972	11176	20382	1.31	3.0E-28	AL045855.2	EST_HUMAN	DKFZp434l068_r1 434 (synonym: hhs3) Homo sapiens cDNA clone DKFZp434l066 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
200	11203		3.1	3.0E-26	AA115895.1	EST_HUMAN	z30d08.1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to qb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); z330f110.1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G985374 G685374
3760	12979	22094	1.44	3.0E-26	AA152464.1	EST_HUMAN	z330f110.1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G985374 G685374 THYROID RECEPTOR INTERACTOR;
3780	12979	22095	1.44	3.0E-26	AA152464.1	EST_HUMAN	G685374 THYROID RECEPTOR INTERACTOR;
6048	15216	24636	9.41	3.0E-26	BF245458.1	EST_HUMAN	60186-9965F1 NIH MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
7313	16531		1.99	3.0E-26	AF039405.1	NT	Homo sapiens MILL (MILL) gene, exons 1-3, and partial cds
8102	17236	28772	2.54	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8102	17236	28773	2.54	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
8129	17263	26807	10.41	3.0E-26	AA583173.1	EST_HUMAN	nr 37dd5_s1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11 OFR repetitive element;
8183	17974		1.58	3.0E-26	AW073434.1	EST_HUMAN	nr 37dd9_x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.11 MER30 repetitive element;
888	9831	19062	6.9	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1834	11042		3.51	2.0E-26	AL038099.2	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hkd2) Homo sapiens cDNA clone DKFZp566L171 3'
3197	12432	21588	4.84	2.0E-26	XB86894.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
7338	16554		3.33	2.0E-26	DR87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7771	16888	28479	4.24	2.0E-26	AB014142.1	EST_HUMAN	nr 89a01_x1 NCI_CGAP_Gcs4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 MER20 repetitive element;
7856	17085		2.02	2.0E-26	AF055086.1	NT	Homo sapiens MHC class 1 region
8522	17553		2.84	2.0E-26	AB0317859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
8733	18284	23683	1.44	2.0E-26	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12orfF3), mRNA
134	9417	18551	11.48	1.0E-26	BE170371.1	EST_HUMAN	QV4-H1T0538-02030-123-a02 HT0538 Homo sapiens cDNA
2014	11216	20425	1.53	1.0E-26	AL038463.2	EST_HUMAN	DKFZp34H1910_1_434 (synonym: hles3) Homo sapiens cDNA clone DKFZp34H1910 5'
2528	11717	20834	1.71	1.0E-26	BE814995.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2647	11830		22.1	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
6014	15284		2.88	1.0E-26	BE165880.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
7469	16877		3.11	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146_r1 566 (synonym: hkd2) Homo sapiens cDNA clone DKFZp566C2146 5'
8780	18357		2.07	1.0E-26	HS50983.1	EST_HUMAN	QH229032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
8895	16107		3.98	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
8225	17398		5.28	9.0E-27	BF44556.1	EST_HUMAN	nr 3cd7_x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.11 OFR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10 9308	18408	2.21	8.0E-27 AW31462.1	EST_HUMAN	NT	W148c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR,b2	
584 9874		5.13	8.0E-27 AL163227.2	EST_HUMAN	THR repetitive element;	Homo sapiens chromosome 21 segment HS21C027	
1420 10639	19801	56.1	8.0E-27 AW162737.1	EST_HUMAN	NT	au87f08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558	
1420 10639	19802	56.1	8.0E-27 AW162737.1	EST_HUMAN	NT	au87f08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558	
2133 11331	20551	1.66	8.0E-27 AW864776.1	EST_HUMAN	PM2-SN0018-22030D-002-a07 SN0018 Homo sapiens cDNA		
3148 12383	21516	3.14	8.0E-27 P12236	SWISSPROT	ADP ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCATOR 3) (ANT 3)		
3327 12556	21693	0.68	8.0E-27 AF161897.1	NT	Homo sapiens WRN (WRN) gene, complete cds		
6077 14523		6.24	8.0E-27 BE928560.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA		
6104 15198	24616	2.63	8.0E-27 N84970.1	EST_HUMAN	J1751F Human fetal heart; Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1		
690 98833		1.34	7.0E-27 Z70584.1	NT	Human endogenous retroviral element HC2		
5122 14301		2.35	7.0E-27 AW628172.1	EST_HUMAN	h15112.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:076040		
7335 16551		4.9	7.0E-27 AJ271795.1	NT	OT8040 ORF2; FUNCTION UNKNOWN;		
8626 17809		1.82	7.0E-27 AV723385.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2		
7314 16532	28021	25.43	6.0E-27 M28697.1	NT	AV723385 HTB Homo sapiens cDNA clone HTBAHE025'		
7145 16322	25803	3.44	5.0E-27 BF688614.1	EST_HUMAN	Human nucleolar protein (B23) mRNA, complete cds		
7145 16322	25804	3.44	5.0E-27 BF688614.1	EST_HUMAN	602121491F1 NIH MGIC 56 Homo sapiens cDNA clone IMAGE:4278527 5'		
8130 17264	28808	2.76	4.0E-27 X89211.1	NT	H. sapiens DNA for endogenous retroviral like element		
2008 11211	20421	7.24	3.0E-27 X60958.1	NT	R. rattus RYAA3 mRNA for a potential ligand-binding protein		
4257 13460	22552	1.33	3.0E-27 BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA		
5362 14592	23669	6.3	3.0E-27 AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08		
6858 16108	25574	3.1	3.0E-27 BF035327.1	EST_HUMAN	601458531F1 NIH MGIC 86 Homo sapiens cDNA clone IMAGE:3862086 5'		
8287 18045		1.78	3.0E-27 AW502868.1	EST_HUMAN	UI-HFBN0-ekg-e-120-Ui,r1 NIH MGIC 50 Homo sapiens cDNA clone IMAGE:3077879 5'		
43 9339	18446	20.19	2.0E-27 AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds		
1860 11067		35.81	2.0E-27 AA565345.1	EST_HUMAN	nk10b10-s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S		
3073 12309		12.63	2.0E-27 AW629172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); h15112.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975878 3' similar to TR:076040		
					O76040 ORF2; FUNCTION UNKNOWN;		

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3190	12425	21558	1.36	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3190	12425	21659	1.36	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6844	16033		2.26	2.0E-27	AA551527.1	EST_HUMAN	nh08hs5_s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1:3 L1 repetitive element;
7528	16733	28223	3.41	2.0E-27	AU121685.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000748 5'
8021	11067		18.89	2.0E-27	AA565345.1	EST_HUMAN	rh01b0_s1 NCI_CGAP_Pr11 Homo sapiens cDNA clone IMAGE:1000698 similar to gb:NM17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
442	8898		2.08	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1004	10235	19388	1.34	1.0E-27	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4057	13267		1.07	1.0E-27	BE350127.1	EST_HUMAN	h109g1_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29_b3 MER29 repetitive element;
5900	15117	24529	5.8	1.0E-27	6005655	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6026	15234	24658	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6026	15234	24857	1.89	1.0E-27	F30158.1	EST_HUMAN	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
6760	15955		2.91	1.0E-27	BE079780.1	EST_HUMAN	RC08-BT0827-140200-011-E08 BT0827 Homo sapiens cDNA
6899	16177	25648	3.53	1.0E-27	DB7449.1	NT	Human mRNA for KIAA02260 gene, partial cds
8196	17328	26870	3.61	1.0E-27	AF111093.1	NT	Bos taurus latrophilin 3 splice variant bba1 mRNA, complete cds
139	8420		1.89	9.0E-28	BE348399.1	EST_HUMAN	hw17c1_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
316	9587	18718	2.2	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR [3] TR:Q07280 TR:Q07313 ;
6355	17448		6.41	8.0E-28	BF377859.1	EST_HUMAN	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
8699	18204		2.25	8.0E-28	AW157571.1	EST_HUMAN	CM2-TN0140-070800-372-g01 TN0140 Homo sapiens cDNA
1189	10410	19584	20.71	7.0E-28	AU142750.1	EST_HUMAN	TR:OB0302_O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element;
7742	16938	26447	10.67	7.0E-28	11411866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8314	17418		2.77	7.0E-28	AV735348.1	EST_HUMAN	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
8971	17841					EST_HUMAN	ae06e35_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains THR:b1 repetitive element; contains element PTR5 repetitive element;
323	9594		3.6	6.0E-28	AA504562.1	EST_HUMAN	w01Bc07_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR:b1 THR repetitive element;
3885	13199	22307	1.47	5.0E-28	RJ79762.1	EST_HUMAN	y8f10_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2588	11774	20894	2.43	4.0E-28	AW195068.1	EST_HUMAN	xn33c09.x1 NC_ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to Sv.GG95_HUMAN
2833	12171	21304	1.12	4.0E-28	4505316 NT		Q83379_GOLGIN-95
3072	12308	21430	4.2	4.0E-28	BE409100.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 1 (MYPFT1), mRNA
5271	14444	23515	12.18	4.0E-28	AF219927.1	NT	Hom sapiens diacylglycerol kinase iota (DGKI) gene, exon 23
6222	15403	24844	2.04	4.0E-28	AI198941.1	EST_HUMAN	qf66110.x1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
7441	16849		4.32	4.0E-28	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen genes families
7576	16781		24.75	4.0E-28	AB038241.1	NT	Ferritin GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
7594	15403	24844	3.74	4.0E-28	AI198941.1	EST_HUMAN	qf66110.x1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
1280	10503		1.85	3.0E-28	AF156382.1	NT	Homo sapiens metalloproteinase-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
6127	15922	26381	2.47	3.0E-28	EF354030.1	EST_HUMAN	MR3-H10713-28050-013-09 HT0713 Homo sapiens cDNA
7509	16714	28202	1.85	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
8776	17708		2.07	3.0E-28	AI831991.1	EST_HUMAN	wf88707.x1 NC_ CGAP Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element;contains element:HGR repetitive element;
8970	17840	23912	1.53	3.0E-28	AI1430460 NT		Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8970	17840	23913	1.53	3.0E-28	AI1430460 NT		Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
88	9381	18511	7.51	2.0E-28	BE02167.1	EST_HUMAN	RC1-PT0284-22030-019-005 BT0254 Homo sapiens cDNA
1173	10394	19546	10.56	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-4
2439	11630	20851	1.92	2.0E-28	AI348634.1	EST_HUMAN	q035b05.x1 NC_ CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2.L1 repetitive element;
5802	15019		6.05	2.0E-28	BF212805.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA
6953	16131		4.38	2.0E-28	AW972305.1	EST_HUMAN	EST384394 IMAGE sequences, MAGI Homo sapiens cDNA
8137	17270	26815	2.58	2.0E-28	AF224669.1	NT	Home sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8756	17697		1.37	2.0E-28	AI063176.1	EST_HUMAN	y79cg9.r1 Scores infant brain TNB Homo sapiens cDNA clone IMAGE:44300 5'
1472	10685	19880	2.38	1.0E-28	D98044.1	NT	Human gene for Ah-receptor, exon 7-9
2188	11383	20607	5.07	1.0E-28	BF333236.1	EST_HUMAN	QY1-B10821-20890-360-B03 BT0821 Homo sapiens cDNA
4568	13760		2.28	1.0E-28	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
6414	15611		6.28	1.0E-28	11428985 NT		Home sapiens similar to ribosomal protein L12 (H. sapiens) (LOC633091), mRNA
8469	15668		3.16	1.0E-28	8922783 NT		Home sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6848	16037	25501	4.97	1.0E-28	AA308744.1	EST_HUMAN	EST178615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
7030	16207	25684	3.28	1.0E-28	4758431 NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	
7030	16207	25685	3.28	1.0E-28	4758431 NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA	
8319	17422		3.88	1.0E-28	AA054182.1	EST_HUMAN	25101.1 Soares retina N2b4R Homo sapiens cDNA clone IMAGE:380448 5'
9106	18091		1.83	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9211	18313	23593	3.18	9.0E-29	AW663987.1	EST_HUMAN	h176g06.x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978268 3'
8873	17770		3.8	8.0E-29	Q00130	SWISSPROT	HYPOTHETICAL PROTEIN
1582	10793	18972	1.81	7.0E-29	AW968447.1	EST_HUMAN	EST378521 MAGE like sequences, MAGI Homo sapiens cDNA
9284	18030		6.88	7.0E-29	AJ132352.1	NT	Reffit's nonvegous mRNA for 45 kDa secretory protein, partial
602	9849	18988	15.71	6.0E-29	AB38748.1	EST_HUMAN	wpsgb01_x1 NC1 CGAP Bm25 Homo sapiens cDNA clone IMAGE:24486985 3' similar to TR:O15475
8829	17621		5.28	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN contains LTR.61 LTR7 repetitive element;
8719	17673		1.47	6.0E-29	BF568097.1	EST_HUMAN	RC3-UT0632-21080-021-05 UT0632 Human sapiens cDNA
5022	14209		1.78	5.0E-28	AL163203.2	NT	602184922F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:43000079 5'
6880	15885		9.84	5.0E-29	AW887541.1	EST_HUMAN	50222_x1 Soares_HS21C003 Homo sapiens chromosome 21 segment HS21C003
3198	12433		2.82	4.0E-29	AI752367.1	EST_HUMAN	cml5cd2_x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cml5cd2 random
5659	14882		7.39	4.0E-29	BE164930.1	EST_HUMAN	QV1-JT0471-28030-121-05 JT0471 Homo sapiens cDNA
6888	15894	25355	5.52	4.0E-29	JO4988.1	NT	Human 30 kB heat shock protein gene, complete cds
4408	13608	22708	1.67	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 5-phospho-ribosyl-1-hydroxypterin synthase, complete cds
4144	13935	23039	1.07	3.0E-29	BF332328.1	EST_HUMAN	QV1-ET0821-12080-360-503 BT0821 Homo sapiens cDNA
6854	16042	26506	2.62	3.0E-29	AW303317.1	EST_HUMAN	xv17f03_x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.12 MER19 repetitive element;
6928	16121		2.61	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7818	17011	26524	2.7	3.0E-29	AA403053.1	EST_HUMAN	zg2501.1 Soares_nht Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
8518	17550		1.98	3.0E-29	DG8882.1	NT	G1335769 GAG-POL POLYPROTEIN
499	9751	18878	1.54	2.0E-29	AF084869.1	NT	Human HsLM15 mRNA for HsLM15, complete cds
499	9751	18879	1.54	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-B (env) gene, complete cds
1519	10733	19803	6.77	2.0E-29	AI963604.1	EST_HUMAN	wr65d10_x1 NC1_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546
1519	10733	19904	6.77	2.0E-29	AI963604.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
							wr65d10_x1 NC1_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4284	13487	22558	1.91	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6914	16102	25568	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
6914	18102	25569	4.35	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25806	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7147	16324	25807	4.53	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8012	17152		1.9	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnaj (SPP31), mRNA
8047	17183		2.01	2.0E-29	AW880701.1	EST_HUMAN	Q96-O70032-080300-155-d01 OT0032 Homo sapiens cDNA
8284	17391		1.8	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
6714	15909	25383	11.36	1.0E-29	AW983880.1	EST_HUMAN	RC1-HN003-229300-021-004 HN0003 Homo sapiens cDNA
5620	15137	24548	3.11	9.0E-30	AA761215.1	EST_HUMAN	nz2c07_5.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:12883323' similar to contains MER4_b1 MER4 repetitive element;
8398	17475		4.04	9.0E-30	11422745	NT	Homo sapiens zinc/finger regulated transporter-like (ZIRTL), mRNA
5797	15014		9.51	8.0E-30	F08988.1	EST_HUMAN	HSC23E051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
6550	15748	25206	3.85	8.0E-30	AA388873.1	EST_HUMAN	EST97317 Thymus l/Homo sapiens cDNA 5' end similar to EST containing O family repeat
1504	10717		1.52	7.0E-30	BE081133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA
1743	10955	20138	1.39	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	12388	21520	2.68	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
9235	14489		2.32	6.0E-30	X51765.1	NT	Human lambda-immunoglobulin constant region complex (germline)
3989	13203	22311	40.02	5.0E-30	A1389862.1	EST_HUMAN	Ig92g3_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:21162763' similar to contains Aliu repetitive element;
5285	18132		5.38	5.0E-30	U87834.1	NT	Human acetylhydrolase (ACO2) gene, exon 7
7484	16872		3.56	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7714	16913	26421	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
7714	16913	26422	7.8	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2111	11310	20523	2.02	4.0E-30	AW837471.1	EST_HUMAN	CY3-DT0043-090200-080-d08 DT0043 Homo sapiens cDNA
2111	11310	20524	2.02	4.0E-30	AW837471.1	EST_HUMAN	CY3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
6746	16941	25401	4.27	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091189-035-f08 ST0181 Homo sapiens cDNA
1160	10382		1.64	3.0E-30	A138955.1	EST_HUMAN	qq83c05_x1 Scores_total_fetus_Np2HF8_9w Homo sapiens cDNA clone IMAGE:1838920 3' similar to contains MER29_b2 MER29 repetitive element;
3740	12960	22075	0.84	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-8
7759	16655	28463	2.59	3.0E-30	P34056	SWISSPROT	TRANSCRIPTION FACTOR AP-2
681	8924	18055	0.91	2.0E-30	AW857315.1	EST_HUMAN	CM0-C10307-310100-158-h03 CT0307 Homo sapiens cDNA
1092	10316		2.41	2.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1473	10886	18861	4.84	2.0E-30	BE175877.1	EST_HUMAN	RCG5-H10582-110400-013-H08 HT0582 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2675	11857	21072	8.48	2.0E-30	BE785232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2870	12108	21237	8.13	2.0E-30	AF114158.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3771	12899	22105	1.85	2.0E-30	AW206581.1	EST_HUMAN	U1-H-B11-efc-c-12-0-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4787	13976	23079	1.85	2.0E-30	BE298945.1	EST_HUMAN	6011198860-F NIH MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
4787	13976	23080	1.85	2.0E-30	BE298945.1	EST_HUMAN	6011198860-F NIH MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
6633	15829	25291	6.69	2.0E-30	C18839.1	EST_HUMAN	C18839 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-570C01 5'
6665	15860	25318	2.21	2.0E-30	BE670617.1	EST_HUMAN	7837c12x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHS A_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
6665	15860	25319	2.21	2.0E-30	BE670617.1	EST_HUMAN	7837c12x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHS A_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR;
7072	16249	25722	2.78	2.0E-30	AW971988.1	EST_HUMAN	EST383637 MAGE sequences MAGL Homo sapiens cDNA
7102	16279	25759	5.6	2.0E-30	AW470791.1	EST_HUMAN	ha33dd8x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR 63 THR repetitive element;
281	9565	18698	16.27	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN-570C01 5'
544	9795	18919	3.42	1.0E-30	AW468897.1	EST_HUMAN	hd30b6x1.x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810981 3' similar to contains MER11.2 MER1 MER1 repetitive element;
723	9865	19103	2.58	1.0E-30	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2779	11376	20598	19.88	1.0E-30	AA664377.1	EST_HUMAN	ec77bb07.81 Strategene lung (#337210) Homo sapiens cDNA clone IMAGE:8685399 3'
2425	11616	20838	2.33	1.0E-30	BF347728.1	EST_HUMAN	602022560-F NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4157891 5'
2982	12200	21334	1.51	1.0E-30	5803091 NT	Homosapiens methionine aminopeptidase; eIF-2-associated p67 (MNP67) mRNA	
3019	12255	21384	0.91	1.0E-30	AA315045.1	EST_HUMAN	EST186868 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
6886	15566	25023	2.19	1.0E-30	BF183230.1	EST_HUMAN	601809832F1 NIH MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
9037	18228		9.1	1.0E-30	I455593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3748	12988	22082	0.91	9.0E-31	T73025.1	EST_HUMAN	#937224 Homo sapiens cDNA clone IMAGE:85570 5'
3748	12988	22083	0.91	9.0E-31	T73025.1	EST_HUMAN	#937224 Homo sapiens cDNA clone IMAGE:85570 5'
1084	10309	19461	2.7	8.0E-31	8923389 NT	Homosapiens hypothetical protein FLJ20420 (FLJ20420), mRNA	
2376	11569		13.17	8.0E-31	AL165208.2	NT	Homosapiens chromosome 21 segment HS21C008
718	9860		1.45	7.0E-31	AA372637.1	EST_HUMAN	EST84855 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2628	11811	21028	2.27	7.0E-31	BE326517.1	EST_HUMAN	hw05a11-x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2628	11811	21029	2.27	7.0E-31	BE326517.1	EST_HUMAN	hw05a11-x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8871	17769	23840	2.52	7.0E-31	X51755.1	NT	Human limbde-immunoglobulin constant region complex (germline)

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3658	12879			2.63	8.0E-31 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6509	15705			6.07	8.0E-31 AF055068.1	NT	Homo sapiens MHC class 1 region
7324	16540	26029		2.02	8.0E-31 AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA10050505 5
8455	17512	24020		1.83	8.0E-31 AW372888.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
8594	18152			2.61	8.0E-31 BE84488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	9477	18609		1.74	5.0E-31 MG06894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
197	9477	18610		1.74	5.0E-31 MG06894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
6612	15808			9.55	5.0E-31 BF0568540.1	EST_HUMAN	7K06FD4_x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537 SIMILAR TO POGO ELEMENT.: contains L1L1 repetitive element;
603	9850			4.69	4.0E-31 AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2 POLYPEPTIDE_N-ACETYLGLACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE_N-ACETYLGLACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1580	10803	18978		0.95	4.0E-31 Q10473	SWISSPROT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA
1787	10987			2.49	4.0E-31 AL1632280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2742	11921			1.88	4.0E-31 5730038	NT	Homo sapiens SET domain and matrix transposase fusion gene (SETMAR) mRNA
8634	17824			1.25	4.0E-31 AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
8019	17871			1.44	4.0E-31 AE0088881.1	NT	Homo sapiens gene for activin receptor type II B, complete cds
2555	11742	20960		5.53	3.0E-31 6005871	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
6228	15407	24849		7.95	3.0E-31 4826853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8 (19kD, ASH1) (NDUFB8) mRNA
6512	15708			2.89	3.0E-31 AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
6961	16129	28597		3.74	3.0E-31 D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
7228	18447	25937		2.88	3.0E-31 P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
7712	16811			7.41	3.0E-31 BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1883	11080	20281		1.84	2.0E-31 AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-03 LT0051 Homo sapiens cDNA
2308	11502	20724		2.54	2.0E-31 AL119245.1	EST_HUMAN	DKFZp761G1513_r1 761 (synonym: Namy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2404	11596	20816		4.8	2.0E-31 AA158824.1	EST_HUMAN	BB88111_s1 Strategene fetal retina 83/202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR:12 TIR repetitive element;
5542	14766	24132		2.77	2.0E-31 BE360127.1	EST_HUMAN	htsg01_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 bs MER29 repetitive element;
6795	15990			2.34	2.0E-31 AA877764.1	EST_HUMAN	htsg04_s1 NCI CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPONSOBLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6830	16024	25489	4.65	2.0E-31	7661535 NT	Homo sapiens B9 protein (B9), mRNA	
7098	16275	25754	3	2.0E-31	BE408611.1	EST_HUMAN	601304125F1_NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
7098	16275	25755	3	2.0E-31	BE408611.1	EST_HUMAN	601304125F1_NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
8685	17585			2.14	2.0E-31	AF148512.1	Homo sapiens hexokinase II gene, promoter region
8712	18380			2.48	2.0E-31	AI114527.1	EST_HUMAN
16	8312	18415	7.1	1.0E-31	U83163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1638	10852	20030	6.59	1.0E-31	O85371	SWISSPROT	OLFACTOORY RECEPTOR 2C1
1638	10852	20031	6.59	1.0E-31	O85371	SWISSPROT	OLFACTOORY RECEPTOR 2C1
1638	10852	20032	6.59	1.0E-31	O85371	SWISSPROT	OLFACTOORY RECEPTOR 2C1
4637	13831	22918	1.87	1.0E-31	AL134378.1	EST_HUMAN	DKFZ541B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZ541B235 5'
4637	13831	22919	1.87	1.0E-31	AL134378.1	EST_HUMAN	DKFZ541B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZ541B235 5'
5322	14544	23624	3.51	1.0E-31	AW391679.1	EST_HUMAN	MR3-ST0220-151-289-028-a08_1 ST0220 Homo sapiens cDNA
5726	14944	24340	2.11	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cab1 repeat region
7480	16697	26182	2.54	1.0E-31	AI086434.1	EST_HUMAN	Q121103.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR_Q16595
8257	17384	26917	6.47	1.0E-31	AW303317.1	EST_HUMAN	xx17f03_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Ali repetitive element contains MER19.12 MER19 repetitive element;
5950	15168	24578	2.53	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAA G01 5'
2045	11246	20456	7.85	8.0E-32	AI056770.1	EST_HUMAN	oxf5e07_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4876	14084	23159	0.96	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 12/ PORE MEMBRANE PROTEIN OF 121 KD (P145)
8538	17583			3.22	7.0E-32	X17283.1	NT
1041	10267	19418	48.91	5.0E-32	AF116827.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part. with 5' breakpoint between orphon and neighbouring non-amplified region
939	10172			2.6	4.0E-32	AL1163246.2	NT
6336	15516	24982	3.11	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C048
6336	15516	24983	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
462	9715	18850	3.57	3.0E-32	Y17283.1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
1454	10587	18841	10.88	3.0E-32	AV731560.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK C07 5'
6875	16066	25534	8.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
6875	18066	25535	8.4	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
7489	16706	26192	9.12	3.0E-32	AA177621.1	EST_HUMAN	Z95a07_x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;

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Table 4
Single Exon Probes Expressed In HEGLA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8568	17587		5.38	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
8950	14491	23579	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (thorax) (Drosophila) homolog; translocated to, 4 (MLL T4) mRNA
8950	14491	23580	3.58	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (thorax) (Drosophila) homolog; translocated to, 4 (MLL T4) mRNA
9112	17830		2.92	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
5883	15081	24493	5.72	2.0E-32	Z38133.1	NT	H_sapiens mRNA for myosin
5883	15081	24494	5.72	2.0E-32	Z38133.1	NT	H_sapiens mRNA for myosin
9228	18008	23847	1.47	2.0E-32	AV736448	EST_HUMAN	CB Homo sapiens cDNA clone CBFBIA08 5'
9228	18008	23848	1.47	2.0E-32	AV736448	EST_HUMAN	CB Homo sapiens cDNA clone CBFBIA08 5'
26316	11819		1.51	1.0E-32	D84430.1	NT	Homo sapiens mRNA for phenylalanyl tRNA synthetase, complete cds
3059	12295		1.32	1.0E-32	BE743289.1	EST_HUMAN	601573207F1 NIH_MGCC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
6106	15200	24618	6.26	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
6653	15848	25307	7.33	1.0E-32	AA720574.1	EST_HUMAN	nw21g02.s1 NCI_CGAP_GCBO Homo sapiens cDNA clone IMAGE:12411383 similar to TR:OB88539 mRNA
3458	12881		5.61	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:OB88539 OB88539
5837	15054		3.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-18, and partial cds, alternatively spliced
6712	15907	25368	2.29	9.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
7378	16594		7.28	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
63	9359	18480	4.34	7.0E-33	50311736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
63	9359	18481	4.34	7.0E-33	50311736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2127	11328	20544	2.68	7.0E-33	AI560115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_UJ2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR_11 OFR repetitive element;
2811	11785		9	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
3208	12442		18.26	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGE sequences, MAGL Homo sapiens cDNA
4472	13870	22761	0.96	7.0E-33	AA1157487.1	EST_HUMAN	z056e01.r1 Stratagene endothelial cell 8317223 Homo sapiens cDNA clone IMAGE:590328 5'
7405	16817	26107	4.81	7.0E-33	BF347228.1	EST_HUMAN	602021164F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
7800	16893	26508	2.26	7.0E-33	AW971588.1	EST_HUMAN	EST383397 MAGE sequences, MAGL Homo sapiens cDNA
8545	17570	23891	5.15	7.0E-33	AA01416.1	EST_HUMAN	n01h01.s1 NCI_CGAP_Phs1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.11 L1 repetitive element;
3717	12837		1.15	8.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6647	15842	25303	4.52	8.0E-33	J04388.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6681	15876	25335	3.6	6.0E-33	11429188	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
1747	10859		1.81	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100T00-21-a02 FT0169 Homo sapiens cDNA
1846	11054		1.22	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1863	11070	20260	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1863	11070	20261	4	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2237	11432		3.29	5.0E-33	AL103285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4035	13245	22348	0.88	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
8343	17440		1.31	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1136	10359		1.64	4.0E-33	AL103207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2095	11295	20507	2.46	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2384	11577		2.74	4.0E-33	AA028621.1	EST_HUMAN	ab51b11.11 Stratagene clone 537218 Homo sapiens cDNA clone IMAGE:8443175' similar to contains Alu repetitive element; contains MER28_b2 MER28 repetitive element;
2510	11689	20916	16.8	4.0E-33	AL103210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4480	13878	22768	1.55	4.0E-33	AW283318.1	EST_HUMAN	U1-H-B12-ah1-c-03-0-U1_51 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:5101385' similar to z71a08_r1 Stratagene clone (#337204) Homo sapiens cDNA clone IMAGE:5101385' similar to dbX12871_mca1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
5397	14626	23739	24.3	4.0E-33	AA053053.1	EST_HUMAN	ht09g01_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:31462563' similar to contains MER28_b3
1097	10321		6.43	3.0E-33	BE350127.1	EST_HUMAN	MER29 repetitive element;
1098	10321		3.04	3.0E-33	BE350127.1	EST_HUMAN	ht09g01_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:31462563' similar to contains MER28_b3
2413	12016		2.84	3.0E-33	AV647851.1	EST_HUMAN	ME647851 GLC Homo sapiens cDNA clone GLCFC09 3'
17	8313		0.77	2.0E-33	AI100189.1	EST_HUMAN	qb67g03_x1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR_r1 OFR repetitive element;
104	8313		2.52	2.0E-33	AI100189.1	EST_HUMAN	qb67g03_x1 Soares_fetal_heart_NbH-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR_r1 OFR repetitive element;
4411	13611		4.41	2.0E-33	BE150039.1	EST_HUMAN	MRD-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA
6006	14183	23282	25.82	2.0E-33	AA026883.1	EST_HUMAN	ab51g11.11 Stratagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:8443885' similar to gbX00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5125	14304	23393	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-β2 (SIRP-b2), mRNA
5125	14304	23394	1.41	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5638	16056	24462	1.83	2.0E-33	AI227492.1	EST_HUMAN	q198d01_x1 Soares_NhlMPu_S1 Homo sapiens cDNA clone IMAGE:1880161 3'
8	9304		1.87	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7887	17057	26578	2	1.0E-33	AV986818.1	EST HUMAN	QV3-BN0047-230200-102-803 BN0047 Homo sapiens cDNA Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
8167	17289	26842	5.98	1.0E-33	U68022.1	NT	w08806_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2482410 3'
8841	17750		2	1.0E-33	AI827191.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9024	8304		5.11	1.0E-33	AF003528.1	NT	
9059	17890	23898	1.63	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
9248	18017		2.54	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
2137	11335	20553	1.18	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
1446	10659	19834	2.78	7.0E-34	T70815.1	EST_HUMAN	yd15e05_1.1 Saccharomyces cerevisiae fetal liver spleen 1NF1 S Homo sapiens cDNA clone IMAGE:108320 5'
8618	17813		2.89	7.0E-34	H12866.1	EST_HUMAN	y14c10_1.1 Saccharomyces cerevisiae placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
477	9729	18862	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
477	9729	18863	1.31	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
8418	17490	24010	1.7	6.0E-34	U03686.1	NT	Mus musculus DAB1/J hair-specific (hac1-) gene
1845	11053		3.27	6.0E-34	7706500	NT	Homo sapiens Npk38-binding protein Npk38BP (LOC51729), mRNA
5084	14274	23357	4.37	6.0E-34	U30883.1	NT	Human splicing factor SRp55-1 (SRp55) mRNA, complete cds
61736	15931	23591	2.28	5.0E-34	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
7247	16467	25658	2.25	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
7806	16299		1.91	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1867	11171	20377	2.12	4.0E-34	AI804687.1	EST_HUMAN	184cd6_x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2249194 3'
2679	11881	21075	0.94	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
3137	12372	21503	1.09	4.0E-34	5803186	NT	Homo sapiens splicing factor 3e, subunit 3, 60kD (SF3A2), mRNA
7711	16910		5.88	3.0E-34	BFC35327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1485	10708	18881	11.87	1.0E-34	P12238	SWISSPROT	ADP,ATP CARRIER PROTEIN LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3654	12875	21983	1.4	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4047	13257	22358	0.98	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4047	13257	22359	0.98	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4476	13674		5.59	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0508-240400-016-h08 BT0508 Homo sapiens cDNA clone
5728	14947	24344	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3886999 5'
5728	14947	24345	2.28	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886999 5'
6991	16169	25841	10.13	1.0E-34	AL036835.1	EST_HUMAN	DKFZp564A1563_1 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564A1563 5'
8804	18316		2.28	1.0E-34	AA807097.1	EST_HUMAN	cc31c11_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb>x68203

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9050	17922		4.53	1.0E-34	AL103210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3624	12845	21984	1.17	9.0E-35	AW683302.1	EST_HUMAN	hh77b08_y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968797 5'
230	9508		17.85	8.0E-35	6031180	NT	Homo sapiens prohibitin (PHB) mRNA
1708	10921	20106	3.14	8.0E-35	BF589937.1	EST_HUMAN	nae33ae08_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1708	10921	20107	3.14	8.0E-35	BF589937.1	EST_HUMAN	nae33ae08_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4883	14071	23168	4.02	8.0E-35	BF183195.1	EST_HUMAN	601803688F1 NIH_WGC_18 Homo sapiens cDNA clone IMAGE:4040324 5'
7281	16500	25883	2.31	8.0E-35	BE378480.1	EST_HUMAN	601238648F1 NIH_WGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
8535	17560		3.51	8.0E-35	BF589282.1	EST_HUMAN	602184624T1 NIH_WGC_42 Homo sapiens cDNA clone IMAGE:3300660 3'
6887	15085	24499	1.62	7.0E-35	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL) mRNA
1417	10930	19798	1.02	8.0E-35	AA757415.1	EST_HUMAN	sh53h03_s1 Soares testis NHT Homo sapiens cDNA clone 1309897 3'
1827	11141	20337	1.3	8.0E-35	6005975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
4030	13240	22344	0.69	8.0E-35	AW287191.1	EST_HUMAN	U1-H-BW0-aid-d-09-0-U_1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731433 3'
6427	15624	25089	5.25	8.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF) interacting (TRIO), mRNA
143	9425	18859	70.69	5.0E-35	AF54830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1684	10898	20083	1.66	5.0E-35	XG3392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2758	11817	21131	2.17	5.0E-35	AB007686.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2870	12208	21344	1.15	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), prop1, colo1, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds.
4403	13803	22703	1.74	5.0E-35	AF023268.1	NT	
6523	15719		3.88	5.0E-35	BE890992.1	EST_HUMAN	601431884F1 NIH_WGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
7753	16830		3.48	5.0E-35	AA001786.1	EST_HUMAN	2h84f12_r1 Soares fetal spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1436	10950	18824	34.03	4.0E-35	BE257907.1	EST_HUMAN	601109778F1 NIH_WGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1788	10988	20183	8.81	4.0E-35	H91193.1	EST_HUMAN	y09807_r1 Soares fetal liver spleen_1NFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element.
4819	14008		0.63	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6136	14314		0.88	4.0E-35	BE408102.1	EST_HUMAN	601300705F1 NIH_WGC_21 Homo sapiens cDNA clone IMAGE:3635401 5'
6169	15361		1.9	4.0E-35	BE350127.1	EST_HUMAN	ht05601_x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146286 3' similar to contains MER29_b3 MER28 repetitive element.
6628	15824	25286	7.14	4.0E-35	AL046596.1	EST_HUMAN	DKE2p434L148_r1 434 (synonym: htcs3) Homo sapiens cDNA clone DKE2p434L148 5'
1558	10772	19845	48.16	3.0E-35	BE298192.1	EST_HUMAN	601125280F1 NIH_WGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2289	11494			3.28	3.0E-35 AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5359	14589	23665	24.64	3.0E-35 BF433100.1	EST_HUMAN	7n25a0021 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q8QZH7 F-BOX PROTEIN FBL2_;	
5359	14589	23668	24.64	3.0E-35 BF433100.1	EST_HUMAN	7n25a0021 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7 Q8QZH7 F-BOX PROTEIN FBL2_;	
108	11959	18528	1.05	2.0E-35 N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT	
1196	10416	19570	0.8	2.0E-35 T11609.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds	
2184	11381	20605	6.37	2.0E-35 ABO18413.1	NT	hi86a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to SW_TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12_;	
2844	11827	21042	1.22	2.0E-35 AW865005.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	
3283	12514	21644	1.02	2.0E-35 6912459	NT	Hi19a12.11 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:274078 5'	
3283	12514	21645	1.02	2.0E-35 6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	
3532	12755		1.11	2.0E-35 ABO20702.1	NT	Homo sapiens mRNA for KIAA0595 protein, partial cds	
3888	13104	22221	0.69	2.0E-35 BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP4328	
3888	13104	22222	0.69	2.0E-35 BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP4328	
4673	13887		2.75	2.0E-35 HA49239.1	EST_HUMAN	1q19a12.11 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:274078 5'	
5481	14708	24063	2	2.0E-35 BF532417.1	EST_HUMAN	Q7D-BT0701-2199-D04 BT0701 Homo sapiens cDNA	
7378	16592	26080	5.53	2.0E-35 X99417.1	NT	H_sapiens PROS-27 mRNA	
8289	12514	21644	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
8289	12514	21645	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
8470	17523	24023	1.28	2.0E-35 BE094978.1	EST_HUMAN	601486774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'	
8470	17523	24024	1.28	2.0E-35 BE094978.1	EST_HUMAN	601486774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898699 5'	
9026	17876		8.58	2.0E-35 AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010	
9144	11959	18528	2	2.0E-35 N88965.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT	
48	9345	18455	4.75	1.0E-35 AA8311949.1	EST_HUMAN	Imfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	
48	9345	18456	4.75	1.0E-35 AA8311949.1	EST_HUMAN	Imfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1	
760	10001	19147	72.69	1.0E-35 AW389473.1	EST_HUMAN	IL2-ST0162-131098-006-d12 ST0162 Homo sapiens cDNA	
760	10001	19148	72.69	1.0E-35 AW389473.1	EST_HUMAN	IL2-ST0162-131098-006-d12 ST0162 Homo sapiens cDNA	
919	10154		2.05	1.0E-35 T83947.1	EST_HUMAN	yd93601.11 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2507	11695	20913	1.56	1.0E-35	7705984	NT	Homo sapiens hypothetical protein (LOC51233), mRNA h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2723	11802	21118	1.21	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element; h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2723	11902	21119	1.21	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element; Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3108	12343	21471	1.33	1.0E-35	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
3127	12362	21491	1.95	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF08 3'
3127	12362	21492	1.95	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCEF08 3'
4414	13814	22709	4.84	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4414	13814	22710	4.84	1.0E-35	7656905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
6893	18076	25592	3.9	1.0E-35	AU158595	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
6893	18076	25593	3.9	1.0E-35	AU158595	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
8237	17368		4.28	1.0E-35	AI525119.1	EST_HUMAN	primate-7.D01.r bimorph Homo sapiens cDNA 5'
8321	18273		2.31	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBNL1), mRNA
8537	17562		2.05	1.0E-35	11418110	NT	Homo sapiens casein kinase 1 epsilon (CSNK1E), mRNA
8915	17803		2.34	1.0E-35	BE192832.1	EST_HUMAN	601584833F1 NIH MGIC_7 Homo sapiens cDNA clone IMAGE:3338985 5'
2881	12119	21250	1.79	7.0E-36	AW857579.1	EST_HUMAN	CMI-CT0315-081289-083-d07 CT0315 Homo sapiens cDNA
3082	12318		5.8	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
63650	15540	24894	5.98	7.0E-36	U08872.1	NT	Human carcinoidembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
63650	15540	24895	5.98	7.0E-36	U08672.1	NT	Human carcinoidembryonic antigen gene family member 12 (CGM12) gene, exons L and LN
8704	17668	23448	2.64	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
1973	11177	20383	1.77	6.0E-36	7706622	NT	Homo sapiens ninjurin 2 (NINJ2), mRNA
2382	11975		.588	6.0E-36	AB035346.1	NT	Homo sapiens trypsin inhibitor precursor (HUMAN)
3618	12839	21958	0.65	6.0E-36	BFE15101.1	EST_HUMAN	UI-H-BW-1-anvc-12-0-j1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5353	14583	23059	6.31	6.0E-36	AI435169.1	EST_HUMAN	gb.M11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN); h006h02.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
6125	15309	24742	3.34	6.0E-36	AW780143.1	EST_HUMAN	PS2282 IMPORTIN ALPHA-2 SUBUNIT; h095cd9.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MER9.b2
8081	17216	26750	2.28	6.0E-36	AI380488.1	EST_HUMAN	MER9 repetitive element;
1356	9418	18552	9.88	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2708	11987	21104	47.02	5.0E-36	BE388498.1	EST_HUMAN	601285537F1 NIH MGIC_44 Homo sapiens cDNA clone IMAGE:36807289 5'
3590	12811	21931	2.13	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4798	13987	23093	2.18	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (APISL1), mRNA

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4758	13987	23094	2.18	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (AP15L1), mRNA
8287	9418	18552	4.4	5.0E-36	A 277735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8593	17602	24006	2.39	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1232	10450	18606	1.85	4.0E-36	B E100368.1	EST_HUMAN	PM3-BN0176-100400-001-g04-BN0176-Homo sapiens cDNA
1444	10657	19833	1.45	4.0E-36	P 0286	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1622	10835	20011	1.15	4.0E-36	B E982574.1	EST_HUMAN	601286574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:36283885'
2188	111386		5.46	4.0E-36	AW_247772.1	EST_HUMAN	2829020_Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:28202020 5'
3328	12557	21694	0.79	4.0E-36	B E889289.1	EST_HUMAN	6011282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36041685'
3328	12557	21695	0.79	4.0E-36	B E889289.1	EST_HUMAN	6011282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36041685'
5161	14940	23429	0.59	4.0E-36	AA 05361.1	EST_HUMAN	OK05b11_s1 Soares cDNA clone IMAGE:15068093' similar to SW_D3H1_RAT_P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
5691	14911	24305	2.59	4.0E-36	11497041	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
6359	15539	24993	1.89	4.0E-36	M 3320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
7559	16764	26255	2.9	4.0E-36	AA 00370.1	EST_HUMAN	ZU63c10.1 Soares _testis_NHT Homo sapiens cDNA clone IMAGE:743250 5'
8809	17607		1.56	4.0E-36	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8857	18156		3.54	4.0E-36	AV 753629.1	EST_HUMAN	AV753629 TP Homo sapiens cDNA clone TPGAB101 5'
9285	18032		1.38	4.0E-36	D 23217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
703	8945	16081	2.65	3.0E-36	AF 098810.1	NT	Homo sapiens neuregulin III-alpha gene, partial cds
1489	10702	19876	0.96	3.0E-36	AF 110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1489	10702	19877	0.96	3.0E-36	AF 110239.1	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2262	11457	20875	3.92	3.0E-36	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
4505	13702	22798	8.01	3.0E-36	10181139	NT	Mus musculus Junctophilin 1 (Jp1-pending), mRNA
7671	16870	26373	1.79	3.0E-36	B F095327.1	EST_HUMAN	60145853 F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:33620985'
3134	12369	21500	6.47	2.0E-36	B E259267.1	EST_HUMAN	60110634 F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:33427065'
4978	14165	23255	23.75	2.0E-36	AW 880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5434	14661	23801	2.36	2.0E-36	AF 267747.1	NT	Mus musculus p47-phox gene, complete cds
5591	14815	24189	3.46	2.0E-36	T 03756.1	EST_HUMAN	EST706848 Infant Brain, Banto Soares Homo sapiens cDNA clone IMAGE:1006848 5'
69115	16132	24541	13.08	2.0E-36	T 639629.1	EST_HUMAN	yc446071_1 Stratagene liver (#337224) Homo sapiens cDNA clone IMAGE:835085'
895	10130	19292	1.73	1.0E-36	BE 409310.1	EST_HUMAN	60130093 F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36354405'
2113	11312	20527	1.28	1.0E-36	BE 148523.1	EST_HUMAN	RC1-HT0217-131198-021-h07 HT0217 Homo sapiens cDNA
2113	11312	20528	1.28	1.0E-36	BE 148523.1	EST_HUMAN	RC1-HT0217-131198-021-h07 HT0217 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2168	11368	20585	1.21	1.0E-36	BF073761.1	EST HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
3318	12548		1.63	1.0E-38	AF156982.1	NT	Homo sapiens human endogenous retrovirus W pro-6-19 protease (pro) gene, partial cds
5746	14985		5.34	1.0E-36	AI80774.1	EST HUMAN	wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:23078862 3' similar to contains Ali repetitive element;
6445	15842	25108	4.67	1.0E-38	AA1148034.1	EST HUMAN	z051812.x1 Stratagene endothelial cell 837223 Homo sapiens cDNA clone IMAGE:580398 5'
6445	15842	25109	4.67	1.0E-38	AA1148034.1	EST HUMAN	z051812.x1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:580398 5'
7115	16282	25773	5.47	1.0E-36	BF364169.1	EST HUMAN	QV3-AN1023-Q10560198-h01 NN1023 Homo sapiens cDNA
7521	16226	26217	3.97	1.0E-36	AW897636.1	EST HUMAN	CN3-HNC0061-140405-147-h12 NN0061 Homo sapiens cDNA
7819	17134	26864	4.03	1.0E-36	AW504143.1	EST HUMAN	UJ-HFBN0-alec-c03-0-U1 r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
8468	17521		4.59	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
8944	17821		3.71	1.0E-36	AL1163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
9209	17892		2.95	1.0E-36	AI2021723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6248	15428	24869	2.31	9.0E-37	AW009277.1	EST HUMAN	ws80907.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2504245 3'
6248	15428	24870	2.31	9.0E-37	AW009277.1	EST HUMAN	ws80907.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2504245 3'
8745	17690		2.13	9.0E-37	W2818.1	EST HUMAN	T3D4 Human retina cDNA fsp5091-cloned sublibrary Homo sapiens cDNA not directional
3330	12559	21697	0.98	8.0E-37	4757979	NT	Homo sapiens chimerin (chimaerin) 2 (CHIN2) mRNA
5584	14808	24181	3.76	8.0E-37	BE150127.1	EST HUMAN	h08901.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.63 MER28 repetitive element;
5584	14808	24182	3.76	8.0E-37	BE150127.1	EST HUMAN	h08901.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.63 MER28 repetitive element;
5604	14828	24204	4.96	8.0E-37	AW840840.1	EST HUMAN	RC1-CN0008-210100-012-e09_1 CN0008 Homo sapiens cDNA
6423	15620	25084	8.42	8.0E-37	X87344.1	NT	H_sapiens DMA, DMB, HLA-Z1, IPP2, TAP1, LMP2, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
1291	10506		3.81	7.0E-37	AI042800.1	EST HUMAN	DKFZp44E0422_T1_424 (synonym: hts3) Homo sapiens cDNA clone DKFZp44E0422 5'
7342	16558	26048	9.31	7.0E-37	AI817700.1	EST HUMAN	wt25b11.x1 NCI_CGAP_Bm125 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12 PTR5 repetitive element;
7471	16679	28181	4.11	7.0E-37	AI536702.1	EST HUMAN	tm87603.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element;
9080	17904		3.34	6.0E-37	AF2021723.1	NT	Homo sapiens Sadi unc-84 domain protein 2 (SUN2) mRNA, partial cds
5705	14924	24317	4.29	5.0E-37	AA307123.1	EST HUMAN	EST178035 Colorectal carcinoma (HCC) cell line Homo sapiens cDNA 5' end
5705	14924	24318	4.29	5.0E-37	AA307123.1	EST HUMAN	EST178035 Colorectal carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7494	16701		5.03	5.0E-37	7657117	NT	Homo sapiens glycine C-acetyltransferase-CoA ligase) (GCAT), mRNA
8463	17518		6.75	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2383	11581	20798	4.78	4.0E-37	AA702794.1	EST HUMAN	z190b04.s1 Soares_fetal liver spleen INF1S1 Homo sapiens cDNA clone IMAGE:4480753

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7602	16805	26300	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
7602	16805	26301	1.77	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
1984	11187	20397	2.81	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L241B_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L241B	
1984	11187	20398	2.81	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L241B_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L241B	
2478	11668		4.67	3.0E-37	AW981150.1	EST_HUMAN	EST373222 MAGE sequences, MAGF Homo sapiens cDNA	
2920	12158		3.85	3.0E-37	AW981150.1	EST_HUMAN	EST373222 MAGE sequences, MAGF Homo sapiens cDNA	
388	9680	18817	0.74	2.0E-37	DS9780.1	NT	Homo sapiens mRNA for AML1, complete cds	
388	9880	18818	0.74	2.0E-37	DS9780.1	NT	Homo sapiens mRNA for AML1, complete cds	
1088	10312	19465	2.82	2.0E-37	AU31202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'	
1088	10312	19468	2.82	2.0E-37	AU31202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002166 5'	
1633	11137	20333	4.55	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047	
3871	13087	22203	6.5	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrofendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA	
4231	13434	22528	1.04	2.0E-37	4828685	NT	Homo sapiens DEAD1H (Asp-Glu-Ala-Asp-His) box polypeptide 1 (DDX1) mRNA	
5935	15171	24696	3.38	2.0E-37	AA346720.1	EST_HUMAN	EST52831 fetal heart Homo sapiens cDNA 5' end	
6477	15674	25145	3.78	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406 5'	
8094	17228	28768	20.18	2.0E-37	AJ78013.1	NT	Homo sapiens J domain containing protein 1 isoform 5 (JDP1) mRNA, complete cds	
8908	18021		3.29	2.0E-37	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	
9252	18021		3.91	2.0E-37	11417972	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA	
2057	11258	20473	4.06	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081	
3181	12398		1.04	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-2410400-016-h03 CT0347 Homo sapiens cDNA	
3838	13154	22271	1.05	1.0E-37	AF188011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds	
4959	14148	23238	2.15	1.0E-37	BF571719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0150 Homo sapiens cDNA	
6693	15698	25348	3.8	1.0E-37	AA171406.1	EST_HUMAN	zp21ib02.1 Stratagene neurepithelium (#837231) Homo sapiens cDNA clone IMAGE:610059 5' similar to L1.12 L1 repetitive element;	
7288	16507	25998	6.48	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds	
8796	17722		2.73	1.0E-37	BE771814.1	EST_HUMAN	CIM3-FT00086-140700-243-d07 FT00086 Homo sapiens cDNA	
5584	14788	24159	1.78	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA	
1229	10447	18603	1.67	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA	
2462	11653	20975	1.26	8.0E-38	BF346221.1	EST_HUMAN	6020-8401F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153392 5'	
2149	11347	20564	9.52	7.0E-38	AW972825.1	EST_HUMAN	EST3734820 MAGE sequences, MAGF Homo sapiens cDNA	
4208	13411	22505	0.7	7.0E-38	H19082.1	EST_HUMAN	YN51107.1 Soares adult brain N285HB55Y Homo sapiens cDNA clone IMAGE:171973 5'	
3007	12243	21314	2.28	6.0E-38	BF033033.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3559348 5'	
8322	17424		7.1	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12orf3), mRNA	

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8830	17742	29933	10.53	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2X0, complete cds
9223	16119	23811	1.25	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
734	8975	19114	2.25	5.0E-38	AW971819.1	EST_HUMAN	EST38908 MAGE sequences, MAGL Homo sapiens cDNA
2417	11608	20830	9.18	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
3685	12806	22026	0.88	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type I (DQ2), transcript variant 2, mRNA
3849	12808	22026	1.69	5.0E-38	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DQ2), transcript variant 2, mRNA
6201	11608	20830	1.22	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIIR gene (partial), exon 8
6099	15389	24731	3.24	5.0E-38	BEET1610.1	EST_HUMAN	601450148F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3854074 5'
119	9405	18536	5.47	4.0E-38	Z25498.1	NT	B_taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
119	8405	18537	5.47	4.0E-38	Z25498.1	NT	B_taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1165	10387	19538	2.48	3.0E-38	11425947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2070	11270	4.56	3.0E-38	AEG03530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions	
3674	12995	1.86	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (Hira-like) (HIRP4), mRNA	
3838	13055	22169	1.6	3.0E-38	PS3538	SWISSPROT	SSU72 PROTEIN
3838	13055	22170	1.6	3.0E-38	PS3538	SWISSPROT	SSU72 PROTEIN
4817	13811	1.61	3.0E-38	BE279301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'	
5981	18069	24811	7.19	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8329	15510	24958	6.88	3.0E-38	BF073664.1	EST_HUMAN	CM3-FT0181-14Q700-241-107 FT0181 Homo sapiens cDNA
6658	15983	25323	3.23	3.0E-38	HB85494.1	EST_HUMAN	yy88b04.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
6658	15863	25324	3.23	3.0E-38	HB85494.1	EST_HUMAN	yy88b04.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
7865	17065	2.14	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048	
9086	10387	18538	1.84	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
52	8348	18463	1.8	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1387	10601	19768	4.68	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
1623	10836	20012	1.58	2.0E-38	AA437353.1	EST_HUMAN	2w30d01.r1 Soares ovary tumor NbHOt Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-Oligosaccharide ALPHA-1,2-MANNOSIDASE
1623	10836	20013	1.58	2.0E-38	AA437353.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-Oligosaccharide ALPHA-1,2-MANNOSIDASE
4579	13773	22888	10.15	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5150	14329	23449	0.87	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5150	14329	23420	0.67	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5173	14317	23408	0.75	2.0E-38	AA437181.1	EST_HUMAN	2w61d09.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR-G817957 G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4;
6822	15818	788	2.0E-38	BE165980.1	EST_HUMAN	MRI3-HT0487-15G200-113-g01 HT0487 Homo sapiens cDNA	

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7787	16982	28495	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.51 NCI_CGAP_Pt23 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:ER12316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.
7787	16982	28496	2.23	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.51 NCI_CGAP_Pt23 Homo sapiens cDNA clone IMAGE:1102812 3' similar to TR:ER12316 E212316 NADP DEPENDENT LEUKOTREINE B4 12-HYDROXYDEHYDROGENASE.
8024	17161	26698	6.35	2.0E-38	BE712790.1	EST_HUMAN	QV2-HT0688-08080-293-a05 HT0688 Homo sapiens cDNA
8153	17285	26828	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LGR8) mRNA, partial cds
8153	17285	26829	3.85	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LGR8) mRNA, partial cds
8375	17461		8.04	2.0E-38	AV7728988.1	EST_HUMAN	AV72688B HTC Homo sapiens cDNA clone HTCAH07 5'
8377	17462		2.07	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
8881	17651		1.59	2.0E-38	M59830.1	NT	Human topoisomerase I pseudogenes 2
8883	17661	23982	3.8	2.0E-38	HS5641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788_5'
8757	17698		1.99	2.0E-38	ST74908.1	NT	E1 beta=pyruvate dehydrogenase delta [promoter] [human, placenta, genomic, 1250 nt]
9243	18014		2.44	2.0E-38	11418248	NT	Homo sapiens sulfotransferease-related protein (SULTX3) mRNA
							zg62b02.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1101	10325		2.54	1.0E-38	AA401570.1	EST_HUMAN	MER19 repetitive element;
1968	11172	20378	2.74	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
1988	11191	20401	1.19	1.0E-38	7661968	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2458	11649	20871	4.38	1.0E-38	AF270531.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2576	11762	20983	1.1	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGI1), mRNA
4137	13343	22444	0.96	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4310	13511	22805	0.67	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4315	13516	22810	1.58	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4316	13516	22811	1.58	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4597	13781	22882	1.02	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5672	14892	24284	4.04	1.0E-38	7305380	NT	Mus musculus otogelin (Oog), mRNA
5672	14892	24285	4.04	1.0E-38	7305380	NT	Mus musculus otogelin (Oog), mRNA
6254	15435	24874	2.8	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
6881	16072	25541	8.97	1.0E-38	BE550127.1	EST_HUMAN	ht09g01.1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.1s MER29 repetitive element;
8122	17256	26798	1.81	1.0E-38	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
8534	18087		1.97	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C0084

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 Table 4
 Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
56	8353	18469	5.88	8.0E-39	4502312	NT	Homo sapiens ATPase, H ⁺ -transporting, lysosomal ('vacuolar proton pump') 16kD (ATP6C) mRNA
1398	10612	19776	1.29	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA whsf10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:PB7890 P87890
1797	11006		2.74	8.0E-39	AIB23404.1	EST_HUMAN	POL PROTEIN :
2063	11284	20477	5.62	7.0E-39	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7388	16800	28088	2.68	6.0E-39	BF331829.1	EST_HUMAN	QV1-BT0531-040900-357-02 BT0631 Homo sapiens cDNA
9152	17955		2.33	6.0E-39	BE670394.1	EST_HUMAN	7634603.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6 CE00828.
1016	10244	18386	3.22	5.0E-39	AF003528.1	NT	Homo sapiens X-linked epidermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2842	12180	21314	8.37	5.0E-39	AJ750154.1	EST_HUMAN	ai36604.x1 Barstead color HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
8845	17754		2.06	5.0E-39	11420289	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT :contains LTR7.11 LTR7 repetitive element ;
557	9807	18932	97.11	4.0E-39	AB015810.1	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803) mRNA
3548	12771	21889	0.94	4.0E-39	AL163210.2	NT	Chlorococcus aestuans mRNA for ribosomal protein S4X, complete cds
8863	17765		3.91	4.0E-39	11418177	NT	Homo sapiens chromosome 21 segment HS21C010
8883	17848		2.14	4.0E-39	BE838452.1	EST_HUMAN	QV0-FN0083-260800-278-058 FN0083 Homo sapiens cDNA
49	9348	18457	18.73	3.0E-39	AA631949.1	EST_HUMAN	fmc16 Regional genomic DNA specific cDNA library/Homo sapiens cDNA clone CR12-1
49	9346	18458	18.73	3.0E-39	AA631949.1	EST_HUMAN	fmc16 Regional genomic DNA specific cDNA library/Homo sapiens cDNA clone CR12-1
49	9346	18459	18.73	3.0E-39	AA631949.1	EST_HUMAN	fmc16 Regional genomic DNA specific cDNA library/Homo sapiens cDNA clone CR12-1
8368	17455	26583	6.17	3.0E-39	AI084557.1	EST_HUMAN	ox63a10.s1 Soares_NHHMPU_S1 Homo sapiens cDNA clone IMAGE:1680988 3' similar to SW:GTR5_RAT
8368	17455	26584	6.17	3.0E-39	AI084557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE :
8413	17487		5.85	3.0E-39	I377903.1	EST_HUMAN	ox63a10.s1 Soares_NHHMPU_S1 Homo sapiens cDNA clone IMAGE:1680988 3'
907	10142		8.08	2.0E-39	BE409203.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE :
922	10157		13.75	2.0E-39	AI525119.1	EST_HUMAN	ox63a10.s1 Soares_reline N204HR Homo sapiens cDNA clone IMAGE:3636289 5'
1039	10265		3.85	2.0E-39	AF000573.1	NT	prommra-7.D01.r bytumor Homo sapiens cDNA 5'
1516	10730		98	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homogenotise 1,2-dioxogenase gene complete cds
1843	11147	20347	2.64	2.0E-39	AL163248.2	EST_HUMAN	PM0-BT0340-21-1289-0103-402 BT0340 Homo sapiens cDNA
2592	11778	20997	1.47	2.0E-39	BS370207.1	NT	fnw21902.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4397	15598	22699	1.65	2.0E-39	BS370207.1	EST_HUMAN	HS21C048
							Hom sapiens chromosome 21 segment HS21C048
							RC4-FN0037-280700-011-810 FN0037 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe Seq ID No.	Exon Seq ID No.	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5437	14684	23817	4.29	2.0E-39	AA509880.1	EST_HUMAN	ng88603_s1_NCL_CGAP_Pt8 Homo sapiens cDNA clone IMAGE:941693
6242	15423	24884	2.22	2.0E-39	AA080867.1	EST_HUMAN	Zn06f02_r1 Strategene hNT neuron (#K37233) Homo sapiens cDNA clone IMAGE:546651 5'
7970	17149	26885	2.7	2.0E-39	D86984.1	NT	Human mRNA for KIAA0209 gene, partial cds
1502	10715	19887	3.01	1.0E-39	A 006345.1	NT	Homo sapiens Kv1.0QT1 gene
1502	10715	19888	3.01	1.0E-39	A 006345.1	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
1517	10731	198900	8.07	1.0E-39	7657020	NT	EST_HUMAN EST364065 MAGE gene sequences, MAGB Homo sapiens cDNA
4663	13857	22855	7.37	1.0E-39	AW951895.1	EST_HUMAN EST364065 MAGE gene sequences, MAGB Homo sapiens cDNA	
4663	13857	22858	7.37	1.0E-39	AW951895.1	EST_HUMAN EST364065 MAGE gene sequences, MAGB Homo sapiens cDNA	
4713	13904	23004	11.24	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
5519	14744	24111	4.29	1.0E-39	A 278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
5519	14744	24112	4.29	1.0E-39	A 278170.1	NT	Mus musculus mRNA for neuronal interacting factor X1 (NIX1) (Nix1 gene)
6098	15258		1.72	1.0E-39	11436738	NT	Homo sapiens tubby-like protein 3 (TULP3), mRNA
6240	15421	24862	2.06	1.0E-39	D 8132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8791	17718		1.28	1.0E-39	U 07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
5622	98112	16835	1.44	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1242	10458	18616	12.31	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1242	10458	18617	12.31	9.0E-40	4755145	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sarcoma fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1450	10683	19838	1.29	9.0E-40	4507512	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3768	12886	22102	0.8	9.0E-40	4503764	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3950	14488	2279	4.18	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4502	13541	22632	0.6	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3006	12242	21373	0.88	8.0E-40	AA078165.1	EST_HUMAN 7H15A04 Chromosome 7 HeLa cDNA library Homo sapiens cDNA clone 7H15A04	
3898	13114		7.24	8.0E-40	BE3985411	EST_HUMAN 601298958F1 NIH MGCG_8 Homo sapiens cDNA clone IMAGE:3619166 5'	
6383	15983	25019	2.32	7.0E-40	U 86925.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
6383	15583	25020	2.32	7.0E-40	U 60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7473	16881	28164	2.72	7.0E-40	AL 63246.2	NT	Human sapiens chromosome 21 segment HS21C046
2686	11867	21080	5.57	6.0E-40	AA 381275.1	EST_HUMAN EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family	
2686	11867	21081	5.57	6.0E-40	AA 361275.1	EST_HUMAN EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family	
5632	14856		2.07	6.0E-40	BE 64798.1	EST_HUMAN BE40901X1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:3210480 3'	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6057	15226	24845	4.62	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
6057	15226	24846	4.62	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7054	16241	25715	10.58	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
7054	16241	25718	10.58	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
2555	11751	20971	3.15	5.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1842	11050	20241	2.08	4.0E-40	AI686005.1	EST_HUMAN	t91b01_x1 NCI CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:Q73505 OT73505 POL PROTEIN.
2078	11278		4.83	4.0E-40	AF003628.1	NT	Homo sapiens X-linked arthritrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4383	13584	22886	9.15	4.0E-40	7862117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
6480	15657	25128	4.42	4.0E-40	AA742809.1	EST_HUMAN	nv3e10_x1 NCI CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
6787	15682	25442	2.71	4.0E-40	BE009416.1	EST_HUMAN	PN0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
6787	15682	25443	2.71	4.0E-40	BE009416.1	EST_HUMAN	PN0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
7304	16522	26013	1.89	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4114	13321	22421	0.89	3.0E-40	AI628949.1	EST_HUMAN	wh1207_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4889	14977		0.63	3.0E-40	AA055118.1	EST_HUMAN	zf16h9.61 Scores_felat_heart_NbHH19W Homo sapiens cDNA clone IMAGE:377153 3'
5951	15167	24580	7.57	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6591	15787	25246	5.04	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7256	18475	25987	1.91	3.0E-40	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
7593	16787	26281	1.91	3.0E-40	BE350127.1	EST_HUMAN	Itg6g01_x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3
7816	17009	26522	14.52	3.0E-40	6005813	NT	Homo sapiens serine/threonine protein kinase (NDR), mRNA
330	9860		5.68	2.0E-40	AI223036.1	EST_HUMAN	q852h108_x1 Scores_tes1is NHT Homo sapiens cDNA clone IMAGE:1838847 3'
804	10043				xr24e10_x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW.RS5_MOUSE		
1793	11002		8.68	2.0E-40	AW303868.1	EST_HUMAN	P87461_40S RIBOSOMAL PROTEIN S5.
1903	11109	20302	3.35	2.0E-40	4506183	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 7 (PSMA7) mRNA, and translated products
1903	11109	20303	3.35	2.0E-40	4506183	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 7 (PSMA7) mRNA, and translated products
2039	11240	20448	1.44	2.0E-40	AI988582.1	EST_HUMAN	w80a1_x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q811929 Q811929 ZINC FINGER PROTEIN;
2135	11333	20552	1.8	2.0E-40	5435292	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3080	12326	21449	4.72	2.0E-40	5453592	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA	
4922	14110	23208	1.68	2.0E-40	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080	
4922	14110	23207	1.68	2.0E-40	AL183280.2	NT	Homo sapiens chromosome 21 segment HS21C080	
893	10128			1.72	1.0E-40	AA225989.1	EST_HUMAN	
2584	11770	20980	4.35	1.0E-40	BF036881.1	EST_HUMAN	nc089a9 s1 NCI CGAP_Pri1 Homo sapiens cDNA clone IMAGE:1007608	
2646	11829			2.88	1.0E-40	BE018348.1	EST_HUMAN	
3267	12500			1.01	1.0E-40	4507142	NT	
4611	13805	22886	5.6	1.0E-40	4508012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products	
6120	15304	24736	2.37	1.0E-40	AA573201.1	EST_HUMAN	nja204_s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'	
6120	15304	24737	2.37	1.0E-40	AA573201.1	EST_HUMAN	nja2104_s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:985167 3'	
7491	16898	26183	6.81	1.0E-40	AU149345.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM402122 3	
8909	18232			8.76	1.0E-40	BF344112.1	EST_HUMAN	
3791	13009	22124	0.91	9.0E-41	W015986.1	EST_HUMAN	MR2-C10222-211099-002-010 C10222 Homo sapiens cDNA clone IMAGE:284602 5'	
6433	15630	25085	2.38	8.0E-41	AL163203.2	NT	za38a02.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone HS21C063	
638	11979	19233	1.42	7.0E-41	AL084384.1	EST_HUMAN	wp04h04_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3	
838	11979	19234	1.42	7.0E-41	AL084384.1	EST_HUMAN	wp04h04_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3	
4680	13854	22851	1.12	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'	
4680	13854	22852	1.12	7.0E-41	BE389592.1	EST_HUMAN	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603955 5'	
5261	14434	23508	7.39	7.0E-41	11431114	NT	Homo sapiens hypothetical protein (FLJ10986), mRNA	
6638	14881	24270	3.45	7.0E-41	11419208	NT	Homo sapiens disintegrin and metalloprotease domain 22 (ADAM22), mRNA	
7872	17151	26886	1.69	7.0E-41	4758445	NT	Homo sapiens glutamine nucleotide binding protein 10 (GNG10) mRNA	
9250	18229			5.86	7.0E-41	11417972	NT	
285	9559	18693	1.26	6.0E-41	AB037163.1	NT	Homo sapiens DSCR5 mRNA, complete cds	
2081	11281	20497	1.72	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	
1771	10981	20171	2.49	5.0E-41	T62628.1	EST_HUMAN	yc03e10_s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:798628 3'	
5901	15118			2.22	5.0E-41	BE087042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
398	9651			1.87	4.0E-41	BE156318.1	EST_HUMAN	QVO-HTC367-150200-114-g09 HT0367 Homo sapiens cDNA
1106	10330	19480	1.12	4.0E-41	AU119344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'	
1414	10227	19783	16.08	4.0E-41	A1027117.1	EST_HUMAN	OM45a06_s1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:000597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE: contains LTR5_b1 LTR5 repetitive element;	

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1414	10627	19784		16.08	4.0E-41	AIR27117.1	EST_HUMAN
1427	10640	19811		2.73	4.0E-41	AB006681.1	NT
1612	10825	20000		5.77	4.0E-41	AI50406.1	EST_HUMAN
2841	12080	21204		4.37	4.0E-41	AJ229041.1	NT
4126	12080	21206		4.37	4.0E-41	AJ229041.1	NT
5879	13332	22430		2.46	4.0E-41	X92985.1	NT
6890	16169	26540		1.77	4.0E-41	AV75295.1	EST_HUMAN
8174	17306			4.92	4.0E-41	BF3104583.1	EST_HUMAN
8998	18121			10.3	4.0E-41	AV710480.1	EST_HUMAN
9186	17977	23858		1.79	4.0E-41	AV708431.1	EST_HUMAN
955	10188	19343		1.4	4.0E-41	BE878118.1	EST_HUMAN
				2.08	3.0E-41	AB030176.1	NT
4327	13528	22622		3.69	3.0E-41	AB026898.1	NT
5438	14685	23818		7.72	3.0E-41	X871689.1	NT
5825	15042	24446		1.7	3.0E-41	AB037808.1	NT
8220	17350	26888		1.82	3.0E-41	AJ229041.1	NT
8808	17792			1.85	3.0E-41	BF125922.1	EST_HUMAN
1782	10757	18831		29.38	2.0E-41	U43701.1	NT
1928	11132	20327		1.52	2.0E-41	AA331940.1	EST_HUMAN
2165	11382	20606		1.27	2.0E-41	DB69862.1	NT
2223	11428	20654		5.66	2.0E-41	X89631.1	NT
2780	10757	18831		18.14	2.0E-41	U43701.1	NT
3300	12531	21663		38.49	2.0E-41	AA448549.1	EST_HUMAN
4624	13818	22908		1.43	2.0E-41	AL163287.2	NT
4624	13818	22909		1.43	2.0E-41	AL163287.2	NT
6366	15546	25001		6.72	2.0E-41	AF038404.1	NT
6487	15684	25151		2.25	2.0E-41	M86944.1	NT
6487	15684	25152		2.25	2.0E-41	M86944.1	NT
8020	17159	26895		3.94	2.0E-41	AA312687.1	EST_HUMAN
3171	12406	21540		1.16	1.0E-41	BE69375.1	EST_HUMAN

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3171	12406	21541	1.16	1.0E-41	BE869735.1	EST_HUMAN	601445647 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4584	13758	22855	10.98	1.0E-41	6678468 NT	Mus musculus tubulin alpha B (Tubab), mRNA	
8462	17517		2.57	1.0E-41	11528291 NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	
469	9722	18853	8.13	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
2079	11279	20495	2.22	8.0E-42	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
8508	18236		29.5	8.0E-42	AA463896.1	EST_HUMAN	nm012021 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943586 similar to TR:G434304 G434304 367BP EXPRESSED SEQUENCE TAG mRNA
8528	18109		1.24	8.0E-42	AW088062.1	EST_HUMAN	xc87804_x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR_12 OFR repetitive element
940	10173		3.08	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6838	18043	28507	2.35	7.0E-42	AI204358.1	EST_HUMAN	qf58g12_x1 Scarecs_lestis_N-IT Homo sapiens cDNA clone IMAGE:1754278 3'
1823	11031	20224	16.53	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
1823	11031	20225	16.53	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
2253	11448		2.87	6.0E-42	AW238658.1	EST_HUMAN	xp28018_x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741788 3' similar to contains L1_m1 L1 repetitive element
133	9416		5.67	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
444	9698	18834	1.43	5.0E-42	BE217813.1	EST_HUMAN	hy1611_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
493	9748		3.18	5.0E-42	5730038 NT	Homo sapiens SET domain and mariner transposase fusion gene (SETTMAR) mRNA	
494	9747		2.91	5.0E-42	5730038 NT	Homo sapiens SET domain and mariner transposase fusion gene (SETTMAR) mRNA	
5868	15280	24712	2.51	5.0E-42	11417957 NT	Hom sapiens myotubularin related protein 3 (MTM3), mRNA	
6166	15348	24786	1.74	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7559	16774	29267	2.28	5.0E-42	8923102 NT	Hom sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA	
761	10002	19149	18.41	4.0E-42	AF055068.1	NT	Homo sapiens MHC class I region
761	10002	19150	18.41	4.0E-42	AF055068.1	NT	Homo sapiens MHC class I region
1073	10288	19448	2.86	4.0E-42	AF188011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4178	13380	22481	1.79	4.0E-42	X59417.1	NT	H_sapiens PROS-27 mRNA
4235	13438	22531	5.5	4.0E-42	4508498 NT	Hom sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA	
4582	13776	22869	16.6	4.0E-42	4508008 NT	Hom sapiens zinc finger protein 177 (ZNF177) mRNA	
5198	14372	23459	1.04	4.0E-42	7861635 NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA	
7242	16462	26951	1.76	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-04040-018-h11 ST0278 Homo sapiens cDNA
7242	16462	25952	1.76	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-04040-018-h11 ST0278 Homo sapiens cDNA
7951	17090	28620	3.51	4.0E-42	BF035227.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1476 10689	198686		2.54	2.0E-42	BF376834.1	EST_HUMAN	RCC-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2356 11549	20770		1.77	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCCB08 5'
2375 11568			3.93	2.0E-42	AW89344.1	EST_HUMAN	RCC-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2389 11582	20789		24.12	2.0E-42	AW250059.1	EST_HUMAN	2819283_3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819283 3'
5554 14778	24145		17	2.0E-42	AW895388.1	EST_HUMAN	EST367438 MAGE_1 sequences, MAGC Homo sapiens cDNA
5554 14778	24146		17	2.0E-42	AW895388.1	EST_HUMAN	EST367438 MAGE_1 sequences, MAGC Homo sapiens cDNA
8228 17358	26897		2	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
741 9881	19124		1.41	1.0E-42	X57147.1	NT	Human endogenous retrovirus pH-E.1 (ERV9)
1049 10275	19428		1.78	1.0E-42	AW295809.1	EST_HUMAN	U1-H-B11_afh-e-04-O-U1_s1NCL CGAP_Subs Homo sapiens cDNA clone IMAGE:2721871 3'
1109 10333	19483		1.58	1.0E-42	AL1251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1109 10333	19484		1.58	1.0E-42	AL1251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1249 11889	19628		12.22	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase A/GGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1249 11889	19629		12.22	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase A/GGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1675 10887	20073		1.1	1.0E-42	11423219 NT	EST_HUMAN	EST367438 MAGE_1 sequences, MAGC Homo sapiens rec (LOC51201), mRNA
2509 11898	20915		2.09	1.0E-42	5174458 NT	EST_HUMAN	Homo sapiens origin recognition complex, subunit 5 (yeast homolog) like (ORC5L) mRNA, and translated products
2819 12157	21292		10.03	1.0E-42	4505524 NT	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3688 12909	22028		2.23	1.0E-42	7662027 NT	EST_HUMAN	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET11) mRNA
3777 12995	22111		1.02	1.0E-42	5031610 NT	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3800 13116	22233		1.09	1.0E-42	AL163287.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C087
4232 13435	22529		2.23	1.0E-42	AL163280.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
4768 13949	23050		2.4	1.0E-42	5803122 NT	EST_HUMAN	Homo sapiens proteasome inhibitor (PI31), mRNA
4753 13949	23051		2.4	1.0E-42	5803122 NT	EST_HUMAN	Homo sapiens proteasome inhibitor (PI31), mRNA
4788 13977	23081		6.15	1.0E-42	4509758 NT	EST_HUMAN	Homo sapiens nanodin receptor 3 (RFR3) mRNA
4887 14075	23173		1.22	1.0E-42	AB033114.1	EST_HUMAN	Homo sapiens mRNA for KIAA1288 protein, partial cds
7562 16767	26258		1.67	1.0E-42	11437455 NT	EST_HUMAN	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
7104 16281	25781		6.25	9.0E-43	4757969 NT	EST_HUMAN	Homo sapiens chromosome-like (CDYL) mRNA
7607 16810	26305		3.42	9.0E-43	AA435718.1	EST_HUMAN	2778a07_s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:278332 3'
658 9804	18030		14.02	8.0E-43	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
658 9804	19031		14.02	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
707 8949	18085		4.54	8.0E-43	8923276 NT	EST_HUMAN	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
707	9949	19086	4.54	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287). mRNA
707	9949	19087	4.54	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287). mRNA
3620	12841	21860	8	7.0E-43	AW246442.1	EST_HUMAN	2822251_5prime_NCI_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
6707	16902		6.35	7.0E-43	AI836748.1	EST_HUMAN	wp68901_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468986 3' similar to TR:O15475
1351	10568		18.5	6.0E-43	AA4491890.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN contains LTR7_b1 LTR7 repetitive element;
2652	11740		2.84	6.0E-43	AY708201.1	EST_HUMAN	nt72d06_s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:90803 similar to gb:LO5095 80S RIBOSOMAL PROTEIN_L30 (HUMAN);
5793	15010	24414	2.46	6.0E-43	9965973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6045	15213	24633	1.97	6.0E-43	AW468897.1	EST_HUMAN	hd30b04_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1_3 MER1 MER1 repetitive element;
7688	18685		6.52	6.0E-43	AL119158.1	EST_HUMAN	Dkf7Zp781L712_r1_761 (synonym: hamy2) Homo sapiens cDNA clone DKf7Zp781L712 5'
140	9422		2.31	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
509	9761	18987	2.47	5.0E-43	AA382780.1	EST_HUMAN	EST86033 Testis 1 Homo sapiens cDNA 5' end
2798	12039	21161	1.47	5.0E-43	AY732578.1	EST_HUMAN	AY732578 HTF Homo sapiens cDNA clone HTFAN06 5'
8868	16080	25557	5	5.0E-43	AA465288.1	EST_HUMAN	aa33308_r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
7187	16364	25844	2.85	5.0E-43	AI735244.1	EST_HUMAN	cc62c10_x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:Pe0591 P90591 P014 GENE ..
7348	16584	26053	5.41	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN007/280400304-c02 SN007 Homo sapiens cDNA
7542	16747	28241	1.88	5.0E-43	W28011.1	EST_HUMAN	55aaN Human retina cDNA randomly primed sublibrary Hom sapiens cDNA
7983	16428	25915	2.26	5.0E-43	X15804.1	NT	Human mRNA for alpha-actinin
880	11943	19367	9.67	4.0E-43	AF003528.1	NT	Human sepius X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6131	15315		2.02	4.0E-43	11416703	NT	Homo sapiens protocadherin beta 6 (PCDHBB6), mRNA
6519	15715	25150	4.94	4.0E-43	AI244341.1	EST_HUMAN	qj78e02_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
6519	15715	25181	4.94	4.0E-43	AI244341.1	EST_HUMAN	qj78e02_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13 MER10 repetitive element;
7852	17042	28559	1.73	4.0E-43	T77380.1	EST_HUMAN	yd72h10_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'
8438	17502		3.09	4.0E-43	R2050.1	EST_HUMAN	yp06005_r1 Soares infant brain 1NIIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element;
1221	10439		2.8	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1670	10883	20067	4.5	3.0E-43	X97869.1	NT	H_sapiens gene encoding La autoantigen AML1-EV1-1=AML1-EV1-1 fusion protein [rearranged translocation] human, leukemic cell line SKH1, mRNA Mutant, 5338 nt]
3547	12770	21898	1.47	3.0E-43	S69002.1	NT	nk65d06_s1 NCI CGAP_Pi7 Homo sapiens cDNA clone IMAGE:101419
4277	13480	22578	1.1	3.0E-43	AA548154.1	EST_HUMAN	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
5975	15189	24808	4.19	3.0E-43	U65487.1	NT	ba88f11_s1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:388413 3' similar to contains THR_12 THR repetitive element;
6513	15709		8.19	3.0E-43	AA458824.1	EST_HUMAN	Homo sapiens hypothetical protein (HSAA011916), mRNA
6724	15919	26378	2.48	3.0E-43	7681721	NT	Homo sapiens SET domain and marinier transposase fusion gene (SETMAR) mRNA
8218	17347	26887	2.04	3.0E-43	5730038	NT	Homo sapiens SET domain and marinier transposase fusion gene (SETMAR) mRNA
188	9467		10.09	2.0E-43	A1190764.1	EST_HUMAN	qdb1c09_x1 Soares_nHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7 PTR7 repetitive element;
6563	15759		7.03	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
7752	16848		8.09	2.0E-43	T03007.1	EST_HUMAN	FB1G5_Fatal brain, Strategene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1627	10840	20016	4.61	1.0E-43	AF_54836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1627	10840	20017	4.61	1.0E-43	AF_54836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1680	10892	20079	2.93	1.0E-43	A1163284.2	NT	Homo sapiens chromosome 21 segment HS21C084,
2683	11865	21077	3.71	1.0E-43	BF548283.1	EST_HUMAN	602022313F1_NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157688 5'
5939	15155	24566	7.88	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
5939	15155	24587	7.88	1.0E-43	4507168	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
6071	14518	23560	1.79	1.0E-43	R1975.1	EST_HUMAN	Y840e01.11 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOLSE_P28656 BRAIN PROTEIN DN38:
6486	15683		2.88	1.0E-43	AF_98490.1	NT	Homo sapiens 8q22.1 region and MTGB8 (CBFA2T11) gene, partial cds
6730	15625	25384	39.18	1.0E-43	AV963676.1	EST_HUMAN	EST375749 MAGE sequences, MAGH Homo sapiens cDNA
7535	18740	26231	7.71	1.0E-43	A1984961.1	EST_HUMAN	wr87h01_x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
7905	17120	26851	3.87	1.0E-43	1142437B	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
8379	17484		3.42	1.0E-43	AL137984.1	EST_HUMAN	DKF2p76/D1015_11761 (synonym:1namy2) Homo sapiens cDNA clone DKF2p76/D1015 5'
8685	17684	23980	2.23	1.0E-43	A1675416.1	EST_HUMAN	wb99004_x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:2313775 3'
8914	17802	23927	3.14	8.0E-44	11418322	NT	Homo sapiens cadherin EGFLAG seven-pass G-type receptor 1 (CELSR1), mRNA
900	10135	19297	7.56	8.0E-44	A1222985.1	EST_HUMAN	qk23g01_x1 Soares_S1 Homo sapiens cDNA clone IMAGE:1B45552 3'
900	10135	19298	7.56	8.0E-44	A1222985.1	EST_HUMAN	qk23g01_x1 Soares_S1 Homo sapiens cDNA clone IMAGE:1B45552 3'
7723	16922	28431	3.57	8.0E-44	Y10498.2	NT	Homo sapiens mRNA for thymidine kinase, partial
8185	17317	26861	2.01	8.0E-44	L28139.1	NT	Homo sapiens myosin mRNA, partial cds
8636	17825	23974	3.72	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA
8679	17890	23984	1.44	8.0E-44	11418085	NT	Homo sapiens putative nuclear protein (HRHIFB2122), mRNA

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Table 4
Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9046	18142	23749	2.3	8.0E-44	11418098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
665	9811		0.83	7.0E-44	R06035_1	EST_HUMAN	yesSeq01.1.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124920 5'
2200	11397	20821	1.88	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2821	12159	21283	1.71	7.0E-44	Af048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2821	12159	21284	1.71	7.0E-44	Af048728.1	NT	Homo sapiens minisatellite ms32 repeat region
3844	13061	22175	2.85	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4227	13430	22522	1.29	7.0E-44	Af231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4227	13430	22523	1.29	7.0E-44	Af231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6524	15720	25184	4.61	7.0E-44	AU158839_1	EST_HUMAN	AU158839_Y79AA1 Homo sapiens cDNA clone Y79AA10000496 3'
8248	17375	26809	3.42	8.0E-44	AV954050_1	EST_HUMAN	EST3681120 MAGE sequences, MAGC Homo sapiens cDNA
308	9881		2.5	5.0E-44	A1289880_1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
337	9805		2.23	5.0E-44	A1289880_1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
8424	15821	25085	4.3	5.0E-44	AI589523_1	EST_HUMAN	In40d02_x1 NCI_CGAP_Bin25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
8872	16094		2.33	5.0E-44	AU124571_1	EST_HUMAN	OFFR OFFR repetitive element;
3392	12619	21750	2.73	4.0E-44	AL163303_2	NT	AU124571_N12TRM4 Homo sapiens cDNA clone NT2RM4000218 5'
5039	14223		1.73	4.0E-44	AI435225_1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7789	16983	28487	3.15	4.0E-44	UR0878_1	NT	b11d02_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
1756	10967		1.21	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM) mRNA, complete cds
2497	11686	20863	3.27	3.0E-44	BE880626_1	EST_HUMAN	Homo sapiens karyopherin alpha 6 (imip alpha 7) (KPNA6), mRNA
3063	12298	21423	6.4	3.0E-44	AA169854_1	EST_HUMAN	60149129F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3693839 5'
1056	10282	19432	2.91	2.0E-44	4B26685	NT	#p1805_1.1 Strategene fetal retina 93/202 Homo sapiens cDNA clone IMAGE:609777 5'
1056	10282	19433	2.91	2.0E-44	4B26685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1216	10433	19589	5.8	2.0E-44	5803200	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1216	10433	19590	5.8	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMSP21), mRNA
1319	10534	19638	2.92	2.0E-44	AF133588_1	NT	Homo sapiens transmembrane trafficking protein (TMSP21), mRNA
1376	10560	19766	1.34	2.0E-44	BE465325_1	EST_HUMAN	hw14g06_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31B2838 3' similar to SW_OXYB_HUMAN
2120	11319	20537	1.6	2.0E-44	AF070651_1	NT	P22058 OXYSTEROL-BINDING PROTEIN :
2571	11756		1.59	2.0E-44	5901933	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3447	12672	21807	1.06	2.0E-44	D87675_1	NT	Homo sapiens adapter-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4567	13761	22857	1.87	2.0E-44	AW864979_1	EST_HUMAN	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
6256	15437	24876	4.1	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
6256	15437	24877	4.1	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8283	17399		1.56	2.0E-44 BE244802.1	EST_HUMAN	TCBAP1E2785 Pediatric pre-B cell acute lymphoblastic leukemia Bayor-HGSC project=TCBA_Homo sapiens cDNA clone TCBAP1E2785	
54	9351	18466	5.21	1.0E-44	7857334 NT	Homo sapiens Missnapen/NIK-related kinase (MINK), mRNA	
54	9351	18487	5.21	1.0E-44	7857334 NT	Homo sapiens Missnapen/NIK-related kinase (MINK), mRNA	
587	9835	18954	2.08	1.0E-44 AW853132.1	EST_HUMAN	RC1-C10248-030300-026-h12 C10248_Homo sapiens cDNA	
1205	10424		1.61	1.0E-44 AW894803.1	EST_HUMAN	RC1-BN039-110300-012-b01 BN039_Homo sapiens cDNA	
1553	10767		6.02	1.0E-44 AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
2191	11388	20610	4.39	1.0E-44 AAA34554.1	EST_HUMAN	ZW53d02/r1 Soares_total_fetus_Nb2hFB_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to ZW53d02/r1 Soares_total_fetus_Nb2hFB_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to	
2191	11388	20611	4.39	1.0E-44 AAA34554.1	EST_HUMAN	Soares_total_fetus_Nb2hFB_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to ZW53d02/r1 Soares_total_fetus_Nb2hFB_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to	
2715	11884	21111	1.46	1.0E-44 AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$	
3706	129226		4.68	1.0E-44 AA55889.1	EST_HUMAN	aa01tc09_s1 Soares_NHHMPU_S1 Homo sapiens cDNA clone DCBBTE03 5'	
7584	16789		11.94	1.0E-44 AV714608.1	EST_HUMAN	AV714608 DCB Homo sapiens cDNA clone DCBBTE03 5'	
8061	17186	26735	4.59	1.0E-44	10092684 NT	Homo sapiens Sushi domain (SCR repeat) containing (BK56A6.2), mRNA	
8117	17251	26791	3.02	1.0E-44 AW846967.1	EST_HUMAN	RC1-CT0198-150989-011-C08 CT0198_Homo sapiens cDNA	
8117	17251	26792	3.02	1.0E-44 AW846967.1	EST_HUMAN	RC1-CT0198-150989-011-C08 CT0198_Homo sapiens cDNA	
4576	13770	22895	1.21	9.0E-45	8922391 NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
4576	13770	22896	1.21	9.0E-45	8922391 NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
2490	11880	20807	16.54	8.0E-45	5174718 NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	
5112	14282	23379	7.98	8.0E-45	5174718 NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA	
2911	12148		1.44	7.0E-45 AL160131.1	NT	Novel human gene mapping to chromosome 22 aud83n07_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to	
3956	13171		7.02	8.0E-45 AW157570.1	EST_HUMAN	SW:R13A_HUMAN P40428 60S RIBOSOMAL PROTEIN L13A;	
9008	18340		1.27	6.0E-45	114163213 NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA	
902	10137		1.9	5.0E-45 AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003	
1971	11175	20381	4.35	5.0E-45 BF333627.1	EST_HUMAN	CM4-CN0044-180200-515-101 CN0044_Homo sapiens cDNA	
3178	12411	21547	2	5.0E-45 AI523786.1	EST_HUMAN	tg9407_x1 NCI_OGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE_P09084 PAIRED BOX PROTEIN PAX-1.;	
5445	14671	23828	8.89	5.0E-45 AA397781.1	EST_HUMAN	z172603_s1 Soares_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element;	
6778	15973	25430	2.31	5.0E-45	475923 NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA	

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8192	17324	26867	2.63	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1152	10374	19525	11.82	4.0E-45	X65826.1	NT	H.sapiens ART4 gene
2255	11450	20689	3.38	4.0E-45	BE65622.1	EST_HUMAN	6011944-AQF1 NIH_MGC_C_7 Homo sapiens cDNA clone IMAGE:3538425 5'
8261	17588		1.68	4.0E-45	BEE04076.1	EST_HUMAN	ho36104_x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29 b3
8298	18285	23684	2.19	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12orf3), mRNA
8907	17798		2.18	4.0E-45	BFF76077.1	EST_HUMAN	602084032F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
3305	12535		0.97	3.0E-45	T71480.1	EST_HUMAN	jd3560771 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:110245 5'
4063	12535		0.95	3.0E-45	T71480.1	EST_HUMAN	jd3560771 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:110245 5'
5244	14417		1.88	3.0E-45	AJ289473.1	NT	Homo sapiens mRNA for TRAF and TNF receptor associated protein (trap gene)
6713	15908	25387	2.57	3.0E-45	4758455	NT	Homo sapiens golgi autoantigen, golgin subfamily 8, 2 (GOLGA2) mRNA
7168	16345	26824	16.25	3.0E-45	AL63227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7168	16345	25625	16.25	3.0E-45	AL63227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9127	18274		1.98	3.0E-45	X85211.1	NT	H.sapiens DNA for endogenous retroviral like element
2468	11657		1.59	2.0E-45	AL63218.2	NT	Homo sapiens chromosome 21 segment HS21C018
2988	12234	21364	0.98	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5886	15103	24514	5.4	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophosphatidase) gene, promoter and exon 1
7381	18077	26084	21.36	2.0E-45	BE824350.1	EST_HUMAN	MRO-HTT023-180800-201-a02 HT0923 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR-G1144569 Q1144569 R_SLY1
7732	16920	28437	4.48	2.0E-45	AA458770.1	EST_HUMAN	aa871121_1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:27458688 3'
8037	17173	28712	2.46	2.0E-45	AW270280.1	EST_HUMAN	x072603_x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:27458688 3'
8037	17173	28713	2.46	2.0E-45	AW270280.1	EST_HUMAN	x072603_x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:27458688 3'
9169	17984		2.9	2.0E-45	11418157	NT	Homo sapiens calcium channel voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
122	9868		3.43	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606163 5'
415	8868		3.82	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606163 5'
479	9731	18865	0.98	1.0E-45	4500412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1182	10403	19557	1.87	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3067	12303	21428	12.47	1.0E-45	U32169.1	NT	Human pro-α2 chain of collagen type XI (COL11A2) gene, complete cds
3467	12692	21826	0.69	1.0E-45	8659858	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4473	13871	22762	6.02	1.0E-45	BE398633.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
6814	16009	25412	4.31	1.0E-45	BE87843.1	EST_HUMAN	60151126F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
8502	17541	24029	4.45	1.0E-45	11416098	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
8898	17664		7.85	1.0E-45	11526291	NT	Human hypothetical protein FLJ20454 (FLJ20454), mRNA

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8702	17887		6.94	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9133	17942	23881	2.75	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
6684	16859		11.57	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7210	16387	25869	8.54	9.0E-46	AW246864.1	EST_HUMAN	2822449 5' prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'
2405	11597	20817	20.16	8.0E-46	AI43261.1	EST_HUMAN	t32f08_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
2405	11597	20818	20.16	8.0E-46	AI43261.1	EST_HUMAN	TUBULIN_BETA-1 CHAIN (HUMAN); t32f08_x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_ma2
6482	15678		5.81	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0506-280200-012-C12 HT0506 Homo sapiens cDNA
8165	17287		3.37	8.0E-46	114191729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
4578	13772		10.04	7.0E-46	BE38165.1	EST_HUMAN	60127729F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4820	14009		1.25	7.0E-46	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
5682	14902	24285	3.83	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
8832	17743		1.33	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2711	11890	21107	6.12	6.0E-46	AI884381.1	EST_HUMAN	wm31f08_x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437375 3' similar to contains MER19.12
2711	11890	21108	6.12	6.0E-46	AI884381.1	EST_HUMAN	MER19 repetitive element; t32f08_x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437375 3' similar to contains MER19.12
5724	14942	24338	9.61	6.0E-46	AI655448.1	EST_HUMAN	ts58h10_x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363
7928	16404		2.87	6.0E-46	BE784971.1	EST_HUMAN	60147849F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880985 6'
209	9489		6.85	5.0E-46	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3502	12726	21862	1.86	5.0E-46	BE377194.1	EST_HUMAN	7db1901_x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3502	12726	21863	1.86	5.0E-46	BE377194.1	EST_HUMAN	7db1901_x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
5977	15191	24808	1.87	5.0E-46	BF590442.1	EST_HUMAN	nas38f07_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258757 3' similar to TR:O75202
8059	15249	24871	4.32	5.0E-46	BF5347228.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
847	9893		2.39	4.0E-46	AA601143.1	EST_HUMAN	no54e09_s1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156870 5'
1679	10881	20077	8.19	4.0E-46	AW770544.1	EST_HUMAN	hi8ec03_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							FIBULIN-1 ISOFORM A PRECURSOR (HUMAN); LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;

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Table 4
Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1679	10801	20078	8.19	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008830 3' similar to gb:X14008_m1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2898	11876	21080	18.7	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5411	14639	23768	2.3	4.0E-46	N36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
5411	14639	23769	2.3	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
8856	17829	23807	1.88	4.0E-46	AB02059.1	NT	Homo sapiens DNA for Human P2Xm1, complete cds
2250	11445	20867	1.82	3.0E-46	7657203	NT	Homo sapiens acidic 32 kDa protein mRNA (HSU15552), mRNA
2392	11585	20803	2.31	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
6701	15896	25357	6.58	3.0E-46	AI831462.1	EST_HUMAN	wj49c04.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
8105	17239	28777	2.69	3.0E-46	D31765.1	NT	Human mRNA for KIAA0081 gene, partial cds
847	10084	18243	6.45	2.0E-46	AA468846.1	EST_HUMAN	ned8a06.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:380408 3' similar to contains THR.b2 THR repetitive element;
1544	10758		1.74	2.0E-46	AA676246.1	EST_HUMAN	ZI27a11.s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431996 3'
1618	10831	20006	4.27	2.0E-46	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44) and F1P3 (F1P3) genes, complete cds
4984	14181	23270	1.44	2.0E-46	AA399288.1	EST_HUMAN	ZQ1750_RS-P1_1PROTEIN_;
6285	15468	24907	7.31	2.0E-46	8910569	NT	Mus musculus sperm tail associated protein (Span), mRNA
6498	15985		4.32	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
7798	18991		1.77	2.0E-46	7657233	NT	Hom sapiens small acidic protein (IMAGE:145052), mRNA
8422	18241		2	2.0E-46	B17028854.1	EST_HUMAN	601765225F1 NIH MGIC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
8689	18135		1.33	2.0E-46	IH48391.1	EST_HUMAN	y32d01.r1 Scares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:206977 5'
8727	17878		1.27	2.0E-46	AA001786.1	EST_HUMAN	zb84f12.r1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
9031	18127	23812	5.9	2.0E-46	AW277214.1	EST_HUMAN	xq76h03.x1 NCI_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2756789 3'
1240	10456	18815	7.9	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2246	11441	20665	4.25	1.0E-46	AW978516.1	EST_HUMAN	EST3806825 MAGE sequences, MAGP Homo sapiens cDNA
2384	11557	20779	3.53	1.0E-46	H97330.1	EST_HUMAN	EST480585 WATM1 Homo sapiens cDNA clone 48b095
3216	12450	21582	4.7	1.0E-46	AAA31912.1	EST_HUMAN	np78802.s1 NCI_CGAP_P72 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76777 H.sapiens MT-11 mRNA, (HUMAN),
4890	14078		2.9	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5535	14759	24128	5.85	1.0E-46	BF194707.1	EST_HUMAN	7e92b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
5643	18960	24250	5.13	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272185), mRNA

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5643	18060	24251	5.13	1.0E-46	8923762	NT	Homo sapiens centaurin alpha 2 protein (HSA272195), mRNA
7439	14759	24128	4.91	1.0E-46	BF194707.1	EST_HUMAN	7682b01_x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3843705 3'
8451	17509	24017	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284f1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4216398 5'
8451	17509	24018	1.5	1.0E-46	BF531102.1	EST_HUMAN	602072284f1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4216398 5'
9244	18015		1.63	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCBA Homo sapiens cDNA clone DCBAIE03 5'
775	10014		4.91	8.0E-47	AJ271735.1	NT	Homo sapiens Xo pseudodentalosomal region, segment 1/2
4952	14139	23233	2.1	9.0E-47	AV770926.1	EST_HUMAN	HYPOTHETICAL 12.4 KD PROTEIN;
8879	18228	23689	1.93	9.0E-47	114179868	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1777	10987	20179	44.01	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
1777	10987	20180	44.01	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
2676	11858	21073	1.3	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2RSE) mRNA
2889	12228	21360	2.14	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
2513	11702	20917	3.72	6.0E-47	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
6847	18038	25500	5.32	6.0E-47	AL6505198.1	EST_HUMAN	b28Bn02_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:22986859 3'
5918	15133	24542	5.84	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
7375	18591		6.37	5.0E-47	MT78590.1	EST_HUMAN	EST00738 Fetal brain, Strategene (cat#586206) Homo sapiens cDNA clone HFBCF07
1404	10617	19783	4.3	4.0E-47	4557558	NT	Homo sapiens ET-1 binding protein p300 (EP300) mRNA
8151	17283		6.74	4.0E-47	AV516590.1	EST_HUMAN	x066b07_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE Q84252_VIRAL_INTEGRATION_SITE PROTEIN INT-6 [1];
5551	9802	18928	2.54	3.0E-47	BEG07634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:38897721 5'
5551	9802	18929	2.54	3.0E-47	BEG07634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:38897721 5'
828	10066	18219	7.18	3.0E-47	NS71483.1	EST_HUMAN	Y534b04-31 Soares, multiple sclerosis, 2NbIMSP Homo sapiens cDNA clone IMAGE:277327 3'
953	10186	18342	10.62	3.0E-47	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3273	12506	21637	0.78	3.0E-47	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3943	13159		6.42	3.0E-47	U83181.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
4356	13568	22963	1.87	3.0E-47	M12959.1	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
5662	14885	24273	4.5	3.0E-47	AV408800.1	EST_HUMAN	U1HF-B10-adv-d-07-0-U1r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
5662	14885	24274	4.5	3.0E-47	AW408800.1	EST_HUMAN	U1HF-B10-adv-d-07-0-U1r1 Homo sapiens cDNA clone IMAGE:3063205 5'
5907	15124		1.87	3.0E-47	A1222413.1	EST_HUMAN	q04607_x1 Soares, NFL_T_GBC_S Homo sapiens cDNA clone IMAGE:1843718 3'
150	8432	18568	1.51	2.0E-47	4505318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MPT2), mRNA
975	10207	18381	2.74	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
976	10207	18382	2.74	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1573	10786	19961	1.75	2.0E-47	7682109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
1652	10868	20048	4.28	2.0E-47	AA524514.1	EST_HUMAN	ng43h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:3978073'
4340	13542	22633	2.14	2.0E-47	45048686	NT	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4378	13580	22679	1.98	2.0E-47	AA569592.1	EST_HUMAN	nt23gb7.s1 NCI_CGAP_Pri1 Homo sapiens cDNA clone IMAGE:914652
4378	13580	22680	1.98	2.0E-47	AA569592.1	EST_HUMAN	nt23gb7.s1 NCI_CGAP_Pri1 Homo sapiens cDNA clone IMAGE:914652
4508	13704	22768	2.32	2.0E-47	5174648	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R), mRNA
4827	14016	23115	1.05	2.0E-47	AW985168.1	EST_HUMAN	EST77239 MAGE sequences, MAGI Homo sapiens cDNA
5167	14348		0.78	2.0E-47	AJ041126.1	EST_HUMAN	ov61hb3.x1 Soares tests_NIH_Homo sapiens cDNA clone IMAGE:16418453'
6447	15844	25111	3	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6447	15844	25112	3	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8489	18272	23879	2.83	2.0E-47	R42423.1	EST_HUMAN	yf82e08.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:298668 3' similar to contains OFFR repetitive element;
1409	10622	19788	6.74	1.0E-47	AI333429.1	EST_HUMAN	qp98n03.x1 Soares fetal_lung_NbHL91W Homo sapiens cDNA clone IMAGE:1931189 3'
3812	13030	22139	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3812	13030	22140	0.92	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5106	14286	23371	2.55	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-402 ST0197 Homo sapiens cDNA
6102	15196	24614	8.41	1.0E-47	AI890886.1	EST_HUMAN	at1Ba06.x1 Barstead aorta HP1RB6 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M22895 RAS-RELATED PROTEIN RAP-1A (HUMAN);
6738	15933		6.84	1.0E-47	AW664648.1	EST_HUMAN	h84a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978972 3' similar to gb:M26328 KERATIN, TYPE I CYTOSKELELETAL 18 (HUMAN);
1591	10804	19879	4.07	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alphaIE subunit (CACNA1E) gene, exons 7-9, and partial cds, alternatively spliced
3531	12754	21887	0.75	9.0E-48	BF359847.1	EST_HUMAN	CN2-MT0100-310700-390-105 MT0100 Homo sapiens cDNA
7677	16876	26381	3.33	9.0E-48	BE983813.1	EST_HUMAN	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
1267	10473		2.18	8.0E-48	4501900	NT	Homo sapiens aminopeptidase 1 (ACY1), mRNA
1258	10473		1.89	8.0E-48	4501900	NT	Homo sapiens aminopeptidase 1 (ACY1), mRNA
3100	12336	21463	3.19	8.0E-48	AW768477.1	EST_HUMAN	hk61b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:>64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3100	12336	21464	3.19	8.0E-48	AW768477.1	EST_HUMAN	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
497	9750		1.35	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
498	9750		17.38	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1488	10701	19875	1.1	7.0E-48	6912719	NT	Homo sapiens toulased-like kinase 1 (TLK1), mRNA
1614	10927	20002	4.69	7.0E-48	5739038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5903	15120	24531	24.85	7.0E-48	11416831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
3576	12799	21925	0.7	8.0E-48	A1761111.1	EST_HUMAN	wf09n03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6832	16125	25591	2.22	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
6888	16168	25638	3.11	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:632627 3' similar to
3280	14466	21642	1.56	5.0E-48	4826891	NT	contains Alu repetitive element;
7528	16734	26224	4.02	4.0E-48	AB204420.1	EST_HUMAN	tu47602.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2254154 3'
1391	10605	19769	1.14	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDFE12 5'
1845	11149	20350	24.98	3.0E-48	4886170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1845	11149	20351	24.98	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3398	12823	21754	1	3.0E-48	AF172453.1	NT	Homo sapiens opioid growth factor receptor mRNA, complete cds
3609	12830	21851	0.78	3.0E-48	AV684531.1	EST_HUMAN	h14b12.x1 NCI_CGAP_Gu1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
4223	13438		0.69	3.0E-48	AA109541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B_;
5661	14835	24210	2.35	3.0E-48	BE084571.1	EST_HUMAN	ZD493.1r1 Scares_fetal_liver_spleen_1NF5_S1 Homo sapiens cDNA clone IMAGE:429844 5'
7451	19659	26148	10.07	3.0E-48	BF5614170.1	EST_HUMAN	MR4-BT0657-060400-201->10 BT0657 Homo sapiens cDNA clone IMAGE:3082287 3'
47	9344	18454	1.14	2.0E-48	AA1631840.1	EST_HUMAN	U1-H-BW1-ani-a-10-0-U1_si NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082287 3'
4529	13725	22822	1.18	2.0E-48	BE246085.1	EST_HUMAN	fmc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
6298	15478	24821	4.24	2.0E-48	AB040934.1	NT	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Bayor+HSCC project TCBAP3842
6298	15479	24922	4.24	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6304	15485	24929	3.75	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p85)) (RELA), mRNA
8448	14481	23532	2.71	2.0E-48	AA465007.1	EST_HUMAN	ZB80G03.1r1 Soares ovary tumor NbHO-T Homo sapiens cDNA clone IMAGE:810052 5'
8799	18191	23760	1.52	2.0E-48	BE737154.1	EST_HUMAN	601305064F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782 5'
58	8354	18471	3.21	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
883	10119	19281	12.45	1.0E-48	4502165	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1053	10308	19459	2.62	1.0E-48	7857430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1083	10308	19460	2.62	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1303	10519	18878	3.47	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 6 (RBM6), mRNA
1884	11091	20282	16.6	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21/C102
3463	12688	21624	1.05	1.0E-48	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21/C046
5163	14342	23421	1.34	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment

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6189	15371	24812	2.4	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
6843	16032	25497	6.77	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
8411	18216		1.41	1.0E-48	W26785.1	EST_HUMAN	15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
1978	11178	20387	1.76	8.0E-49	AB028497.1	NT	Mus musculus MyoP7DZ mRNA for myosin containing PDZ domain, complete cds
5689	14910	24303	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20) mRNA
5690	14910	24304	3.04	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20) mRNA
6558	15754	25217	5.17	8.0E-49	U23850.1	NT	Human insulin 1,4,5 triphosphate receptor type 1 mRNA, partial cds
7433	18642	26134	1.69	8.0E-49	AI623722.1	EST_HUMAN	ts28df12X1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; element contains element PTR5 repetitive element;
138	9853	18788	2.75	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
138	9853	18789	2.75	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
398	9853	18789	2.43	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
398	9853	18789	2.43	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	9853	18788	3.58	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
389	9853	18789	3.58	7.0E-49	5729890	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1228	10446	19802	3.33	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5424	14651	23787	1.65	7.0E-49	AI807191.1	EST_HUMAN	wf25h04_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2258683 3' similar to TR:O54923 O54923 RSEC15.;
202	8482	18815	52.05	6.0E-49	AW731740.1	EST_HUMAN	ba55g05_x1 NIH MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse L1R4p3 protein mRNA from a repetitive element, complete (MOUSE);
4093	13301	22401	0.65	6.0E-49	AL162091.1	EST_HUMAN	Dkf72p761A138_S1_761 (synonym: hemg2) Homo sapiens cDNA clone Dkf72p761A138_3'
7828	17020	26535	2.57	6.0E-49	AW452218.1	EST_HUMAN	UI-H-B13_d10-a-05-0-UJ_s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:30680483'
8166	17298	28840	3.61	6.0E-49	AA368558.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8166	17298	28841	3.61	6.0E-49	AA368558.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
8795	18104		4.03	6.0E-49	AA707587.1	EST_HUMAN	zj28cd8_s1 Soares_fetal_liver_spleen_1NFL_S1 Homo sapiens cDNA clone IMAGE:451694 3'
719	9981	16058	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
719	9981	18059	13.78	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1763	10974	20162	7.07	5.0E-49	AA172121.1	EST_HUMAN	#28c07 r1 Stratagene neuroepithelium (#907231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233226 G233226 RTVL-H PROTEIN; contains LTR7.13 LTR7 LTR7 repetitive element;
2707	11898	21103	11.9	5.0E-49	U117714.1	NT	Homo sapiens putative tumor suppressor S113 (S113) mRNA, complete cds
3240	12474	21605	12.59	5.0E-49	1143635	NT	Homo sapiens similar to ribosomal protein S27 (metallopanstimulin 1)(H_sapiens) (LOC63362), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
531	9782	18904	35.35	4.0E-49 AW189533.1	EST_HUMAN	x05b01.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:00350_2B CE06703	
8852	18333	3.3	4.0E-49 AA210798.1	EST_HUMAN	zr90f5.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'		
8742	17687		3.88	4.0E-49 AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	
567	9817	18939	1.68	3.0E-49 X68988.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase	
2810	11794		2.85	3.0E-49 AA016131.1	EST_HUMAN	ze31c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.k3 L1 repetitive element;	
5004	14191	23281	2.37	3.0E-49 U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40	
6259	15440	24878	10.15	3.0E-49 H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12	
7849	17040	28557	2.43	3.0E-49 AA337581.1	EST_HUMAN	EST25f7 Endometrial tumor Homo sapiens cDNA 5' end	
667	8913		2.98	2.0E-49 BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA	
3188	12423	21558	1.34	2.0E-49 N26448.1	EST_HUMAN	y2230f6.71 Soares melanocyte 2NbHm Homo sapiens cDNA clone IMAGE:2675571 5'	
4823	14012	23111	0.61	2.0E-49 BF511848.1	EST_HUMAN	U1-H-BI4-aps-d-02-0-L1 s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:30888538 3'	
6494	16891		2.82	2.0E-49 M8633.1	EST_HUMAN	EST025583 Fetal brain, Strategene (cat#3362016) Homo sapiens cDNA clone HFECY50	
909	10144		5.03	1.0E-49 BF035327.1	EST_HUMAN	601458531f1 NIH_MGC_C_66 Homo sapiens cDNA clone IMAGE:3862086 5'	
1538	10751	19924	47.43	1.0E-49 4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA	
1770	10980	20170	4.77	1.0E-49 BE255216.1	EST_HUMAN	60111576f1 NIH_MGC_C_16 Homo sapiens cDNA clone IMAGE:3356273 5'	
5283	14454		1.02	1.0E-49 7706703	NT	Homo sapiens putative G-protein coupled receptor (SH120), mRNA	
5372	14601	23711	4.6	1.0E-49 BF131007.1	EST_HUMAN	601820053f1 NIH_MGC_C_58 Homo sapiens cDNA clone IMAGE:4052052 5'	
6175	15357	24798	3.23	1.0E-49 BE39810.1	EST_HUMAN	601280330f1 NIH_MGC_C_8 Homo sapiens cDNA clone IMAGE:3520883 5'	
6175	15357	24787	3.23	1.0E-49 BE39811.1	EST_HUMAN	yw78g12.s1 Soares placenta_816weeks_2NbHP868W Homo sapiens cDNA clone IMAGE:3520883 5'	
6207	15388	24831	2.52	1.0E-49 N25884.1	EST_HUMAN	similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN); yw78g12.s1 Soares placenta_816weeks_2NbHP868W Homo sapiens cDNA clone IMAGE:258406 3'	
6207	15388	24832	2.52	1.0E-49 N25884.1	EST_HUMAN	similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);	
7617	16820	26315	1.92	1.0E-49 AV751477.1	EST_HUMAN	AV751477 NP0 Homo sapiens cDNA clone NPDAWE04 5'	
7888	17048	28687	4	1.0E-49 11427356	NT	Homo sapiens breyfeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA	
8220	17397		1.68	1.0E-49 BE158343.1	EST_HUMAN	MRO-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA	
8844	17629		2.64	1.0E-49 11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA	
9187	18115		1.42	1.0E-49 11418123	NT	Homo sapiens KIAA0033 gene product (KIAA0033), mRNA	
5018	14205		1.16	8.0E-50 AF01475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds	
173	9454	18585	2.7	8.0E-50 AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002	
728	9988	19108	2	8.0E-50 X65097.2	NT	Homo sapiens mRNA for VIP receptor 2	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
726	8888	19107	2	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2	
1734	10948	20129	3.93	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA	
2444	11635	20855	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA	
2444	11635	20856	1.38	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA	
2660	11841	21055	2.33	8.0E-50	4829858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA	
7847	17087	26818	1.89	8.0E-50	AA833467.1	EST HUMAN	GLUTATHIONE S-TRANSFERASE TESTIS/BRAIN (HUMAN); np82d08.s1 NCI CGAP_B72 Homo sapiens cDNA clone IMAGE:1130891 3' similar to gb:J05459	
625	9870	18992	0.7	7.0E-50	BE088591.1	EST HUMAN	QVO-BT0703-280400-211-008 BT0703 Homo sapiens cDNA	
7341	16557	28045	21.23	7.0E-50	AI872137.1	EST HUMAN	wm5g11.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'	
4336	13537		0.72	6.0E-50	BE784381.1	EST HUMAN	601589565f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3948577 5'	
6533	15729			4.02	6.0E-50	BE044078.1	EST HUMAN	
7392	16808	26095	5.86	6.0E-50	AA312079.1	EST HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end	
7392	16808	26098	5.98	6.0E-50	AA312079.1	EST HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end	
1762	10973	20160	0.98	5.0E-50	BF332938.1	EST HUMAN	CMO-BT0792-300500-398-005 BT0792 Homo sapiens cDNA	
1762	10973	20161	0.98	5.0E-50	BF332938.1	EST HUMAN	CMO-BT0792-300500-398-005 BT0792 Homo sapiens cDNA	
8258	17383	26916	2.05	5.0E-50	AA403053.1	EST HUMAN	ZB2901.r1 Sacculi testis NHT Homo sapiens cDNA clone IMAGE:726889 6' similar to TR:G1337769	
827	10161			3.35	4.0E-50	AA601143.1	EST HUMAN	G1337769 GAG-POL POLYPROTEIN; nos4ae09.s1 NCI CGAP_SST_Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
3425	12850	21780	1.59	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN); Homo sapiens chromosome 21 segment HS21C048	
1807	11113			5.69	3.0E-50	MI8048.1	NT	Human endogenous retrovirus RTVL-H2
2484	11674	20891	3.11	3.0E-50	BE259198.1	EST HUMAN	601109717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'	
3268	12501	21632	1.28	3.0E-50	AA746142.1	EST HUMAN	ab03f08.s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'	
3733	12853	22070	1.01	3.0E-50	AW755254.1	EST HUMAN	CNYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 41151935 similar to CNYA5 Cardiomyopathy associated gene 5	
5259	14432	23507	0.72	3.0E-50	AW583866.1	EST HUMAN	hg26e01.x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2948744 3' similar to SW_C1TC_HUMAN	
6354	15534	24987	4.64	3.0E-50	AF233436.2	NT	Homologous P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC contains Alu repetitive element; cds	
6354	15534	24988	4.64	3.0E-50	AF233436.2	NT	Homologous P11588 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC contains Alu repetitive element; cds	
7667	16866	26367	1.83	3.0E-50	11436955	NT	Homologous Grb2-associated binder 2 (KIAA0571), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
80001 16435	25922	5.9	3.0E-50	AJ245621.1	NT		Homo sapiens CTL2 gene
787 10028		5.16	2.0E-50	AF055086.1	NT		Homo sapiens MHC class 1 region
1087 10311	19464	5.21	2.0E-50	4557752	NT		Homo sapiens midline 1 (Optib/BBB syndrome) (MID1) mRNA
3255 12488	21619	0.7	2.0E-50	AF11168.2	NT		Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
4898 14088	23178	1.7	2.0E-50	AWB69159.1	EST_HUMAN	MR3-SEN0068-040500-008-01	SIN0068 Homo sapiens cDNA
4898 14088	23180	1.7	2.0E-50	AWB69159.1	EST_HUMAN	MR3-SEN0068-040500-008-01	SIN0068 Homo sapiens cDNA
6816 15812	25269	10.73	2.0E-50	X06566.1	NT		Human HALPHA44 gene for alpha-tubulin, exons 1-3
6816 15812	25270	10.73	2.0E-50	X06566.1	NT		Human HALPHA44 gene for alpha-tubulin, exons 1-3
8164 17296		2.75	2.0E-50	AF023861.1	NT		Macaca mulatta cyclophilin A mRNA, complete cds
468 9721	18852	2.18	1.0E-50	AL183209.2	NT		Homo sapiens chromosome 21 segment HS21C009
2333 11528		11.32	1.0E-50	AJ271755.1	NT		Homo sapiens Xq pseudautosomal region, segment 1/2
9224 18126		1.7	9.0E-51	D25217.2	NT		Homo sapiens mRNA for KIAA0027 protein, partial cds
4686 13769	22858	18.64	8.0E-51	AA610842.1	EST_HUMAN	NP88608.x1 NCI CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1	
6358 15538	24982	1.97	8.0E-51	11439587	NT		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN); Homo sapiens PDZ-73 protein (PDZ73/NY-CO-38), mRNA
2880 12217	21352	0.7	7.0E-51	AW274720.1	EST_HUMAN	XN34603.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q8Z340	
3250 12483	21615	1.43	7.0E-51	AW889219.1	EST_HUMAN	Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN;	
3338 12567	21705	0.77	7.0E-51	AW274720.1	EST_HUMAN	XN34603.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q8Z340	
4149 13355	22457	1.26	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2229_r1_434 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434B2229_5'	
4149 13355	22458	1.28	7.0E-51	AL078628.1	EST_HUMAN	DKFZp434B2229_r1_434 (synonym: hesc3) Homo sapiens cDNA clone DKFZp434B2229_5'	
4344 13548	22837	2.74	7.0E-51	AW295803.1	EST_HUMAN	U1-H-BW0-0ip_b-05-0-U..st NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729817.3	
8183 17315	26858	2	7.0E-51	AF181449.1	NT		Homo sapiens HSPC331 mRNA, partial cds
1513 10727	19898	1.08	6.0E-51	8878783	NT		Homo sapiens putative DNA binding protein (M96), mRNA
1948 11152	20354	8.28	6.0E-51	7657268	NT		Homo sapiens KIAA0629 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0629), mRNA
3450 12875	21810	15.12	6.0E-51	7657268	NT		Homo sapiens KIAA0629 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0629), mRNA
4298 13497	22592	0.85	6.0E-51	8910553	NT		Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4298 13497	22593	0.85	6.0E-51	8910553	NT		Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
5653 14876	24283	6.45	6.0E-51	AF070083.1	NT		Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
5653 14876	24284	6.45	6.0E-51	AF070083.1	NT		Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6070 14517	23559	2.46	6.0E-51	11429665	NT		Homo sapiens cerebral cell adhesion molecule (LOC51148), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7608	17001	26513	2.12	6.0E-51	11526289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
8060	17195	26733	1.75	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
8060	17195	26734	1.75	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
801	10040	19191	10.27	5.0E-51	AL168203.2	NT	Homo sapiens chromosome 21 segment HS21C003
813	10051	19205	1.85	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
888	11983	1684	0.97	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1587	10800	18878	1.72	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated p41 homolog (POH1) mRNA
2553	11741	20857	8.98	5.0E-51	A1007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3920	13136	22253	2.4	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3920	13136	22254	2.4	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5104	14284	23368	2.25	5.0E-51	AB037892.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
7828	17021	26536	4.86	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
132	9415	18550	20.31	3.0E-51	AL587348.1	EST_HUMAN	tr81c09_x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1184	10405	19559	34.42	3.0E-51	AL587348.1	EST_HUMAN	tr81c09_x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4318	13519	22614	2.02	3.0E-51	AL169142.1	NT	Novel human gene mapping to chromosome 22
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
371	9637	18770	1.81	2.0E-51	4507798	NT	EST_HUMAN
696	89338	19068	0.84	2.0E-51	BE391063.1	EST_HUMAN	601265684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
695	89338	19059	0.84	2.0E-51	BE391063.1	EST_HUMAN	601265684F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
							Z30805.1 Stratogene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:G233226 G233226 RTV-L PROTEIN; contains LTR7.3 LTR7 repetitive element;
1663	10876	20081	10.84	2.0E-51	AA233352.1	EST_HUMAN	I27603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2137732 3'
3713	12933	22061	3.07	2.0E-51	A1492415.1	EST_HUMAN	U1-H-B11-ed1-d22-q-U1-s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
4493	13691	22784	0.62	2.0E-51	AW1317826.1	EST_HUMAN	6014704461 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3B73563 5'
5664	14888	24276	3.73	2.0E-51	BE782015.1	EST_HUMAN	ts74807_x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW.TRKC_HUMAN
6917	16110	25576	2.68	2.0E-51	A1917078.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR;
6964	18142	25611	8.5	2.0E-51	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-801 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7871	14640	23770	9	2.0E-51	A1732851.1	EST_HUMAN	ab34f09_x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW_NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7871	14640	23771	9	2.0E-51	A1732851.1	EST_HUMAN	ab34f08_x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW_NME1_MOUSE P35438 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
8967	17837	23811	1.62	2.0E-51	11419159 NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (thymux) (Drosophila) homolog; translocated to 4 (MLL T.4), mRNA	
114	9402	18531	18.07	1.0E-51	4505281NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA	
1485	10698		45.14	1.0E-51	A1742248 CB_Homo sapiens cDNA clone CBFBCC12 5'	EST_HUMAN	A1742248 CB_Homo sapiens cDNA clone CBFBCC12 5'
5048	14230	23314	0.83	1.0E-51	BE779039.1	EST_HUMAN	801484985F1 NIH_GRC_67 Homo sapiens cDNA clone IMAGE:38668246 5'
5391	14620	23734	3.38	1.0E-51	T18862.1	EST_HUMAN	b120561 Testis 1 Homo sapiens cDNA clone b120561
8248	18392		3.62	1.0E-51	A1760590 MDS_Homo sapiens cDNA clone b12056	EST_HUMAN	A1760590 MDS_Homo sapiens cDNA clone MDSCBB22 5'
7280	18499	25691	1.97	9.0E-52	R91638.1	EST_HUMAN	YJ10h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198567 5' similar to SP:YGAF_ECOLI_P13739 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
7280	18499	25692	1.97	9.0E-52	R91638.1	EST_HUMAN	YJ10h04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198567 5' similar to SP:YGAF_ECOLI_P13739 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
8737	17683		4.59	9.0E-52	AA777621.1	EST_HUMAN	Z85607.1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR_k3 THR repetitive element ;
155	9437	18571	6.6	8.0E-52	AA720574.1	EST_HUMAN	mw21g02.51 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR_k3 THR repetitive element ;
1487	10700	18874	1.22	8.0E-52	X84690.1	NT	H_sapiens mRNA for laminin-5_alpha3/b chain
1630	10843	20020	2.78	8.0E-52	11968028 NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	
1630	10843	20021	2.78	8.0E-52	11968028 NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	
3971	10843	20020	8.23	8.0E-52	11968028 NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	
3971	10843	20021	8.23	8.0E-52	11968028 NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA	
1165	10415		2.09	6.0E-52	BE072409.1	EST_HUMAN	Q173-BT0537-271289-049-d07 BT0537 Homo sapiens cDNA partial cds ; S171 gene, partial cds
1669	10882	20068	7.15	6.0E-52	AF08807.1	NT	t246h04_Y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW_PGBM_MOUSE_Q05793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;
7761	16957	29466	2.04	6.0E-52	SE048172.1	EST_HUMAN	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4433	13633	22729	1.94	5.0E-52	Z78898.1	NT	Homo sapiens flow-sorted chromosome 6 HindIII fragment, SC6pa18H7
1637	10851	20028	1.58	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1758	10989	20154	1.94	4.0E-52	47588493	NT	Homo sapiens nucleophorin 155kD (NUP155) mRNA
3901	13117	22234	0.8	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (Tiam1) mRNA
4650	13844	22935	0.97	4.0E-52	5174590	NT	Homo sapiens 5,10-methylene tetrahydrofolate dehydrogenase, 5,10-methyltetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase (MTHFD) mRNA
6632	15828	25280	4.42	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4) mRNA
8564	17584		5.5	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9033	17805		6.28	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
4098	13278		14.34	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
569	9819	18940	2.3	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
569	9819	18941	2.3	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2483	11654	20876	15.22	2.0E-52	BE207575.1	EST_HUMAN	b686b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb:X16433 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2693	11873		25.07	2.0E-52	BF677892.1	EST_HUMAN	602084710f5_NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
4897	14184	23272	4.01	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5038	14222	23306	1.36	2.0E-52	AI141802.1	EST_HUMAN	q866d05.s1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5038	14222	23307	1.36	2.0E-52	AI141802.1	EST_HUMAN	q866d05.s1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5537	14761	24128	3.39	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-23129-03-E12 CT0214 Homo sapiens cDNA
5819	15036	24437	1.85	2.0E-52	11414868	NT	Homo sapiens interleukin 21 receptor (IL2R), mRNA
6869	15854		10.82	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
7116	16283	25774	5.48	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7116	16283	25775	5.48	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
7756	16952	28458	6.11	2.0E-52	AI831462.1	EST_HUMAN	wj48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR b2 THR repetitive element;
7756	16952	28459	6.11	2.0E-52	AI831462.1	EST_HUMAN	wj48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR b2 THR repetitive element;
7769	16985	28478	3.72	2.0E-52	AV175377.1	EST_HUMAN	AV716377 DCB Homo sapiens cDNA clone DCBAE03 5'
7892	17108		2.13	2.0E-52	W70280.1	EST_HUMAN	2d49e12.r1 Soares_fetal_heart_NbH-H9W Homo sapiens cDNA clone IMAGE:344038 5'
8140	17212		3.66	2.0E-52	11417890	NT	xn72a07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700038 3' similar to contains Alu repetitive element;contains element LTR2 repetitive element;
8365	18375	23591	12.95	2.0E-52	AW236297.1	EST_HUMAN	wf67d05.x1 Soares_NL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TRQ16859 Q16859 CARBOXYLESTERASE ;
8783	17712		4.63	2.0E-52	AI809885.1	EST_HUMAN	

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
539	9780	18914	1.76	1.0E-52	AA634445.1	EST_HUMAN	ZU75112 s1 Scores_NHT testis testis clone IMAGE:743879 3'
1379	10583	19759	3.28	1.0E-52	4504026 NT	Homo sapiens glutamate-ammonia ligase (glutamine synthetase) (GLUL) mRNA pol-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]	
3024	12280	21388	1.82	1.0E-52	S61070.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6365	14585	23681	3.88	1.0E-52	M29426.1	NT	Human PMS2 related (hPMNSR2) gene, complete cds
5827	15044	24448	2.75	1.0E-52	U38864.1	NT	Human adidase C gene for fructose-1,6-bisphosphate aldolase
6284	15445	24884	2.57	1.0E-52	X07292.1	NT	Human serine protein tyrosine phosphatase PTTPCAAX1 (hPTTPCAAX1) mRNA, complete cds
7350	16566	26056	15.62	1.0E-52	U48298.1	NT	Human serine protease (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
7413	16825		2.87	1.0E-52	11426321 NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA	
3773	12891	22106	0.85	9.0E-53	4506084 NT	Homo sapiens clone IMAGE:4132783 5'	
8614	17611		3.78	7.0E-53	BF238465.1	EST_HUMAN	601804771 F1 NIH MGIC_54 Homo sapiens cDNA clone IMAGE:4132783 5'
9057	18245		6.71	7.0E-53	A1421782.1	EST_HUMAN	lf44f07_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098077 3' similar to contains THR, t1
4076	13286	22384	6.55	5.0E-53	4758543 NT	Homo sapiens heterocystous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA	
8668	17842		1.81	5.0E-53	AW813563.1	EST_HUMAN	RC3-S10197-151059-011-910 ST0197 Homo sapiens cDNA
51	9348	18461	2.25	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
51	9348	18482	2.25	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7788	168962	28473	3.53	4.0E-53	BF128701.1	EST_HUMAN	6018108699F1 NIH MGIC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
7788	168962	28474	3.53	4.0E-53	BF128701.1	EST_HUMAN	6018108699F1 NIH MGIC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2622	11808	21023	1.8	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEc1 to ORCtL4 gene region, section 1/2 (DLEc1, ORCtL3, ORCtL4 genes, complete cds)
3712	12832	22050	1.7	3.0E-53	AW050836.1	EST_HUMAN	w222g07_x1 Scores_Dlecgtaefc_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4588	13782	22874	0.81	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-1240300-055-D03 UM0081 Homo sapiens cDNA
6562	15758	25221	5.16	3.0E-53	ST72043.1	NT	GIF-growth inhibitory factor [human, brain, Generic, 205 n]
6788	15983		8.94	3.0E-53	5901953 NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA	
8463	17536		1.41	3.0E-53	11426423 NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA	
484	9717		5.34	2.0E-53	AA368656.1	EST_HUMAN	EST77725 Pancreas tumor III Homo sapiens cDNA 5' end
2286	11491	20711	43.99	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
2501	11690		11.69	2.0E-53	4502316 NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 3110; Vacuolar proton-ATPase, subunit E, V-ATPase, subunit E (ATP8E), mRNA	
3212	12446	21579	0.8	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4036	13246	22349	2.27	2.0E-53	MG1873.1	NT	Human Krueppel-related DNA-binding protein (TFI4) gene, partial cds
5406	14634	23746	2.32	2.0E-53	BF332740.1	EST_HUMAN	PM1-CT0398-170800-001-g03 CT0386 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5406	14634	23747		2.32	2.0E-53 BF334740.1	EST_HUMAN	PMI-CT0398-170808-001-g03 CT0398 Homo sapiens cDNA
6880	16071			6.07	2.0E-53 AW245876.1	EST_HUMAN	2822865_5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822865 5'
1447	10560	19835		1.18	1.0E-53 AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
3387	12614	21747		1.42	1.0E-53 AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4 genes, complete cds)
4984	14171	23281		1.03	1.0E-53 BE286386.1	EST_HUMAN	6011178725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
6801	15988	25454		12.97	1.0E-53 X785336.1	NT	H_sapiens mRNA for tRNA core protein A1
8359	17451	26581		1.49	1.0E-53 AW245422.1	EST_HUMAN	2822843_3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822843 3'
3218	12452	21585		0.82	9.0E-54 4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5330	18050	23634		5.29	9.0E-54 4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
212	9492	18624		5.45	8.0E-54 BE386785.1	EST_HUMAN	68012712863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1803	11012	20205		2.01	8.0E-54 4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4747	13938	23041		0.71	8.0E-54 4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) USP13 mRNA
4747	13938	23042		0.71	8.0E-54 4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) USP13 mRNA
5129	13938	23041		0.72	8.0E-54 4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) USP13 mRNA
5128	13938	23042		0.72	8.0E-54 4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) USP13 mRNA
5631	14855	24238		22.45	8.0E-54 6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8) mRNA
389	9683	18820		1.42	7.0E-54 AA812537.1	EST_HUMAN	6178c12_s1 Soares_lestis_NH-T Homo sapiens cDNA clone 1377046 3' similar to contains MERSO.13 MERSO repetitive element
1758	11007	202200		1.3	7.0E-54 Y16845.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2171	11368	20589		8.45	7.0E-54 N271177.1	EST_HUMAN	yw6d12_s1 Soares_placenta_8to9weeks_2NbHPt60W Homo sapiens cDNA clone IMAGE:257399 3'
7668	16867	26368		2.02	7.0E-54 8823588	NT	similar to contains LTR7_b3 LTR/repetitive element;
7668	16867	26369		2.02	7.0E-54 8823588	NT	Homo sapiens gdf6-like protein (GLP) mRNA
7839	17031			8.56	7.0E-54 AI160189.1	EST_HUMAN	qb7g03_s1 Soares_fetal_hear_NbH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR_11 OFR repetitive element;
24	9320	18424		4.02	8.0E-54 AB0039818.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
390	8684	18821		1.74	8.0E-54 8822148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
390	9684	18822		1.74	8.0E-54 8822148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3251	12484	21616		1.3	8.0E-54 8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3981	13195	22303		1.16	8.0E-54 4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4457	13655	22749		0.75	6.0E-54 AV754748.1	EST_HUMAN	AV754748 TP Homo sapiens cDNA clone TPGAAAC10 5'
4891	14079			1.7	6.0E-54 Y09846.1	NT	H_sapiens snc pseudogene, p66 isoform
5024	14079			2.37	8.0E-54 Y09846.1	NT	H_sapiens she pseudogene, p86 isoform

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7860	18425	25912	4.04	6.0E-54	AW813567.1	EST_HUMAN	RC3_ST0187-151098-011-f08 ST0187 Homo sapiens cDNA ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
2119	11318	20536	3.92	5.0E-54	PE1523	SWISSPROT	
187	9468		74.6	4.0E-54	AF110103.1	NT	Tupaia belangeri beta-actin mRNA, partial cds EST177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
883	10198	19351	100.21	4.0E-54	AA306764.1	EST_HUMAN	
1774	10984	20175	3.46	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1774	10984	20178	3.46	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3168	12403		1.84	4.0E-54	AI065086.1	EST_HUMAN	wd28d11.x1 Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711
93	9388	18515	11.44	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPAGE POLYPROTEIN
2587	11773		1.32	3.0E-54	AI08757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7852	18852	28350	4.71	3.0E-54	BF348600.1	EST_HUMAN	IL-BT189-180389-007 BT189 Homo sapiens cDNA
							602019408F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155121 5'
7808	17123	26854	3.14	3.0E-54	AA383362.1	EST_HUMAN	Zf0112.1 Soares_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
8484	17619	24022	2.69	3.0E-54	AW984559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN
8512	18337		2.75	3.0E-54	AV748965.1	EST_HUMAN	EST368629 MAGE gene sequences: MAGE resequencing
648	8894	19018	8.02	2.0E-54	5031800 NT	EST_HUMAN	RC1-B10313-131188-011-809 BT0313 Homo sapiens cDNA
1373	10587	19753	1.05	2.0E-54	4507184 NT	EST_HUMAN	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
2504	11692	20812	2.47	2.0E-54	AV163175.1	EST_HUMAN	au92g03.y1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to gb:X53777 6QS
2560	11748	20868	2.11	2.0E-54	AL163210.2	NT	SW_CUL1_HUMAN Q13616 CULLIN HOMOLOG 1
							Homo sapiens chromosome 21 segment HS21Cq10
2847	12086	21215	1.44	2.0E-54	AV057524.1	EST_HUMAN	wy60b12.x1 Soares_NSF_F8_9N_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552827 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING
3523	12747		6.73	2.0E-54	AA532925.1	EST_HUMAN	n45g09.s1 NCL_CGAP_P9 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 6QS
4187	13391		3.82	2.0E-54	4502842 NT	EST_HUMAN	RIBOSOMAL PROTEIN L23 (HUMAN); Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4434	13634		1.21	2.0E-54	AF208161.1	NT	
4438	13638		1.27	2.0E-54	AL163201.2	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5166	14345	23434	0.6	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5598	14780	24148	4.56	2.0E-54	11426637 NT	EST_HUMAN	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
5595	14819	24195	12.42	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
5595	14819	24196	12.42	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6128	15312	24748	7.59	2.0E-54	11426544 NT	EST_HUMAN	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6973	16151	256222	4.05	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
8217	17348		4.24	2.0E-54	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
8991	17853	23887	1.6	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4461	13659		1.8	1.0E-64	BT-315418.1	EST_HUMAN	601589230F1 NIH_MGC_19 Homo sapiens cDNA clone Zn62880 similar to 5'-end region of Human AU077541 Sugeno cDNA library Homo sapiens cDNA clone IMAGE:4128835 5'
9168	17863		3.74	1.0E-54	AU077341.1	EST_HUMAN	gamma-glutamyl transpeptidase mRNA, 5 end
1322	10537		0.87	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1326	10540		2.14	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
7750	16946		2.46	8.0E-55	AW-409714.1	EST_HUMAN	fm22e02.2 NIH_MCC_17 Homo sapiens cDNA clone IMAGE:2860807 5'
1089	10313	19487	1.07	7.0E-55	R06346.1	EST_HUMAN	yf28e04.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127988 5' similar to SP_C561 BOVIN P10897 CYTOCHROME
7762	16958	28487	15.53	7.0E-55	AI561056.1	EST_HUMAN	lq25969.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
7762	16958	26468	15.56	7.0E-55	AI561056.1	EST_HUMAN	lq25969.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2210249 3'
8987	17851		1.49	7.0E-55	H23398.1	EST_HUMAN	ym157g07.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
9136	18263		5.18	7.0E-55	H23398.1	EST_HUMAN	ym157g07.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
8048	17182	28722	2.17	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1740	10952	20134	1.32	5.0E-55	AA704971.1	EST_HUMAN	z198b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482617 3'
1740	10952	20135	1.32	5.0E-55	AA704971.1	EST_HUMAN	z198b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:482617 3'
4782	13971	23074	1.49	5.0E-55	AW206021.1	EST_HUMAN	Ui-H-B11-afy-9-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
5898	15115	24526	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
5898	15115	24527	1.68	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6781	15978	25434	2.25	5.0E-55	4506802	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA), mRNA
8555	17577		3.36	5.0E-55	11417872	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
57	11958	18470	3.36	4.0E-55	AW1657984.1	EST_HUMAN	EST370564 IMAGE sequences, Homo sapiens cDNA
678	9922	19053	46.97	4.0E-55	4828573	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMYA1), mRNA
1442	10656	19830	1.18	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1442	10656	19831	1.18	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
2276	11471	20883	1.45	4.0E-55	BF061411.1	EST_HUMAN	7f52b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to 10716 contains L13 L1 repetitive element;
1503	10716		2.71	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA
1884	11187	20406	2.71	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA
1884	11197	20407	2.71	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2), mRNA
2055	11258	20468	8.48	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
2055	11258	20470	8.48	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
							Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), mRNA

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2550	11738		0.98	4.0E-55	A 271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
3247	12480	21612	0.94	4.0E-55	AL 163300.2	NT	Homo sapiens chromosome 21; segment HS21C100
6578	15774		5.57	4.0E-55	AL 163210.2	NT	Homo sapiens chromosome 21; segment HS21C100
7781	16978		6.6	4.0E-55	W 28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8465	17620		7.9	4.0E-55	BF 303841.1	EST_HUMAN	60 1886575 F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE_4120338 5'
8462	17480		3.27	3.0E-55	BF 78510.1	EST_HUMAN	PM1-H T0603-090300-001-g08 HT0603 Homo sapiens cDNA
9181	17973		1.98	3.0E-55	AL 163284.2	NT	Homo sapiens chromosome 21; segment HS21C084
3812	8848	18781	2.24	2.0E-55	X 37147.1	NT	Human endogenous retrovirus phIE-1 (ERV9)
5558	8808		1.09	2.0E-55	M 10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6555	9901	18027	3.38	2.0E-55	4607286	NT	Homo sapiens synatin-binding protein 1 (STXBP1) mRNA, and translated products
2813	12151	21286	0.82	2.0E-55	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4785	13974	23077	2.73	2.0E-55	B 718988.1	EST_HUMAN	CN1-H T0878-150500-357-g03 HT0876 Homo sapiens cDNA
6819	16013		2.85	2.0E-55	A 002838.1	EST_HUMAN	am98t05.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE_1684185 3' similar to contains
7523	16728	26219	2.48	2.0E-55	AL 119344.1	EST_HUMAN	THR_b2 THR repetitive element; AU116344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
98	9389	18518	1.2	1.0E-55	4505080	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
194	9474	18605	60.19	1.0E-55	U 9823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefl1a2) mRNA, complete cds
581	9830	18949	0.67	1.0E-55	A 026718.1	EST_HUMAN	ov85g09.X1 Soares, testis NRT Homo sapiens cDNA clone IMAGE_1644160 3'
1158	10380	19532	5.24	1.0E-55	A 0202710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1821	11125	20320	2.45	1.0E-55	B 277861.1	EST_HUMAN	60 1120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE_2987027 5'
1821	11125	20321	2.45	1.0E-55	B 277861.1	EST_HUMAN	60 1120118F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE_2987027 5'
2283	11498		8.1	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3) mRNA
2483	11673	20890	79.35	1.0E-55	X 13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2520	11708	20923	5.19	1.0E-55	A 007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2520	11708	20924	5.19	1.0E-55	A 007886.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2573	11758	20978	8.98	1.0E-55	L 54057.1	NT	Homo sapiens CLP mRNA, partial cds
3967	13162	22291	3.78	1.0E-55	AL 163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4282	13485	22584	1.09	1.0E-55	AL 163210.2	NT	Homo sapiens chromosome 21 segment HS21C100
4742	13983		1.08	1.0E-55	N 7261.1	EST_HUMAN	y44g03.11 Soares, fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE_245620 5'
4845	14034	23128	1.85	1.0E-55	AB 037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4845	14034	23127	1.85	1.0E-55	AB 037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5162	14341	23430	0.97	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FJ 20128 (FLJ20128) mRNA

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	149898	24397	6.65	1.0E-55	11433046 NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	
5778	149898	24398	6.65	1.0E-55	11433046 NT	Homo sapiens hect domain and RLD 2 (HERC2), mRNA	
7488	16693	26176	5.28	1.0E-55	AL1632102 NT	Homo sapiens chromosome 21 segment HS21C010	
7488	16693	26177	5.28	1.0E-55	AL1632102 NT	Homo sapiens chromosome 21 segment HS21C010	
7984	18419	28906	2.62	1.0E-55	U509850.1 NT	Human infant brain unknown product mRNA, complete cds	
8003	18438	25925	2.12	1.0E-55	T10045.1 EST_HUMAN	seq1575 b4hB3MA_Co8-HAP-F1 Homo sapiens cDNA clone b4hB3MA-COT8-HAP-Ft61 5' similar to similar seq in Chinese Hamster DHFR-coamplified protein mRNA	
6241	15422	24883	1.68	9.0E-58	BE379074.1 EST_HUMAN	601237702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3509552 5'	
280	11871	21085	5.74	7.0E-58	H18934.1 EST_HUMAN	yr62g03.1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element;	
6353	15553	24985	2.12	7.0E-58	AW361213.1 EST_HUMAN	RCI-CT0252-231089-013-b07 CT0252 Homo sapiens cDNA	
6353	15553	24986	2.12	7.0E-58	AW361213.1 EST_HUMAN	RCI-CT0252-231089-013-b07 CT0252 Homo sapiens cDNA	
1867	10980	20084	1.85	5.0E-58	AW897712.1 EST_HUMAN	RC3-BN0053-172020-01-h01 BN0053 Homo sapiens cDNA	
8651	18324	23589	2.18	5.0E-58	H155099.1 EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'	
29	9325	18428	18.75	4.0E-58	AF141349.1 NT	Homo sapiens beta-tubulin mRNA, complete cds	
29	9325	18428	18.75	4.0E-58	AF141349.1 NT	Homo sapiens beta-tubulin mRNA, complete cds	
2669	11850	21085	3.18	4.0E-58	4507723 NT	Homo sapiens tubulin beta polypeptide (TUBB) mRNA	
2669	11850	21068	3.18	4.0E-58	4507728 NT	Homo sapiens tubulin beta polypeptide (TUBB) mRNA	
2764	9783	18806	3.7	4.0E-58	AF003628.1 NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
2765	11761	20981	1.3	4.0E-58	AI632488.1 EST_HUMAN	wb08f08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW_DCOR_MUSPA	
2765	11761	20982	1.3	4.0E-58	AI632488.1 EST_HUMAN	P27119 ORNITHINE DECARBOXYLASE ;	
5773	14891	24391	5.54	4.0E-58	AF217508.1 NT	wb08f08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW_DCOR_MUSPA	
5773	14891	24392	5.54	4.0E-58	AF217508.1 NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds	
7487	18704	28188	11.06	4.0E-58	AI498066.1 EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'	
7487	18704	28189	11.08	4.0E-58	AI498066.1 EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'	
1349	10584	19128	4.56	3.0E-58	8924028 NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA	
1735	10947	26130	1.43	3.0E-58	6912743 NT	Homo sapiens 5'-acribonylic acid base 2 (XRN2), mRNA	
2118	11317	20535	1.09	3.0E-58	6912687 NT	Homo sapiens oncogene TC21 (TC21), mRNA	
3089	12325	21447	1.68	3.0E-58	AA325828.1 EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end	
3089	12325	21448	1.68	3.0E-58	AA325828.1 EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end	
3824	13042		2.27	3.0E-58	AF055066.1 NT	Homo sapiens MHC class I region	

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3895	13111	22229	0.88	3.0E-56	BE383512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'	
4382	13583	22685	0.6	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA	
4416	13616	22712	5.14	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068	
4570	13784	22860	2.93	3.0E-56	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S_ceratitis homolog)-like (SKIV2L), mRNA	
4817	14006		1.75	3.0E-56	BE883572.1	EST_HUMAN	601438164F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'	
5142	14321	23413	0.76	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PTPNB), mRNA	
5528	14752	24118	1.73	3.0E-56	4769163	NT	Homo sapiens sparclosleeneetin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	
5528	14752	24119	1.73	3.0E-56	4759183	NT	Homo sapiens sparclosleeneetin, cwcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA	
6030	15238	24881	5.37	3.0E-56	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA	
6723	15918	25377	8	3.0E-56	11418104	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA	
7211	16388	25870	2.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA	
7861	17051	26571	5.15	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA	
7861	17061	26572	5.15	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NP1P), mRNA	
8510	17546	23984	1.24	3.0E-56	11434876	NT	Homo sapiens cavolin 3 (CAV3), mRNA	
8510	17546	23985	1.24	3.0E-56	11434876	NT	Homo sapiens cavolin 3 (CAV3), mRNA	
530	9781		2.09	2.0E-56	AA198918.1	EST_HUMAN	zq52e08.s1 Strategene neuroepithelium (#93723) Homo sapiens cDNA clone IMAGE:6452026 3'	
740	11976	19122	1.19	2.0E-56	BE084388.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	
740	11976	19123	1.19	2.0E-56	BE084388.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA	
2945	12183	21316	1.53	2.0E-56	AB031783.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds	
3288	12519		0.92	2.0E-56	AB009881.1	NT	Homo sapiens gene for actwin receptor type IIb, complete cds	
3507	12731	21869	1.14	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'	
6121	15305	24738	1.71	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA	
987	10218		24.65	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds	
3655	12876	21994	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GCG6 Homo sapiens cDNA clone IMAGE:2946452 3'	
3655	12878	21995	1.84	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GCG6 Homo sapiens cDNA clone IMAGE:2946452 3'	
631	8876		2.23	8.0E-57	AW880885.1	EST_HUMAN	QV0-OT0033-070500-162-f03 OT0033 Homo sapiens cDNA	
7773	16988	26481	2.07	8.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds	
7773	16988	26482	2.07	8.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds	
8053	17189	26729	1.8	8.0E-57	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds	
13	9309	18411	0.69	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	
302	9575	18708	2.41	8.0E-57	AV818405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
894	10129	16291	4.82	8.0E-57	AW284599.1	EST_HUMAN	x05d10_x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1785	10985	20191	1.75	8.0E-57	AA498109.1	EST_HUMAN	Z51b12_r1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:757151 5'
5080	14240	23329	0.9	8.0E-57	BE288916.1	EST_HUMAN	600844420_F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860864-5'
5287	18235	23703	2.72	8.0E-57	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5853	15071	24481	13.17	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5853	15071	24482	13.17	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
6398	16677	26034	2.29	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6398	15577	26035	2.29	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8013	9309	18411	3.51	8.0E-57	8823349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
8751	17694		1.48	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A8), mRNA
8902	17795	23925	2.02	8.0E-57	11645732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2597	11782	21001	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2597	11782	21002	1.89	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3238	12472	21604	0.78	7.0E-57	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3859	13075	22180	2.25	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
3859	13075	22181	2.25	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
9253	18270		4.12	5.0E-57	AJ271735.1	NT	Homo sapiens Xo pseudoeutoosomal region; segment 1/2
3736	12956	22072	2.71	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
814	10052	19208	1.2	3.0E-57	450778	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1339	10553		55.7	3.0E-57	AA230278.1	EST_HUMAN	nc13f07_s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2354	11547	20768	1.09	3.0E-57	AA348335.1	EST_HUMAN	P48783_40S RIBOSOMAL PROTEIN S10.; EST54770 Hippocampus II Homo sapiens cDNA 5' end
2684	11845	21059	1.08	3.0E-57	BE876822.1	EST_HUMAN	7133b10_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WP:Y47H9C.2
2684	11845	21060	1.09	3.0E-57	BE876822.1	EST_HUMAN	CE20263;
3536	12759	21690	-2.57	3.0E-57	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (ICln) gene, complete cds
3675	12886		43.06	3.0E-57	AV853964.1	EST_HUMAN	RC3-CT0254-110300-027-410 CT0254 Homo sapiens cDNA
5719	14937	24333	3.4	3.0E-57	BE796537.1	EST_HUMAN	601589896_F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6507	15703	25169	3.32	3.0E-57	W28130.1	EST_HUMAN	4216 Human retina cDNA randomly primed sublibrary-Homo sapiens cDNA
6515	15711	28176	2.34	3.0E-57	11645788	NT	Homo sapiens hypothetical protein FLJ11866 (FLJ11866), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6515 15711	25176	2.34	3.0E-57	115457981	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA	
6734 15929	25398	5.84	3.0E-57	AU117659	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'	
7482 16890	26172	3.42	3.0E-57	AW248374.1	EST_HUMAN	2820473_5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'	
8517 18343	23805	6.01	3.0E-57	W23871.1	EST_HUMAN	2245d11.r1 Soares_fetal_lung_NbHL18V Homo sapiens cDNA clone IMAGE:303549 5'	
8903 18240	19878	1.57	3.0E-57	AW178575.1	EST_HUMAN	RCo-HT012-0508899-001-C06 HT0112 Homo sapiens cDNA	
1492 10705	19878	1.63	2.0E-57	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	
1492 10705	19879	1.63	2.0E-57	AF248219.1	EST_HUMAN	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds	
2365 11558	20780	0.98	2.0E-57	BE172526.1	EST_HUMAN	MRO-HT0559-0104-00-008-h10 HT0559 Homo sapiens cDNA clone IMAGE:1404747 3' similar to at02002_s1 Soares_perithyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1404747 3'	
2688 11889	21083	2.54	2.0E-57	AA845419.1	EST_HUMAN	at02002_s1 Soares_perithyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to at02002_s1 Soares_perithyroid_tumor_NBHPA Homo sapiens cDNA clone IMAGE:1404747 3'	
3417 12642		2.73	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
3905 13121	22239	0.85	2.0E-57	BE073264.1	EST_HUMAN	MRO-BT0551-0103-503 BT0551 Homo sapiens cDNA	
4169 13373	22472	2.44	2.0E-57	AA018299.1	EST_HUMAN	2840c08_r1 Soares retina N264HHR Homo sapiens cDNA clone IMAGE:361450 5'	
4169 13373	22473	2.44	2.0E-57	AA018299.1	EST_HUMAN	2840c08_r1 Soares retina N264HHR Homo sapiens cDNA clone IMAGE:361450 5'	
4511 13707	22800	6.55	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C053	
5522 14747		1.69	2.0E-57	AA016131.1	EST_HUMAN	2834c05_r1 Soares retina N264HHR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L13 L1	
5674 14894		31.59	2.0E-57	BF115266.1	EST_HUMAN	2834f04_x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11	
7819 17012	26525	2.46	2.0E-57	11424084	NT	7n80f04_x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11	
7819 17012	28526	2.46	2.0E-57	11424084	NT	7n80f04_x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570966 3' similar to contains TAR1.11	
7860 17050	28569	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA	
7860 17050	28570	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein	
2198 11356	20817	2.63	1.0E-57	AW503208.1	EST_HUMAN	Homo sapiens partial mRNA for PEX5 related protein	
6878 15873		3.15	1.0E-57	BE043031.1	EST_HUMAN	U1-HF-BND-akt-9-0-U1_r1 NIH_MCG_50 Homo sapiens cDNA clone IMAGE:3038082 3' similar to TR_C00248 O00248	
8680 17650		5.46	1.0E-57	AW70791.1	EST_HUMAN	h32a08_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR_ls3	
8680 17832	23909	1.56	8.0E-58	BB395061.1	EST_HUMAN	h32a08_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR_ls3	
596 9843		2.21	8.0E-58	BB888715.1	EST_HUMAN	601445548F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'	
660 9806	19033	9.69	8.0E-58	AI798376.1	EST_HUMAN	601445548F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'	
660 9806	19034	9.69	8.0E-58	AI798376.1	EST_HUMAN	601445548F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1824	11032	20226	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1824	11032	20227	2.33	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2829	12167		2.9	8.0E-58	7706132	NT	Homo sapiens DHHC protein (LOC51304), mRNA bad5603_r1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR:Q61489 Q61489
4840	14127	23223	6.17	7.0E-58	BE209803.1	EST_HUMAN	DHM1 PROTEIN.
7432	16641		7.04	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
7603	16710	26197	3.9	7.0E-58	AV504109.1	EST_HUMAN	U1-HFBN0-ali-g-10-0-U1_r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
7603	16710	26198	3.9	7.0E-58	AV504109.1	EST_HUMAN	U1-HFBN0-ali-g-10-0-U1_r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079887 5'
2218	11415	20640	1.85	6.0E-58	BE395081.1	EST_HUMAN	601309485F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2343	11538	20760	12.89	6.0E-58	AU130889	EST_HUMAN	AU130889 NT2RP3 Homo sapiens cDNA clone NT2RP3001288 5'
2853	12091	21220	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP_E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bay6r+HGSC project=TCAA Homo sapiens cDNA clone TCAAP_E1219
2853	12091	21221	1.15	6.0E-58	BE242150.1	EST_HUMAN	TCAAP_E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Bay6r+HGSC project=TCAA Homo sapiens cDNA clone TCAAP_E1219
8778	17709		1.8	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
305	9578	18710	4.83	5.0E-58	4507334	NT	Homo sapiens synaptotilin 1 (SYN1), mRNA
717	8858	18097	4.77	5.0E-58	BE763984.1	EST_HUMAN	RCG-N0057-160600-018-005 NT0043 Homo sapiens cDNA CN3-JN0043-240300-127-007 UM0043 Homo sapiens cDNA
1202	10422	19576	3.01	5.0E-58	AV797948.1	EST_HUMAN	CN3-JN0043-240300-127-007 UM0043 Homo sapiens cDNA
1202	10422	18577	3.01	5.0E-58	AV797948.1	EST_HUMAN	CN3-JN0043-240300-127-007 UM0043 Homo sapiens cDNA
1203	10422	18578	2.7	5.0E-58	AV797948.1	EST_HUMAN	CN3-JN0043-240300-127-007 UM0043 Homo sapiens cDNA
1203	10422	19577	2.7	5.0E-58	AV797948.1	EST_HUMAN	CN3-JN0043-240300-127-007 UM0043 Homo sapiens cDNA
3285	12526	21657	4.5	5.0E-58	AA888183.1	EST_HUMAN	698607_s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4246	13448	22539	0.92	5.0E-58	A1636745.1	EST_HUMAN	IS89607_s1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA_P19884 PROFILIN II
5504	14729		2.2	5.0E-58	11496282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6743	14982	24362	6	5.0E-58	H23072.1	EST_HUMAN	ym51h07_r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'
6451	15648	25118	11.24	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8483	18265		2.43	5.0E-58	11326293	NT	Homo sapiens cat eye syndrome chromosomes region, candidate 1 (CECR1), mRNA
9193	17980		3.41	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
378	9844	18778	4.45	4.0E-58	4502302	NT	Homo sapiens ATP transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O), mRNA
806	10045	19196	1.31	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database & Source	Top Hit Descriptor
1464	10677	19850	1.04	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (f9) mRNA
2541	11729	20947	1.09	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating B1/R-domain enzyme APOLLON mRNA, complete cds
2595	11781	20899	1.73	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3287	12528	21659	1.07	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3721	12841	22058	1.23	4.0E-58	5031980	NT	Homo sapiens EGFR-like repeats and discardin I-like domains 3 (EDIL3), mRNA
7883	17071	28598	10.39	4.0E-58	11424059	NT	Homo sapiens 65kDa-associated protein 5 (EB-AP5), mRNA
340	9608		1.87	3.0E-58	R17879.1	EST_HUMAN	yg10ed21r1 Soares_infant brain_1NIB_Homo sapiens cDNA clone IMAGE:3163815
1393	10607	19771	1.82	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
2890	12227		0.76	3.0E-58	R17879.1	EST_HUMAN	yg10ed21r1 Soares_infant brain_1NIB_Homo sapiens cDNA clone IMAGE:3163815'
3143	12378	21508	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1_NIH_MGCC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
3143	12378	21509	3.37	3.0E-58	BF569848.1	EST_HUMAN	602185789F1_NIH_MGCC_45 Homo sapiens cDNA clone IMAGE:4308943 5'
948	10181	19337	12.44	2.0E-58	AF088624.1	NT	Homo sapiens 5'-aminolevulinic synthase 2 (ALAS2) gene, complete cds
							ba08b07.1Y_NIH_MGCC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X81987 M.musculus mRNA for TAX responsive element binding RIBOSOMAL PROTEIN L8 (HUMAN); gb:X81987 M.musculus mRNA for EF HAND CALCIUM protein (MOUSE);
1287	10512		47.14	2.0E-58	BE208532.1	EST_HUMAN	
5371	18052	23878	3.36	2.0E-58	BE807186.1	EST_HUMAN	60149861F1_NIH_MGCC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5371	18052	23710	3.36	2.0E-58	BE807186.1	EST_HUMAN	60149861F1_NIH_MGCC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
							am57602.x1 Johnston frontal cortex_Homo sapiens cDNA clone IMAGE:16398674 3' similar to WP:ZK328.1 CE0565 UBIQUITIN CONJUGATING ENZYME, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
5717	14935	24331	1.81	2.0E-58	A1124874.1	EST_HUMAN	
6145	15329	24764	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6145	16329	24765	3.16	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7327	16543	28032	12.17	2.0E-58	BF307745.1	EST_HUMAN	601890812F1_NIH_MGCC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
7538	18741	28232	1.94	2.0E-58	AV872841.1	EST_HUMAN	hm25108.x1 NCL_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
729	8971	19109	0.76	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1075	10300	18450	3.15	1.0E-58	6274549	NT	
1335	10550	19714	0.84	1.0E-58	AW857192.1	EST_HUMAN	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1335	10550	19715	0.84	1.0E-58	AW857192.1	EST_HUMAN	EST368252 MAGE resequences, MAGD Homo sapiens cDNA
140	10814	19778	1.13	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1639	10853	20033	1.77	1.0E-58	BE466132.1	EST_HUMAN	hy10f08.x1 NCL_CGAP_GCS_Homo sapiens cDNA clone IMAGE:3196935 3'
2815	11789	21015	1.71	1.0E-58	AF2217514.1	NT	Homo sapiens uncharacterized bone marrow protein BM038 mRNA, complete cds
2754	11933	21149	2.78	1.0E-58	4759169	NT	Homo sapiens sterol regulatory element binding transcription factor 2 (SREBF2) mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2783	11181	20389	1.27	1.0E-58	5174444 NT	Homo sapiens G protein-coupled receptor 69A (GPR69A), mRNA	
3511	12735	21874	0.83	1.0E-58	4758081 NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA	
3511	12735	21875	0.63	1.0E-58	4758081 NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2), mRNA	
4980	14177	23288	5.91	1.0E-58	AI141053.1 EST_HUMAN	cz43h01.x1 Soares_NHIMPU_S1 Homo sapiens cDNA clone IMAGE:1678129 3'	
8245	17374		3.08	1.0E-58	X633932.1 NT	H.sapiens immunoglobulin kappa light chain variable region L14	
2198	11383	20815	45.34	8.0E-59	4507378 NT	Homo sapiens TATA box binding protein (TBP), mRNA	
6521	15717	25182	2.25	8.0E-59	AI761863.1 EST_HUMAN	wh50d06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'	
1822	11981		2.44	8.0E-59	BF035327.1 EST_HUMAN	601458331F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'	
4980	14167	23267	1.07	6.0E-59	AV889159.1 EST_HUMAN	MR3-SN0086-040500-008-101 SN0086 Homo sapiens cDNA	
3091	12327	21450	7.79	5.0E-59	AI807484.1 EST_HUMAN	wf48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359836 3'	
4661	13855	22953	7.37	5.0E-59	X83497.1 NT	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat	
6084	14530	23555	8.55	5.0E-59	AV162304.1 EST_HUMAN	eub6c07.x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element;	
7481	16889	20171	3.22	5.0E-59	11434908 NT	Homo sapiens hypothetical protein (LOC57143), mRNA	
803	10042	19194	4.8	4.0E-59	D80008.1 NT	Human mRNA for KIA0184 gene, partial cds	
4803	13992	23100	0.98	4.0E-59	4506758 NT	Homo sapiens ryanoidine receptor 3 (RYR3), mRNA	
4803	13892	23101	0.88	4.0E-59	4506758 NT	Homo sapiens ryanoidine receptor 3 (RYR3), mRNA	
8832	18197		2.83	4.0E-59	AF057720.1 NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD11B4) gene, promoter region and exon 1	
9	9305	4.81	3.0E-59	AV985524.1 EST_HUMAN	EST377532 MAGE sequences, MAGI Homo sapiens cDNA		
231	9509	16637	5.06	3.0E-59	768224 NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA	
1685	10897	20084	11.45	3.0E-59	4505860 NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA	
1685	10897	20085	11.45	3.0E-59	4505860 NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA	
2099	11299	20512	8.64	3.0E-59	AB028035.1 NT	Homo sapiens mRNA for KIAA1112 protein, partial cds	
2099	11299	20513	8.64	3.0E-59	AB028035.1 NT	Homo sapiens mRNA for KIAA1112 protein, partial cds	
3093	12329	21454	3.98	3.0E-59	4502014 NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	
3093	12329	21455	3.98	3.0E-59	4502014 NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA	
3815	13033	22144	1.19	3.0E-59	4508044 NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA	
4692	13883	22985	2.22	3.0E-59	AL163284.2 NT	Homo sapiens chromosome 21 segment HS21C084	
4859	14047	23142	1.63	3.0E-59	7427522 NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA	
5760	14979	24377	2.17	3.0E-59	BB24074 NT	Homo sapiens hypothetical protein PRO1741 (PRC1741), mRNA	
6235	15416	24857	1.83	3.0E-59	5454137 NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA	
8760	17701		5.3	3.0E-59	11417866 NT	Homo sapiens gamma-dutamyltransferase-like activity 1 (GGTLA1), mRNA	
6975	16153		8.01	2.0E-59	AA309774.1 EST_HUMAN	EST180833 Jurkat T-cells V Homo sapiens cDNA 5' end	

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe Seq ID No:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7407	16619	26110	2.31	2.0E-59	AW410568.1	EST_HUMAN	fl0704_x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
7407	16619	26111	2.31	2.0E-59	AW410598.1	EST_HUMAN	fl0704_x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
8506	17544	24030	13.36	2.0E-59	AB31809.1	EST_HUMAN	wb6c12_x1 NC_0042 RTV-H PROTEIN; contains LTR7_b1 LTR7 repetitive element;
9061	18220	23693	4.11	2.0E-59	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
166	9448		12.28	1.0E-59	BE298411.1	EST_HUMAN	60117675/F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2580	11768		3.15	1.0E-59	AA748468.1	EST_HUMAN	aa56hn1_s1 NC_0042 RTV-H PROTEIN; contains LTR7_b1 LTR7 repetitive element;
7431	15498	24943	9.28	1.0E-59	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
772	10012	19160	1.38	8.0E-60	AW977845.1	EST_HUMAN	EST389849 MAGE resequences, MAGO Homo sapiens cDNA
1467	10580	19853	5.94	8.0E-60	4759159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (8kd) (SNRPD3) mRNA
2138	11336	20554	4.87	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6448	15845	25113	4.12	8.0E-60	X17033.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6754	15849	25406	3.84	8.0E-60	11428949	NT	Human mRNA for integrin alpha-2 subunit
7409	16621	26113	5.82	8.0E-60	AL163204.2	NT	Homo sapiens retina and pineal gland (arrestin) (SAG) mRNA
7409	16821	26114	5.82	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
762	10003	19151	24.23	7.0E-60	AF055066.1	NT	Homo sapiens chromosome 21 segment HS21C004
763	10003	19151	103.89	7.0E-60	AT055066.1	NT	Homo sapiens MHC class 1 region
825	10063	19215	1.61	7.0E-60	4504634	NT	Homo sapiens interferkin 10 receptor, beta (IL10RB), mRNA
2098	11298	20511	4.34	7.0E-60	AT077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4180	13364	22464	3.55	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4573	13167	22862	0.62	7.0E-60	AT264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
6879	16070	25540	3.61	7.0E-60	HS8041.1	EST_HUMAN	y1204_x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
7804	17119	28650	1.95	7.0E-60	HS8041.1	EST_HUMAN	y1204_x1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
2145	11343	20561	2.1	6.0E-60	BS864974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
6811	16807		10.84	6.0E-60	I52456.1	EST_HUMAN	OFR repetitive element;
83	8376	18505	0.9	5.0E-60	A1807917.1	EST_HUMAN	wf52c01_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2356212 3'
83	8378	18506	0.9	5.0E-60	A1807917.1	EST_HUMAN	wf52c07_x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2356212 3'
2201	11398	20622	2.69	4.0E-60	AV503208.1	EST_HUMAN	U1-HF-BN0-ekr9-07-0-U1 r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2201	11398	20623	2.69	4.0E-60	AV503208.1	EST_HUMAN	U1-HF-BN0-ekr9-07-0-U1 r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2827	12165		1.39	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to retrovirus-related pol
1827	11035	20230	4.76	3.0E-60	BE562611.1	EST_HUMAN	60133648FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1827	11035	20231	4.76	3.0E-60	BE562611.1	EST_HUMAN	60133648FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1835	11043		4.97	3.0E-60	6031190	NT	Homo sapiens prothrombin (PHB) mRNA
4451	13650	22745	1.67	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5506	14731	24093	2.37	3.0E-60	AW336188.1	EST_HUMAN	RC3-LT0023-200100-01-2-a01 LT0023 Homo sapiens cDNA
6501	15787	25253	8.71	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6501	15787	25254	8.71	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
6507	15892	25353	7.68	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9140	18257		1.5	3.0E-60	AA485286.1	EST_HUMAN	ab07h04_r1 Strategenelung (R837210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.1H LTR10 repetitive element;
32	8328	18433	1.51	2.0E-60	AY008285.1	NT	Homo sapiens scute carrier (SLC25A8) mRNA, complete cds; nuclear gene for mitochondrial product
1428	10841	19812	5.12	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1686	10908	20083	1.43	2.0E-60	M24603.1	NT	Human ber protein mRNA, 5' end
2447	11638	20859	1.02	2.0E-60	AV380450.1	EST_HUMAN	RC1-HT0268-031289-012-102 HT0268 Homo sapiens cDNA
3554	12777	21808	0.7	2.0E-60	4757887	NT	Homo sapiens v-faf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3882	13108	22226	0.86	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6018	14508	23577	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6018	14508	23578	2.21	2.0E-60	4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6126	15310	24747	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
6126	15310	24744	4.04	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
6737	15892	25392	5.05	2.0E-60	L36033.1	NT	Human pre-B cell stimulating Factor homologue (SDF-1b) mRNA, complete cds
7065	16242	25717	4.11	2.0E-60	11891659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
7065	16242	25718	4.11	2.0E-60	11891659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A (SEMA6A), mRNA
7861	17140	28671	1.84	2.0E-60	4507386	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
7861	17140	28672	1.84	2.0E-60	4507386	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8797	17723		6	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2(S. cerevisiae)-like 1 (NHP2L1), mRNA
8938	18186		1.96	2.0E-60	AF068757.1	NT	Homo sapiens sonatastatin receptor subtype 3 (SS1FR3) gene, 5' flanking region and partial cds
8940	17818		1.23	2.0E-60	11418098	NT	Homo sapiens similar to HSPC0222 protein (H. sapiens) (LOC63504), mRNA
8954	17828		1.25	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
538	9778	18692	1.68	1.0E-60	BE178586.1	EST_HUMAN	PN3-HT0605-270200-001-e06 HT0605 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID No:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3880	13096	22213	1.79	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001884 5'
4976	14163	23254	1.83	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6704	15689		3.72	1.0E-60	AJ244041.1	EST_HUMAN	nc04e12.1 NCI_CGAP_Pri1 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1 M1 L1 repetitive element 1
1107	10331	19481	4.23	9.0E-61	AU118344 HEMBA1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA105538 5'
2630	11813	21031	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2506555 3'
2630	11813	21032	1.13	8.0E-61	AW008478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2506555 3'
2803	12141		2.98	8.0E-61	X97147.1	NT	Human endogenous retrovirus pHE-1 (ERV6)
2770	85445	18874	2.65	6.0E-61	BE409310.1	EST_HUMAN	60130038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
821	10059	19212	1.54	6.0E-61	BE409310.1	EST_HUMAN	60130038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1328	10544	19707	12.57	6.0E-61	AF119880.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1807	10820	19986	0.91	6.0E-61	BF257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:350145 5'
1625	10839	20015	3.27	6.0E-61	AA598603.1	EST_HUMAN	nn68h09.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:10588897 3'
3277	12510	21640	11.97	6.0E-61	AU130889 NT2RP3	EST_HUMAN	AU130889 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
5673	14883	24286	3.18	6.0E-61	S79249.1	NT	Ig-beta/B2B=CD76 (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
6227	15408	24850	1.8	6.0E-61	U24498.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
6342	15523	24971	1.86	6.0E-61	AF035737.1	NT	Human sapiens general transcription factor 2-I (GTF2I) mRNA, complete cds
8898	10059	19212	1.62	6.0E-61	BE409310.1	EST_HUMAN	60130038F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1653	10867	20049	2.83	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3001	12237	21367	2.23	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3116	12351	21479	1	5.0E-61	AB020632.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3162	12397	21532	1.6	5.0E-61	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3859	13174		1.78	5.0E-61	AJ2228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5028	9631	18763	0.7	5.0E-61	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5275	14447	23519	1.06	5.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha 1 subunit (CBFA1) gene, exon 2
5275	14447	23520	1.06	5.0E-61	AF001445.1	NT	Homo sapiens core binding factor alpha 1 subunit (CBFA1) gene, exon 2
8480	17529		4.52	4.0E-61	AV731140	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFARBO1 5'
505	9757	18884	1.65	2.0E-61	8922629	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1220	10438	18594	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1220	10438	19595	1.84	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-d01 HT0513 Homo sapiens cDNA
1641	10865	20036	1.64	2.0E-61	N53039.1	EST_HUMAN	y53d11.s1 Scares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:246453 3' similar to gb:L25444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
7045	16222	25698	2.74	2.0E-61	AW500256.1	EST_HUMAN	UL-HFBND-did-f-12-0-U.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7152	16329	25812	3.6	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (38KD) (RPC39), mRNA
7461	16658		22.39	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
441	9695		0.8	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
782	10021	19171	1.88	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1828	11034	20229	4.25	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2163	11361	20579	1.74	1.0E-61	AW827281.1	EST_HUMAN	xn11b09_Y1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:26933369 5' similar to contains element MSR1 repetitive element;
2788	12028	21155	1.09	1.0E-61	BE396333.1	EST_HUMAN	6012751351 NIH_MCG_20 Homo sapiens cDNA clone IMAGE:3614687 5'
3354	12582	21722	0.79	1.0E-61	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4432	13832	22727	0.74	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4432	13632	22728	0.74	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4873	14081	23155	9.51	1.0E-61	AW288181.1	EST_HUMAN	U1-H-BW0-ajt-b-08-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4873	14081	23156	8.51	1.0E-61	AW288181.1	EST_HUMAN	U1-H-BW0-ajt-b-08-0-UJ.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4979	14166	23256	0.79	1.0E-61	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6041	15209	24629	10.68	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds
6504	15701	25167	4.48	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
6564	15760	25222	3.39	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
6850	16039		2.62	1.0E-61	AW989726.1	EST_HUMAN	MRO-BN070-0-010-010-101 BN070 Homo sapiens cDNA
7084	16261	25738	12.12	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
7229	16450	25939	3.5	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
8414	18231	23700	3.11	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8414	18231	23701	3.11	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9115	17833	23877	7.89	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
9280	18097	23803	1.55	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4548	13743	22844	1.6	8.0E-62	AA830420.1	EST_HUMAN	cc86h11_s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone DCBAMA08 5'
1115	10339	19489	1.36	7.0E-62	AV714334.1	EST_HUMAN	P31795_P0L POLYPROTEIN;
3480	12704	21840	0.85	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
7890	17108	28636	4.29	7.0E-62	AI208861.1	EST_HUMAN	q856e0_x1 Scores_ntests_NHT_Homo sapiens cDNA clone IMAGE:1639150 3' similar to TR:O15103 O15103_HYPOTHETICAL_27.3 KD PROTEIN.
2956	12194		1.27	8.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3362	12590		5.35	8.0E-62	1141825	NT	Homo sapiens CGI-58 protein (CGI-58), mRNA

Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{Top}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
6346	15527	24975		3.61	6.0E-62	AI762801.1	EST_HUMAN	wi04d02_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251_3'
6348	15527	24976		3.61	6.0E-62	AI762801.1	EST_HUMAN	wi04d02_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251_3'
6366	16058	25523		2.47	6.0E-62	AV614393.1	EST_HUMAN	MR3-ST0203-130100-025-e09 ST0203 Homo sapiens cDNA
422	9875	18815		2.46	5.0E-62	AJ550528.1	EST_HUMAN	wk51e07_x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204_3' similar to SW:GG95_HUMAN
2370	11563	20784		4.37	5.0E-62	AJ271735.1	NT	Q08379_GOLGIN_95,_contains element MER22 repetitive element;
2370	11563	20785		4.37	5.0E-62	AJ271735.1	NT	Homo sapiens Xo pseudautosomal region; segment 1/2
3397	12624	21755		2.42	5.0E-62	450875.9	NT	Homo sapiens Xo pseudautosomal region; segment 1/2
4319	13520	22615		1.97	5.0E-62	AA431063.1	EST_HUMAN	zw78e09_s1 Scareas_festis_NHT Homo sapiens cDNA clone IMAGE:782344_3' similar to SW:NRDC_RAT
4556	13761			1.27	5.0E-62	AW905887.1	EST_HUMAN	RC5-NN1059-100500-021-H03 Homo sapiens cDNA
6921	16114	25580		4.84	5.0E-62	AV410687.1	EST_HUMAN	fr07g08_x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2961816_5'
7815	17008	26520		2.31	5.0E-62	AA431063.1	EST_HUMAN	P47245_NARDILYSIN
7815	17008	26521		2.31	5.0E-62	AV410687.1	EST_HUMAN	RC5-NN1059-100500-021-H03 Homo sapiens cDNA clone IMAGE:2961816_5'
850	10087	19248		3.3	4.0E-62	AV161479.1	EST_HUMAN	au71d03_y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701_5' similar to gb:M37104
850	10087	19247		3.3	4.0E-62	AV161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
851	10087	19248		3.33	4.0E-62	AV161479.1	EST_HUMAN	au71d03_y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701_5' similar to gb:M37104
851	10087	19247		3.33	4.0E-62	AV161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2421	11612	20834		27.87	4.0E-62	AJ827800.1	EST_HUMAN	au71d03_y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701_5' similar to gb:M37104
2421	11612	20835		27.87	4.0E-62	AJ827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3377	12605			9.57	4.0E-62	4557887	NT	wf12608_x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359_3' similar to
5041	14225			0.86	4.0E-62	AJ243213.1	NT	gb:X57138_ma1 HISTONE_H2B.2 (HUMAN);
5250	14423	23500		0.81	4.0E-62	4758323	NT	wf12608_x1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359_3' similar to
5626	14850	24232		1.84	4.0E-62	4506978	NT	gb:X57138_ma1 HISTONE_H2B.2 (HUMAN);
5786	15003	24407		2.71	4.0E-62	11420654	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6151	15335	24772		1.76	4.0E-62	11421041	NT	Homo sapiens enhancer of zeste (Drosophila) homolog 2 (EZH2) mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6348	15528	24977	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6348	15528	24978	2.14	4.0E-62	7657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
6731	15926	25385	10.84	4.0E-62	AB033089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
7582	16787	26281	2.72	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment SCSpA16D3
7582	16787	26282	2.72	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment SCSpA16D3
7779	16914	26487	22.33	4.0E-62	ST0584.1	NT	thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]
8399	17477	26953	2.09	4.0E-62	11418096	NT	Homo sapiens putative nuclear protein (HRHFB2/22), mRNA
8631	18190		2.62	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
8047	17820	23873	1.7	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9099	17915	23870	7.8	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9099	17915	23871	7.8	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9148	17852	23883	2.58	4.0E-62	11420480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
74	8368	18496	1.85	3.0E-62	45577784	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), mRNA
3011	12247	21376	0.74	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3011	12247	21377	0.74	3.0E-62	AB040908.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3678	12897	22017	15.04	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8635	15830	25292	6.49	3.0E-62	AB1632733.1	EST_HUMAN	WA3304_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2288903 3' similar to contains THR:12
1238	10455	19814	2.67	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7128	16803		5.65	2.0E-62	AF224869.1	NT	Homo sapiens membrane, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8186	17318		26.63	2.0E-62	BF330676.1	EST_HUMAN	QV4-BT0257-081198-017-e03 B10257_Homo sapiens cDNA
1051	10277	19430	2	1.0E-62	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1530	10744	18917	17.89	1.0E-62	L77810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) genes, complete cds
1788	10978	20167	1.58	1.0E-62	AA825207.1	EST_HUMAN	art70e11.1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP-K01H12.1
2865	12103	21234	0.94	1.0E-62	AL038044.1	EST_HUMAN	DKFZp686F104_1166 (synonym: Ifikd2) Homo sapiens cDNA clone DKFZp686F104_5'
3402	12628		2.08	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4528	13722	22818	1.26	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FJ_20212 (FLJ_20212), mRNA
6136	15320	24754	2.5	1.0E-62	AA722878.1	EST_HUMAN	208510_51 Soares_fetal_hear_Nbh19W Homo sapiens cDNA clone IMAGE:409771_3
6136	15320	24755	2.5	1.0E-62	AA722878.1	EST_HUMAN	208510_51 Soares_fetal_hear_Nbh19W Homo sapiens cDNA clone IMAGE:409771_3
6806	16001	25460	2.36	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6806	16001	25461	2.36	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
6940	16084	25552	3.51	1.0E-62	AA465170.1	EST_HUMAN	aa833d08_s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055_3'

Table 4
Single Exon Probes Expressed in HEla Cells

Probe Seq ID No:	Exon Seq ID No:	ORF Seq ID No:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7908	17121	26652	2.64	1.0E-82	Z79898.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
8917	17804		2.3	1.0E-82	11416322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
9129	17940	23880	3.35	1.0E-82	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
343	8611	18738	2.08	9.0E-83	AW016405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA (Tfjujivare) Homo sapiens cDNA clone GEN558C10 5'
2314	11508		1.26	9.0E-83	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (Tfjujivare) Homo sapiens cDNA clone KIAAO350 protein, partial cds
4018	13230	22332	7.81	9.0E-83	AB002348.2	NT	Homo sapiens mRNA 1 for KIAAO350 protein, partial cds
4018	13230	22333	7.81	9.0E-83	AB002348.2	NT	Homo sapiens mRNA 1 for KIAAO350 protein, partial cds
5300	14487	26928	2.91	9.0E-83	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6157	15340	24777	3.67	9.0E-83	11426885	NT	Homo sapiens nucleophathin 88KD (NUP88), mRNA
7610	16813	26309	2	9.0E-83	BF203408.1	EST_HUMAN	60186582BF1 NIH MGCG_17 Homo sapiens cDNA clone IMAGE4098487 5'
2312	11506	20727	1	8.0E-83	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2341	11534	20757	4.33	8.0E-83	5031810	NT	Homo sapiens L2-inducible T-cell kinase (ITK), mRNA
3438	12683	21795	4.09	8.0E-83	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3438	12683	21798	4.09	8.0E-83	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4252	13455	22547	3.98	8.0E-83	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
837	10170		1.24	7.0E-83	A1972137.1	EST_HUMAN	wmt5511_x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:24339608 3'
5358	14588		21.03	6.0E-83	AA420803.1	EST_HUMAN	nc83021_x1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361 60S RIBOSOMAL PROTEIN (HUMAN);
3293	12524	21656	0.98	4.0E-83	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3798	13014	22128	1.48	4.0E-83	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3798	13014	22127	1.48	4.0E-83	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
5846	15063	24471	2.59	4.0E-83	AW750372.1	EST_HUMAN	CM3-BT0585-180100-072-809 BT0585 Homo sapiens cDNA
5846	15063	24472	2.59	4.0E-83	AW750372.1	EST_HUMAN	CM3-BT0585-190100-072-809 BT0585 Homo sapiens cDNA
7692	16891	26309	2.35	4.0E-83	AW134709.1	EST_HUMAN	U1-H-B1-abq-e-02-0-LI_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
7692	16891	26400	2.35	4.0E-83	AW134709.1	EST_HUMAN	U1-H-B1-abq-e-02-0-LI_s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1804	11110	20304	2.09	3.0E-83	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2734	11913	21126	0.97	3.0E-83	J0310.1	NT	Human Mef mRNA-1 gene 1
2773	10462	19823	11.76	3.0E-83	6005983	NT	Homo sapiens zinc finger protein 144 (Me1-18) (ZNF144), mRNA
5859	15077	24490	31.49	3.0E-83	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC33528), mRNA
198	9478	18608	1.26	2.0E-83	U07864.1	NT	Human DNA topoisomerase I mRNA, partial cds
203	9483	18616	1.81	2.0E-83	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EY42), mRNA
504	8756		1.42	2.0E-83	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
836	10074	19231	2.04	2.0E-83	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1549	10762	19896	1.66	2.0E-83	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1548	10762	19897	1.66	2.0E-83	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1737	10949	20132	2.19	2.0E-83	BE410739.1	EST_HUMAN	601301622F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
3120	12355	21484	1.16	2.0E-83	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3253	12486	21618	2.53	2.0E-83	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3883	13099	22216	2.35	2.0E-83	L38991.1	NT	Homo sapiens complete gene, partial cds; cfos gene, complete cds; and unknown gene
4882	14070	23167	1.1	2.0E-83	AF111167.2	NT	Homo sapiens glutaminyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5213	14388	23473	0.67	2.0E-83	6912817	NT	Homo sapiens poly cystic kidney disease-associated protein (PKD1) gene, complete cds
5308	18049	23542	1.88	2.0E-83	11419429	NT	Homo sapiens jun dimerization protein gene, partial cds; and unknown gene
5606	14830	24208	2.73	2.0E-83	BF373541.1	EST_HUMAN	QV1-FT0170-040700-285-c05 FT0170 Homo sapiens cDNA
5608	14830	24207	2.73	2.0E-83	BF373541.1	EST_HUMAN	QV1-FT0170-040700-285-c05 FT0170 Homo sapiens cDNA
7332	18548	26038	27.58	2.0E-83	N78345.1	EST_HUMAN	2b18b05_s1 Soares_fetal lung NbH1.19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:XJ7205_40S RIBOSOMAL PROTEIN S4 (HUMAN);
7355	16571	26062	2.86	2.0E-83	AF0989810.1	NT	Homo sapiens neurexin III-alphai gene, partial cds
7355	16571	26063	2.86	2.0E-83	AF0989810.1	NT	Homo sapiens neurexin III-sigma gene, partial cds
8513	18133	23748	5.24	2.0E-83	11418185	NT	Homo sapiens eaconitase 2, mitochondrial (ACO2), mRNA
4335	13536	22627	2.88	1.0E-83	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4335	13536	22628	2.88	1.0E-83	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
6619	15815		2.88	1.0E-83	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9197	18246		7.48	1.0E-83	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C07
6416	15613	25077	8.1	9.0E-84	AI478186.1	EST_HUMAN	Im50b07_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1053	10278		16.75	8.0E-84	BE280786.1	EST_HUMAN	6011553232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
5730	14949	24348	3.59	8.0E-84	BE888755.1	EST_HUMAN	601508688F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
8320	17423		4.21	8.0E-84	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RAN GAP 1), mRNA
8374	17460		2.3	8.0E-84	T60651.1	EST_HUMAN	y688b02_r1 Strategene lung R8317210 Homo sapiens cDNA clone IMAGE:79178 5'
3503	12727		0.86	7.0E-84	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4743	13834	23037	2.89	7.0E-84	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4743	13834	23038	2.89	7.0E-84	4507480	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7086	16263	25741	4.75	7.0E-84	Y07848.1	NT	Homo sapiens EWS, qai22, mp22 and bam22 genes

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1697	10909	20094	3.93	6.0E-64	A1551892.1	EST_HUMAN	wb51e07_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1697	10909	20095	3.83	6.0E-64	A1551892.1	EST_HUMAN	wb51e07_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3086	12322	21443	4.98	6.0E-64	AV026445.1	EST_HUMAN	ww13e03_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
3086	12322	21444	4.98	6.0E-64	AV026445.1	EST_HUMAN	ww13e03_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
5501	14727	24087	2.09	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5501	14727	24088	2.09	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5507	14732	24094	6.03	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6179	15361	24799	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6179	15361	24800	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
6861	16051	25518	8.49	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC558402), mRNA
6868	16176	25647	2.76	6.0E-64	S76475.1	NT	tkC [human, brain, mRNA, 2715 nt]
7353	16569	26059	9.75	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7353	16569	26060	9.75	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
7587	12322	21443	2.09	8.0E-64	AV026445.1	EST_HUMAN	ww13e03_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
7587	12322	21444	2.09	8.0E-64	AV026445.1	EST_HUMAN	ww13e03_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2528436 3'
8532	17558	23980	4.22	6.0E-64	11526198	NT	Homo sapiens interleukin 1 receptor, beta (IL10RB), mRNA
830	10068	19222	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
830	10068	19223	2.38	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1346	10561	19726	1.1	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0503 protein, partial cds
1426	10639	19809	1.34	5.0E-64	LA0933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1426	10639	19810	1.34	5.0E-64	LA0933.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1686	10898	20086	1.67	5.0E-64	U89358.1	NT	Human [(3')mbt] protein homolog mRNA, complete cds
2778	10687	19882	5.41	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2778	10687	19883	5.41	5.0E-64	7682205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3665	13151	22267	8.01	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CRE3 (ICR53) mRNA, partial cds
4083	13282	22391	0.68	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0503 protein, partial cds
7390	16604	26083	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-016-03 ST0197 Homo sapiens cDNA
7390	16604	26084	4.15	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-016-03 ST0197 Homo sapiens cDNA
2164	11362	20580	12.04	3.0E-64	C8895_1	EST_HUMAN	C18895_Human placenta cDNA (T Fujiiwara) Homo sapiens cDNA clone GEN:569E02 5'
3221	12455	21588	0.7	3.0E-64	BE794281.1	EST_HUMAN	601589565F1_NIH_MGGC_7_Homo sapiens cDNA clone IMAGE:3943577 5'
3420	12845	21774	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA_Homo sapiens cDNA clone DCAAMC01 5'
3420	12845	21775	1.42	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA_Homo sapiens cDNA clone DCAAMC01 5'

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5872	15090	24503	2.5	3.0E-64	BF370000.1	EST_HUMAN	RC6-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
6818	15814	25273	2.49	3.0E-64	AF248953.1	NT	Homo sapiens cdgI matrix protein GM130 (GOLGA2) mRNA, complete cds
6818	15814	25274	2.49	3.0E-64	AF248953.1	NT	Homo sapiens cdgI matrix protein GM130 (GOLGA2) mRNA, complete cds
6823	15819	25277	2.26	3.0E-64	BE208521.1	EST_HUMAN	b672h12 Y NIH MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08669 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
6823	15819	25278	2.26	3.0E-64	BE208521.1	EST_HUMAN	b672h12 Y NIH MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:L08669 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
7790	16984	26498	2.06	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7790	16984	28499	2.06	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8188	17320	26863	5.53	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1098	10320	18472	2.11	2.0E-64	AA605940.1	EST_HUMAN	af08008.s1 Scores _testis_NH1 Homo sapiens cDNA clone IMAGE:1031151 3
1401	10815	19779	3.29	2.0E-64	475770.1	NT	Homo sapiens eIF4E-like cap-binding protein (4EHP) mRNA wro87b01.x1 NCI_CGAP_P_Kid11 Homo sapiens cDNA clone IMAGE:2482281 3; similar to contains element L1 repetitive element;
2491	11681		2.83	2.0E-64	A1927030.1	EST_HUMAN	
2498	11685	20803	8.65	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2498	11685	20804	8.65	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3105	12340	21483	2.07	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA, AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2/2002113 5'
5656	14879	24269	2.65	2.0E-64	AU124387.1	EST_HUMAN	602123474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280395 5'
5968	15088	24500	4.15	2.0E-64	BF668537.1	EST_HUMAN	o228603.x1 Scores _testis Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1676717 3'
5930	16148	24557	2.05	2.0E-64	A078387.1	EST_HUMAN	H_sapiens dopamine receptor D5 pseudogene 1, partial cds
5964	15179	24596	4.1	2.0E-64	M77165.1	EST_HUMAN	602042882F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4180556 5'
7347	16563	26052	2.91	2.0E-64	BF528114.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
7819	16822	26317	5.7	2.0E-64	A1922911.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2452211 3'
7819	16822	26318	5.7	2.0E-64	A1922911.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
7785	16980	26493	2.13	2.0E-64	AV984773.1	EST_HUMAN	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
82446	17507	24018	1.38	2.0E-64	8387387	NT	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
8913	17801		2.65	2.0E-64	H55162.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
2622	9538	18687	2.22	1.0E-64	AF231919.1	NT	eu6051.X1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gbl21698_cds1 PROTHYMOGIN ALPHA (HUMAN);contains element MSR1 repetitive element;
1749	10981	20143	27.24	1.0E-64	A1929419.1	EST_HUMAN	
2873	12210	21348	0.82	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA

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3485	12709	21848	5.83	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3561	12784	21913	1.41	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3591	12784	21914	1.41	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3978	13094	22211	0.78	1.0E-64	8922839	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
8419	17491		2.5	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C045
2241	11438	20660	1.5	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2241	11436	20661	1.5	9.0E-65	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
8098	17203		35.12	9.0E-65	BF7330876.1	EST_HUMAN	QV4-BT0287-081189-017-903 BT0257 Homo sapiens cDNA clone
8042	17178	26717	11.64	8.0E-65	A1928244.1	EST_HUMAN	au8907.x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to au8907.x1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW.RI.21_HUMAN P46778 60S RIBOSOMAL PROTEIN L21 ;
1063	10289	18440	2.01	6.0E-65	AV721898	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBBZC08 5'
1890	11097		20.4	6.0E-65	AA550929.1	EST_HUMAN	nr86410.s1 NCI CGAP_Pri1 Homo sapiens cDNA clone IMAGE:8999379 similar to gb:K03002 SOS RIBOSOMAL PROTEIN L32 (HUMAN);
6700	15895	25358	3.18	8.0E-65	AW083252.1	EST_HUMAN	xG07b09.x1 NCI CGAP_Co21 Homo sapiens cDNA clone IMAGE:2683545 3' similar to TR:Q63308 Q63308 LONG INTERSPersed REPEtitive DNA CONTAINING 7 ORFs; :contains L1,b2,L1 repetitive element;
6768	15963	25420	4.89	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
6788	15963	25421	4.89	6.0E-65	AA427878.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
7450	19858	26147	4.89	6.0E-65	BE567816.1	EST_HUMAN	60/1340485F NIH MGC_53 Homo sapiens cDNA clone IMAGE:3682677 5'
8030	17167	26705	4.81	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
637	8882	18008	0.72	5.0E-65	AF064604.1	NT	Homo sapiens KEO3 protein mRNA, partial cds
1361	10576	18741	1.71	5.0E-65	7681951	NT	Homo sapiens KIAAO56 gene product (KIAAO156), mRNA
1361	10576	18742	1.71	5.0E-65	7681951	NT	Homo sapiens KIAAO56 gene product (KIAAO156), mRNA
2123	11322	20540	1.56	5.0E-65	AB033768.1	NT	Homo sapiens tRP-D-colony10 mRNA for peptidylarginine deiminase type I, complete cds
3222	12458	21589	2.37	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3222	12458	21590	2.37	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
198	8478	18811	2.79	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_-1761 (synonym: Namy2) Homo sapiens cDNA clone DKFZp761G108 5'
753	8894	19138	1.27	4.0E-65	AI266468.1	EST_HUMAN	qm46801.x1 Soares_placenta_8to9weeks_2NbHP869W Homo sapiens cDNA clone IMAGE:1891800 3'
753	8894	19139	1.27	4.0E-65	AI266468.1	EST_HUMAN	qm46801.x1 Soares_placenta_8to9weeks_2NbHP869W Homo sapiens cDNA clone IMAGE:1891800 3'
1086	10310	19463	1.28	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1479	10692	19887	28.34	4.0E-65	4506536 NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA	
2305	11489	20718	3.54	4.0E-65 BE221469.1	EST_HUMAN	hu25604_x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'	
2305	11489	20720	3.54	4.0E-65 BE221469.1	EST_HUMAN	hu25604_x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'	
3928	13142	22258	0.96	4.0E-65 AW983185.1	EST_HUMAN	RC2-BN0033-160200-013-a03 BN0033 Homo sapiens cDNA	
5735	14954	24352	4.42	4.0E-65 AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds	
5735	14954	24353	4.42	4.0E-65 AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds	
6173	15355	24783	2.45	4.0E-65	11545780 NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087) mRNA	
7683	16883	26365	2.72	4.0E-65 AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds	
8754	10310	18463	1.88	4.0E-65	48267 35	Hom sapiens fragile X mental retardation, autosomal homolog 1 (FMR1), mRNA	
8801	17794		5.17	4.0E-65 AB011389.1	NT	Hom sapiens gene for AF-6, complete cds	
9268	9478	18611	1.68	4.0E-65 AL1120419.1	EST_HUMAN	DKFZp761G108_r1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'	
97	8391	18521	1.26	3.0E-65	5031976 NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	
98	9391	18621	1.04	3.0E-65	5031976 NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA	
1239	11946		4.66	3.0E-65 X78352.1	NT	H.sapiens HZF9 mRNA finger protein	
1543	10756	18630	0.92	3.0E-65	4504626 NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products	
1781	11001	20197	1.13	3.0E-65 A1000692.1	EST_HUMAN	ov23603_s1_Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element	
2847	12285	21317	0.99	3.0E-65 DB7078.2	NT	MSR1 repetitive element;	
3244	12477	21610	1.5	3.0E-65	4504626 NT	Hom sapiens mRNA for KIAA0235 protein, partial cds	
3701	12821	22099	1.22	3.0E-65 A1000692.1	EST_HUMAN	Hom sapiens laminin, beta 1 (LAMB1), mRNA	
4851	13845	22896	1.56	3.0E-65	6912385 NT	Hom sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCNA), mRNA	
7927	16403	25898	15.56	3.0E-65 AA430006.1	EST_HUMAN	zv65068_r1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:781042 5'	
3382	12609	21743	7.64	2.0E-65 BF680294.1	EST_HUMAN	602155062_r1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4265066 5'	
5895	15112		5.18	2.0E-65 BE263373.1	EST_HUMAN	601190883_F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:353741 5'	
6133	15317	24750	27.19	2.0E-65 BF576922.1	EST_HUMAN	6021343259_F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4268295 5'	
7249	16469	25961	1.71	2.0E-65	11419247 NT	Homo sapiens SW/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARDP3), mRNA	
8373	17459		11.08	2.0E-65 AA307904.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and similar to similar to endogenous retrovirus	
8868	18111		3.24	2.0E-65 BF246086.1	EST_HUMAN	601654033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'	
90	9383		0.99	1.0E-65 BF125544.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'	
545	9786	18820	1.2	1.0E-65	7657435 NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homolog (RABEF5), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ('Top') Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	11210	20420	1.4	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds hz24e09.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3208888 3'
3351	12579	21719	0.86	1.0E-65	BE466581.1	EST_HUMAN	Homo sapiens glyican 4 (GPC4) mRNA
3975	13189	22287	1.9	1.0E-65	4504032	NT	Homo sapiens glycan 4 (GPC4) mRNA
4188	13393	22288	1.9	1.0E-65	4504032	NT	Homo sapiens glycan 4 (GPC4) mRNA
4189	13393	22491	4.44	1.0E-65	AW028340.1	EST_HUMAN	wx09e09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4239	13442	22492	4.44	1.0E-65	AW028340.1	EST_HUMAN	wx09e09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5055	14237	23125	1.11	1.0E-65	AW062813.1	EST_HUMAN	EST374886 MAGE genes, MAGG Homo sapiens cDNA
5055	14237	23326	1.09	1.0E-65	AW062813.1	EST_HUMAN	xp28c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740898 3'
6770	15985	25423	2.68	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6770	15985	25424	2.68	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
6774	15989		4.14	1.0E-65	11431934	NT	Homo sapiens Inositol 1,4,5-triphosphate receptor, type 1 (ITPR1) mRNA
6866	16063	25529	7.42	1.0E-65	AI191716.1	EST_HUMAN	qd556a02.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1733450 3' similar to gb:M28581 ZINC FINGER PROTEIN 8 (HUMAN) contains MER19_1 MER19 repetitive element;
7243	16463	25953	2.12	1.0E-65	MM26167.1	NT	Human platelet factor 4 variation 1 (PF4var1) gene, complete cds
7358	16574	26068	25.94	1.0E-65	4506630	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
7680	16889	26396	2.8	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
7763	16959	26469	2.63	1.0E-65	AI621017.1	EST_HUMAN	ts76a08.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb:L15533_mra1 PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
8420	17492		2.48	1.0E-65	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
8524	17554	23987	5.48	1.0E-65	11418322	NT	Homo sapiens cochain EGFLAG seven-pass G-type receptor 1 (CELSR1), mRNA
8963	17834		1.47	1.0E-65	11418248	NT	Homo sapiens sulfatase-related protein (SULTR2), mRNA
71	9366	18482	0.83	9.0E-68	AI160311.1	NT	Novel human gene mapping to chromosome 22
71	9366	18483	0.83	9.0E-68	AI160311.1	NT	Novel human gene mapping to chromosome 22
1362	10577	19743	2.59	9.0E-68	5031980	NT	Homo sapiens 26S proteasome-associated pael1 homolog (POH1) mRNA
1362	10577	19744	2.59	9.0E-68	5031980	NT	Homo sapiens 26S proteasome-associated pael1 homolog (POH1) mRNA
1477	10690		4.32	9.0E-68	M37298.1	NT	Human transposon-like element, partial
3877	13083	22209	0.73	9.0E-68	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3877	13083	22210	0.73	9.0E-68	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4690	13890	22890	0.82	9.0E-68	AI131763.1	NT	Novel human gene mapping to chromosome X
7887	17103		1.9	7.0E-68	BE064401.1	EST_HUMAN	RC4-BT0311-141189-01-n06 BT0311 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
4359	13581	22855	1.14	6.0E-68	AI924653.1	EST_HUMAN	CE18595 ;

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Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _c) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4359	13561	22656	1.14	6.0E-66	A1924653.1	EST_HUMAN	wn57107.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
4359	13561	22657	1.14	6.0E-66	A1924653.1	EST_HUMAN	wn57107.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP:F15G9.4A
4359	13561	26428	0.19	6.0E-66	X69181.1	NT	CE18595; CE18595;
7719	16918	19755	2	5.0E-66	B064410.1	EST_HUMAN	H.sapiens mRNA for ribosomal protein L31
1375	10589	5140	0.97	5.0E-66	B0598644.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
5140	14319	23410	0.97	5.0E-66	B0598644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
5140	14319	23411	0.97	5.0E-66	B0598644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
8832	16041	25505	6.48	5.0E-66	11420537	NT	Homo sapiens thyroid hormone receptor binding protein (AlB3), mRNA
800	10039	19190	1.09	4.0E-66	68798876	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2245	11440	20864	4.3	4.0E-66	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2437	11628	708	4.0E-66	A1223364.1	NT	Homo sapiens germ-line DNA upstream of Jak2paa locus	
4783	13982	1015	4.0E-66	9835487	NT	Human endogenous retrovirus, complete genome	
5466	14692	24045	4.68	4.0E-66	11428843	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6020	14510	23568	4.04	4.0E-66	AW965473.1	EST_HUMAN	EST377548 MAGE resequences, MAGI Homo sapiens cDNA
6132	15316	24749	8.3	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
6347	14692	24045	2.06	4.0E-66	11428843	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
6491	15688	25154	10.1	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1430	10643	19814	37.87	3.0E-66	45020388	NT	(SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1430	10643	19815	37.87	3.0E-66	45020388	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1951	11155	20357	0.92	3.0E-66	N55323.1	EST_HUMAN	y227912.r1 Soares_multiple_scleroses_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2.[2] PIR:B5612;
1951	11155	20358	0.92	3.0E-66	N55323.1	EST_HUMAN	y227912.r1 Soares_multiple_scleroses_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2.[2] PIR:B5612;
1951	11155	20359	0.92	3.0E-66	N55323.1	EST_HUMAN	y227912.r1 Soares_multiple_scleroses_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35058 HISTONE H2B.1/H2B.2.[2] PIR:B5612;
2868	11849	21064	3.9	3.0E-66	11141830	NT	Homo sapiens TGFbeta-induced transcription factor 2 (TGIF2), mRNA
3031	12317	21439	7.06	3.0E-66	7682223	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
5562	14785	24155	2.1	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA

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Single Exon Probes Expressed In HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5562	14785	24156	2.1	3.0E-66	11417946 NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA	
8043	17179	26718	7.97	3.0E-66	5453949 NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA	
63	8350	18464	1.32	2.0E-66	7657334 NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	
53	8350	18485	1.32	2.0E-66	7657334 NT	Homo sapiens Misshapen/NIK-related kinase (MINK), mRNA	
428	9293	18395	1.17	2.0E-66	4505524 NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	
428	9293	18396	1.17	2.0E-66	4505524 NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products	
1794	11003	20198	4.01	2.0E-66	AL163301.2 NT	Homo sapiens chromosome 21 segment HS21C101	
3747	12867	22081	0.75	2.0E-66	AL117233.1 NT	Novel human gene mapping to chromosome 1	
4041	13251	22352	0.92	2.0E-66	AF108389.1 NT	Homo sapiens sodium/calcium exchanger isoform Na+/Ca2+ (NCX1) mRNA, complete cds	
4247	13450	22541	1.08	2.0E-66	8923798 NT	Homo sapiens histone deacetylase 8 (HDAC8 gene) (HS-2277724), mRNA	
4658	13852	22948	30.43	2.0E-66	AJ132687.2 NT	Homo sapiens HLA-B gene for human leucocyte antigen B	
4658	13852	23849	30.43	2.0E-66	AJ13267.2 NT	Homo sapiens HLA-B gene for human leucocyte antigen B	
8762	18335		2.62	2.0E-66	11418318 NT	Homo sapiens G-2 and S-phase expressed 1 (GSE1), mRNA	
1638	16871		6.34	1.0E-66	BE887173.1 EST_HUMAN	60150376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909631 5'	
2848	12085	21213	1.61	1.0E-66	AV717817.1 EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	
2848	12085	21214	1.61	1.0E-66	AV717817.1 EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	
4379	12085	21213	3.84	1.0E-66	AV717817.1 EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	
4379	12085	21214	3.84	1.0E-66	AV717817.1 EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'	
5387	14816	23729	5.7	1.0E-66	BF673088.1 EST_HUMAN	602152866F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3284151 5'	
7516	16721	26211	2.08	1.0E-66	AF111167.2 NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene	
9114	17932		1.35	1.0E-66	BE894192.1 EST_HUMAN	6011437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'	
8530	17558		2.6	9.0E-67	114181177 NT	Homo sapiens Ran GTPase activating protein 1 (RAN GAP1), mRNA	
385	8879	18816	2.28	7.0E-67	AW1622232.1 EST_HUMAN	su75d02_XL Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);	
1389	10603	19768	1.83	7.0E-67	AQ383416.1 EST_HUMAN	EST86812 Testis 1 Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid ZK353	
1539	10752	18925	1.19	7.0E-67	W65947.1 EST_HUMAN	Zh58b05.11 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'	
1539	10752	18926	1.19	7.0E-67	W65947.1 EST_HUMAN	Zh58b05.11 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'	
2001	11204	20414	1.12	7.0E-67	7657243 NT	Homo sapiens inositol 1,3,4-triphosphate 5' kinase (ITPK1), mRNA	
2001	11204	20415	1.12	7.0E-67	7657249 NT	Homo sapiens inositol 1,3,4-triphosphate 5' kinase (ITPK1), mRNA	

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	8679	18818	2.8	7.0E-67	AW162232.1	EST_HUMAN	au75d02_x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:27B2083 3' similar to gb:M37104
5777	14885	24395	1.87	7.0E-67	11425572	NT	Homo sapiens ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN); Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
5777	14895	24396	1.87	7.0E-67	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8176	17308	28851	2.1	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit V1a (COX6A1P) pseudogene, complete cds
8330	17408	28933	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8330	17408	26934	1.92	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8789	17716	23961	1.88	7.0E-67	AB011388.1	NT	Homo sapiens gene for Af-8, complete cds
966	9818	18938	2.14	6.0E-67	X68988.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
805	10044	18195	1.06	6.0E-67	Z17227.1	NT	Homo sapiens membrane receptor protein
1280	10495	19654	0.98	6.0E-67	Y14320.1	NT	Homo sapiens PMP89 gene, exons 3-4,5,6 & 7
3133	12369	21499	1.21	6.0E-67	4508434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3416	12841	21770	1.29	6.0E-67	4507332	NT	Homo sapiens mRNA and translated products
3416	12841	21771	1.29	6.0E-67	4507332	NT	Homo sapiens mRNA and translated products
4107	13314	22411	0.79	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4107	13314	22412	0.78	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4716	13907	23008	4.23	6.0E-67	7857020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
4716	13907	23009	4.23	6.0E-67	7857020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
3187	12422	21555	2.95	5.0E-67	AF009660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7/5JA2 to TCRBV1/2S2 (region)
1336	10551	19716	0.74	4.0E-67	R90819.1	EST_HUMAN	yn02d11_1r1 Soares adult brain N2b4hB55Y Homo sapiens cDNA clone IMAGE:167253 5'
7630	16831		2.28	4.0E-67	AA174294.1	EST_HUMAN	mw06e01_s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR_Q10385 Q10385
2765	8884	18009	1.15	3.0E-67	AA333768.1	EST_HUMAN	EST31803 Embryo, 9 week Homo sapiens cDNA 5' end
3431	12658	21786	1.11	3.0E-67	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
4704	13895	22894	3.38	3.0E-67	AW869159.1	EST_HUMAN	MR3-SN0066-040500-008-01 SN0066 Homo sapiens cDNA
4734	13925		1.01	3.0E-67	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
6822	15718	25183	2.27	3.0E-67	BF196068.1	EST_HUMAN	hr81f05_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
7811	17004		24.32	3.0E-67	AA927874.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
193	9473	18604	1.21	2.0E-67	BE348354.1	EST_HUMAN	om18807_s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
855	10091	19253	5.63	2.0E-67	AV818405.1	EST_HUMAN	hw18g09_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136 3' similar to WF_F23H11.9
1113	10337		1.73	2.0E-67	AF167460.1	NT	QV4-ST0234-181199-037-005 ST0234 Homo sapiens cDNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1849	11056	20248	0.91	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O94892
1849	11056	20249	0.91	2.0E-67	BE303037.1	EST_HUMAN	KIAA0798 PROTEIN ; ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976 5' similar to TR:094892 O94892
2350	11543	20766	1.39	2.0E-67	AF308361.1	NT	Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds
2395	11588	20806	3.97	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3444	12669	21804	4.82	2.0E-67	AA625755.1	EST_HUMAN	ZU91901.s1 Seares testis NHT Homo sapiens cDNA clone IMAGE:745392 3'
3979	13193	22301	3.33	2.0E-67	AI163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5720	148338	24334	4.82	2.0E-67	BF240758.1	EST_HUMAN	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
5785	15002	24405	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
5785	15002	24406	2.36	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
7476	16884	26187	1.8	2.0E-67	BF885788.1	EST_HUMAN	602140470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301705 5'
7623	18390	3.79	2.0E-67	11426448	NT	Homo sapiens KIAA0985 protein (KAIA0985), mRNA	
7891	18426	25913	2.14	2.0E-67	BF577169.1	EST_HUMAN	PM2-TN0103-040800-001-c02 TN0103 Homo sapiens cDNA
8635	18189	23759	2.69	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
257	9533	18864	7.29	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
715	98957	19095	1.12	1.0E-67	AA702784.1	EST_HUMAN	2808205.s1 Soares_fetal_liver_spineer_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4722	13913	23014	0.59	1.0E-67	BF439247.1	EST_HUMAN	nab61f08.x1 Soares_NSFF8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'
2142	11340	20558	1.2	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3851	13067	22181	5.82	8.0E-68	AA209456.1	EST_HUMAN	2082h10.r1 Strategene hNT neuron (R83723) Homo sapiens cDNA clone IMAGE:848163 5' similar to SW_SAV_SULAC_Q07580 SAV PROTEIN .
3851	13067	22182	5.82	8.0E-68	AA209456.1	EST_HUMAN	2082h10.r1 Strategene hNT neuron (R83723) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW_SAV_SULAC_Q07580 SAV PROTEIN .
7197	16374	25856	2.52	6.0E-68	11422086	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BEG2), mRNA
8973	17843		1.37	6.0E-68	BE612554.1	EST_HUMAN	601452087F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3855761 5'
812	11942	19203	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
812	11942	19204	1.04	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19220	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
829	10067	19221	5.46	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2735	11914	21127	0.97	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3112	12347	21475	3.04	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4162	13398	0.64	5.0E-68	4826967	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA	
4489	13687	22778	0.75	5.0E-68	AL157645.1	EST_HUMAN	DKEZp547D207_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone DKFZp547D207 5'

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{top}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2483	11683	20899	3.92	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2483	11683	20900	3.92	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
4865	14182		13.93	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
5212	14387	23472	0.72	4.0E-68	7549804	NT	Homo sapiens daidzinase, idotheoyanine, type II (D02), transcript variant 2, mRNA
5898	15271	24899	6.7	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
5898	15271	24700	5.7	4.0E-68	11055891	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6777	15972	25428	5.65	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
6777	15972	25429	5.65	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7573	16778	26271	7.1	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IV, member 1 (PTP4A1), mRNA
7573	16778	26272	7.1	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IV, member 1 (PTP4A1), mRNA
3841	12862	21980	5.48	3.0E-68	AF238082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
6897	15603		5.45	3.0E-68	A1342323.1	EST_HUMAN	q38h02_x1 Soares_sefal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR.12 THR repetitive element;
9188	18108		1.41	3.0E-68	AW394945.1	EST_HUMAN	QV1-DT0072-010200-056-h08 DT0072 Homo sapiens cDNA
2814	14475		26.8	2.0E-68	D00622.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4003	13216	22320	0.89	2.0E-68	B6875788.1	EST_HUMAN	711502_x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:080828 OB0828
4888	13878	22980	1.97	2.0E-68	AB0096881.1	NT	HYPOTHETICAL 88 kD PROTEIN, mRNA
6031	15239		8.84	2.0E-68	R45088.1	EST_HUMAN	Hom sapiens gene for activin receptor type II B, complete cds
6110	15204	24623	4.55	2.0E-68	BF035318.1	EST_HUMAN	yg38q04_s1 Soares infant brain 1NIH Homo sapiens cDNA clone IMAGE:34896_3
79	9372	18502	2.89	1.0E-68	4505222	NT	601458514F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034_5
301	9574	18707	11.39	1.0E-68	AV816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2216	11413	20637	2.32	1.0E-68	AB011149.1	NT	QV4-S10234-181199-037-105 ST0234 Homo sapiens cDNA
2216	11413	20638	2.32	1.0E-68	AB011149.1	NT	Hom sapiens mRNA for KIAA0357 protein, complete cds
3986	13200	22308	0.97	1.0E-68	BE2986032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344_5
5053	14235	23322	0.64	1.0E-68	AA897343.1	EST_HUMAN	bj47912_s1 Soares_cDNA clone cDNA clone IMAGE:1460518_3
5346	14576	23853	1.69	1.0E-68	7682349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0888), mRNA
7428	16839	26132	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7428	16839	26133	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
7478	19898	26168	2.64	1.0E-68	L76416.1	NT	Homo sapiens Mif2 suppressor (MSMT3), mRNA, complete cds
7747	16943	26455	2.44	1.0E-68	11433277	NT	Homo sapiens myosin IC (MYO1C), mRNA
7847	17038	26554	2.74	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80k-H (PRKCSH) gene, exon 4-5
7847	17038	26555	2.74	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80k-H (PRKCSH) gene, exon 4-5
8169	17301	26845	1.88	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8169	17301	26846	1.88	1.0E-68	11418421	NT	Homo sapiens CG178 protein (LOC51832), mRNA
8955	9372	18502	2.07	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
9178	18288	23886	1.69	1.0E-68	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
21	9317	18419	2.67	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA
21	9317	18420	2.67	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBCE) mRNA
1035	10261	19411	3.32	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH) mRNA
1035	10261	19412	3.32	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH) mRNA
4110	13317	22416	0.69	9.0E-69	4757887	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
7465	16673		9.68	9.0E-69	AI117241	EST_HUMAN	AI117241 Homo sapiens cDNA clone HEMBA1000988 5'
3364	12592		1.39	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
5814	16031	24432	5.24	7.0E-69	9866912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
6415	15812	25075	9.31	6.0E-69	AI192764.1	EST_HUMAN	q622h01.X1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE1743601 3' similar to gbL11566 80S RIBOSOMAL PROTEIN L18 (HUMAN);
6415	15812	25076	9.31	6.0E-69	AI192764.1	EST_HUMAN	q622h01.X1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE1743601 3' similar to gbL11566 80S RIBOSOMAL PROTEIN L18 (HUMAN);
9101	18262		4.5	5.0E-69	AV613417.1	EST_HUMAN	hh72e06.X1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE2988354 3' similar to MER29_12 MER29 repetitive element;
526	9777		1.22	4.0E-69	AI873630.1	EST_HUMAN	wm26h111.X1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE2437125 3'
5589	14813	24187	4.72	4.0E-69	AI764973.1	EST_HUMAN	wh57b06.X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE2384819 3' similar to TR055137 O55137 ACYL-COA THIOESTERASE;
5946	15162	24575	3.11	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
5946	15162	24576	3.11	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
391	9885	18823	2.37	3.0E-69	BE268012.1	EST_HUMAN	60110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE3351352 5'
618	9883	18983	1.63	3.0E-69	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
							yd08a02.11 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE24880 5' similar to SP-A488336 A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROPELLIN-LIKE PROTEIN - SEA URCHIN;
4882	14169	23259	2.54	3.0E-69	T80514.1	EST_HUMAN	NT
4882	14169	23259	4.28	3.0E-69	AB031732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
5178	13268	22370	1.54	3.0E-69	AI765888.1	EST_HUMAN	wh68g08.X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE2385758 3'
5299	14486	26927	2.26	3.0E-69	11418185	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6313	15494	24940	8.1	3.0E-69	AF268075.1	NT	Human mRNA for calcium-binding protein T6BP mRNA, complete cds
6929	16122	25589	3.57	3.0E-69	X06233.1	NT	Human mRNA for macrophage migration inhibitory factor (MIF)-related protein
7235	16456	25944	4.89	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15a), mRNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T ₀) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7418	16630		15.56	3.0E-59	AA376388.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
8432	17498		5.21	3.0E-59	11419157	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
126	9663	18802	0.88	2.0E-59	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
126	9663	18803	0.98	2.0E-59	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
410	9663	18802	4.91	2.0E-59	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
410	9663	18803	4.91	2.0E-59	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha/beta protein gene, partial cds
1850	11057	20250		1.85	2.0E-59	BE257857.1	EST_HUMAN
2798	12036		3.59	2.0E-59	AA431157.1	EST_HUMAN	zw71902_r1 Soares testis NHt Homo sapiens cDNA clone IMAGE:781682 5'
1826	10839		11.27	1.0E-59	BF330124.1	EST_HUMAN	RC0-BN0305-200500-031-105 BN0305 Homo sapiens cDNA
1678	10890	20078		2.07	1.0E-59	AF053768.1	NT
5934	15150	24560		4.11	1.0E-59	AVW939699.1	EST_HUMAN
6013	15263	24687		3.25	1.0E-59	AB032973.1	NT
6013	15263	24688		3.25	1.0E-59	AB032973.1	NT
7127	16304	25784	4.82	1.0E-59	BE245070.1	EST_HUMAN	TCBAPIE2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA_Homo sapiens
7127	16304	25785	4.82	1.0E-59	BE245070.1	EST_HUMAN	TCBAPIE2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA_Homo sapiens
7449	16657	26587	25.72	1.0E-59	4504918	NT	cdNA clone TCBAP2678
8369	17456		1.39	1.0E-59	BF125887.1	EST_HUMAN	TCBAPIE2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA_Homo sapiens
8798	17724			3.22	1.0E-59	AB099894.1	EST_HUMAN
2300	12014	20714		1.88	8.0E-70	AA230303.1	EST_HUMAN
4387	13569	22665		1.97	8.0E-70	L77586.1	NT
1782	10992	20187		1.72	7.0E-70	AI497807.1	EST_HUMAN
1782	10992	20188		1.72	7.0E-70	AI497807.1	EST_HUMAN
1899	11106	20288		1.42	7.0E-70	AA282856.1	EST_HUMAN
2031	11232			4.62	7.0E-70	5031688	NT
4210	13413	22508		4.25	7.0E-70	4757723	NT
5433	14860	23789		5.89	7.0E-70	AB032369.1	NT
5433	14860	23800		5.69	7.0E-70	AB032369.1	NT
6054	15222	24641		1.72	7.0E-70	AJ000052.1	NT
6688	15883	25342		5.2	7.0E-70	MT4098.1	NT
6688	15883	25343		5.2	7.0E-70	MT4098.1	NT
6688	16594	25056		6.49	7.0E-70	AF153715.1	NT

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	17259	28801	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
8125	17259	28802	2.19	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
881	10117	19279	2.56	8.0E-70	450216	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2106	11305	20519	4.61	8.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2474	11665	20884	1.66	8.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthetase (LOC555807), mRNA
2518	12018	20820	88.43	5.0E-70	7662307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
2518	12018	20821	88.43	5.0E-70	7662307	NT	Homo sapiens KIAA0782 gene product (KIAA0782), mRNA
8378	17463		2.24	5.0E-70	BE168034.1	EST_HUMAN	MR3-H10487-150200-115-a08 HT0487 Homo sapiens cDNA RCO-BT0522-071299-01-a12 BT0522 Homo sapiens cDNA
1569	10782	19955	2.52	3.0E-70	BE071786.1	EST_HUMAN	RCO-BT0522-071299-01-a12 BT0522 Homo sapiens cDNA
1569	10782	19956	2.52	3.0E-70	BE071786.1	EST_HUMAN	RCO-BT0522-071299-01-a12 BT0522 Homo sapiens cDNA
40	8336	18443	0.74	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
698	8839	19070	18.57	2.0E-70	N42181.1	EST_HUMAN	y07a10_r1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR
696	8839	19071	19.57	2.0E-70	N42161.1	EST_HUMAN	y07a10_r1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3H1_RAT P29266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR
712	8954	19094	3.59	2.0E-70	AI246998.1	EST_HUMAN	φ51b01_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1028	10254	19405	2.8	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1192	10412	19588	0.59	2.0E-70	7681983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1192	10412	19587	0.59	2.0E-70	7681983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1413	10628	19792	1.36	2.0E-70	BE467311.1	EST_HUMAN	h284c12_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
1632	10848	20024	0.93	2.0E-70	AA180083.1	EST_HUMAN	z45h05_r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:612441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1632	10848	20025	0.93	2.0E-70	AA180083.1	EST_HUMAN	z45h05_r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:380214 5' similar to SV:GAG_HTL1A
1716	10928	20113	1.45	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2286	11481		29.63	2.0E-70	AA054010.1	EST_HUMAN	P03345 GAG POLYPROTEIN
2448	11639	20880	2.97	2.0E-70	AB011173.1	NT	Homo sapiens mRNA for KIAA0601 protein, partial cds
3604	12825	21946	0.6	2.0E-70	H37988.1	EST_HUMAN	yp58b04_r1 Scores fetal liver spleen tNFLS Homo sapiens cDNA clone IMAGE:191599 5'
3809	13027	22137	1.12	2.0E-70	AL153207.2	NT	Novel human gene mapping to chromosome X
3916	13132	22250	2.14	2.0E-70	AJ246003.1	NT	Homo sapiens Spsat gene for spastin protein

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4026	13237	22342	3.74	2.0E-70	M69181.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5446	14672	23830	8.15	2.0E-70	X72662.1	NT	H_sapiens gene for schwannomin (CS8)
5446	14672	23831	8.15	2.0E-70	X72662.1	NT	H_sapiens gene for schwannomin (CS8)
5949	15185	24578	2.25	2.0E-70	D12625.1	NT	Human mRNA for NF 1 protein isoform (neurofibromin isoform), complete cds
5958	15174	24589	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
5958	15174	24590	10.47	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6087	14533	23557	1.72	2.0E-70	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetyllactosaminide alpha 2-3-sialyltransferase) (SIALT6) mRNA
6431	15628	25093	4.82	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-h subunit gene (G-s-alpha), exons 4 and 5
7638	16838	26334	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
7638	16838	26335	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8154	17286	26830	10.05	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48KD) (EIF3S8) mRNA
8787	17714	23958	2.3	2.0E-70	11420450	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8787	17714	23959	2.3	2.0E-70	11420450	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3370	12598		3.37	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
7508	16713	26201	19.02	1.0E-70	AV738538	CB_Homo sapiens cDNA clone IMAGE:23092810 5'	AV738538 CB_Homo sapiens cDNA clone IMAGE:23092810 5'
5835	14859	24242	7.21	9.0E-71	AI143870.1	EST_HUMAN	q80401_X1 Soares, testis_NHT_Homo sapiens cDNA clone IMAGE:17380093 similar to TR:O14045
5835	14859	24243	7.21	9.0E-71	AI143870.1	EST_HUMAN	q80401_X1 Soares, testis_NHT_Homo sapiens cDNA clone IMAGE:17380093 similar to TR:O14045
5835	14859	24243	7.21	9.0E-71	AI143870.1	EST_HUMAN	q80401_X1 Soares, testis_NHT_Homo sapiens cDNA clone IMAGE:17380093 similar to TR:O14045
6100	15300	24732	2.08	9.0E-71	AI654903.1	EST_HUMAN	wb52c05_X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:23092883 similar to TR:P97213
8055	15300	24732	5.42	9.0E-71	AI654903.1	EST_HUMAN	wb52c06_X1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:23092883 similar to TR:P97213
8794	15989		4.09	8.0E-71	AA171451.1	EST_HUMAN	zb21d11_11 Strengene neuroepithelium (#B37231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL
6245	16426	24866	8.53	7.0E-71	AA42230.1	EST_HUMAN	TR:G1143061 G1143061 STRAIN XA34 POL
7875	17083	26588	5.4	7.0E-71	AI163210.2	NT	Homo sapiens chromosome 21 segment HS21C10
2177	11374	28598	28.52	5.0E-71	AT056322.1	NT	Homo sapiens SP100/HMG nuclear autoantigen (SP100) mRNA, complete cds
4098	13307	22407	1.2	5.0E-71	AW816405.1	EST_HUMAN	Q44-ST0234+181199-037-105 ST0234 Homo sapiens cDNA
5605	14829	24205	1.82	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6380	15570	25027	21.73	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
7043	16220		3.25	5.0E-71	X13487.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7553	16758	26252	3.73	5.0E-71	11436514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide II, neutrophil-activating peptide-2) (PPBP), mRNA	
7748	16942	28454	2.43	5.0E-71	11438059	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC83525), mRNA	
8692	17680			1.78	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA	
365	9823	18752		112.04	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds	
365	9823	18753		112.04	4.0E-71 AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds	
2839	12078	21201	1.63	4.0E-71	4505890	NT	Homo sapiens plasminogen (PLG), mRNA	
4420	13820	22715	5.57	4.0E-71 AF056322.1	NT	Homo sapiens SP100-LIM nuclear autoantigen (SP100), mRNA, complete cds		
5007	14194	23283	5.98	4.0E-71	7657602	NT	Homo sapiens putative name-binding protein (SOU1), mRNA	
7283	16502	25984	4.32	3.0E-71 AA557683.1	EST_HUMAN		nik5h10.s1.NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;	
1237	10454	19813	10.52	2.0E-71 AL163208.2	NT	Human mRNA for KIAA0272 gene, partial cds		
5344	14574	23651	7.58	2.0E-71 D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds		
5344	14574	23652	7.58	2.0E-71 D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds		
8072	14519	23561	57.87	2.0E-71 AL042439.1	EST_HUMAN	DKFTZp434D1721_11434 (synonym:11tes3) Homo sapiens cDNA clone DKFTZp434D1721 5'		
7222	16399	25983	4.68	2.0E-71 AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds		
7222	16399	25984	4.68	2.0E-71 AF095703.1	NT	Human mRNA for KIAA0272 gene, partial cds		
7285	18504	25985	2.75	2.0E-71 BE018477.1	EST_HUMAN	P54727 UV EXCISION REPAIR PROTEIN RAD23 HOMOLOG B; NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW.R23B_HUMAN		
8112	17246	28786	1.65	2.0E-71 RS5626.1	EST_HUMAN	yJ77C11.11 Scarecrows breast-2NbHBst Homo sapiens cDNA clone IMAGE:154772 5'		
8445	17506		7.26	2.0E-71 T86489.1	EST_HUMAN	ye43609/r1 Scarecfs fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'		
844	9890	18015	1.07	1.0E-71 AI077927.1	EST_HUMAN	oy15e03_s1 Scarecs_senescents_fibroblasts_NbhHSF Homo sapiens cDNA clone IMAGE:16850163' similar to contains LOR1.b2.LOR1 repetitive element;		
949	10182	18338	2.43	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51816), mRNA	
1108	10332	19482	6.48	1.0E-71 AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds		
1348	10563	19728	10.22	1.0E-71 AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p44K230) mRNA, complete cds		
2051	11252	20465	2.23	1.0E-71 AB0117007.1	NT	Homo sapiens PM/S2L16 mRNA, partial cds		
2051	11252	20466	2.23	1.0E-71 AB0117007.1	NT	Homo sapiens neuronal cell death-related protein (LOC51816), mRNA		
2653	11836	21049	4.77	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEY1), mRNA	
3475	12689	21835	2	1.0E-71 AF119865.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds		
3574	12197	21922	7.32	1.0E-71 AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds		
3574	12797	21923	7.32	1.0E-71 AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds		

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3627	12848	21668	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19
3627	12848	21987	0.89	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 similar to Homo sapiens chromosome 19
3722	12942	22059	1.54	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (A FRN) gene, exon 19
4466	13664	22757	2.57	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4592	13786	22878	0.93	1.0E-71	H23176.1	EST_HUMAN	ym56h10.1 Scarce infant brain 1N1B Homo sapiens cDNA clone IMAGE:525285
4810	13889		1.9	1.0E-71	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
6211	15392	24836	13.82	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
6613	15809	25264	4.89	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10598 (FLJ10598), mRNA
6813	15809	25265	4.99	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10598 (FLJ10598), mRNA
7076	16253	25728	8.32	1.0E-71	AY007643.1	NT	Homo sapiens cytochrome c oxidase subunit VI-related protein gene, complete cds
7365	16581		6.68	1.0E-71	AV761217	MDS_Homo sapiens cDNA clone MDSFA03 5'	
7459	16887	26155	2.12	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII A1 polypeptide (F13A1), mRNA
7706	16905	26413	2.19	1.0E-71	11417181	NT	Homo sapiens leucyl/cystein aminopeptidase (LNPEP), mRNA
7706	16905	26414	2.19	1.0E-71	11417181	NT	Homo sapiens leucyl/cystein aminopeptidase (LNPEP), mRNA
8838	17748		8.79	1.0E-71	AB011139.1	NT	Homo sapiens gene for AF-8, complete cds
4113	9866	18805	0.89	9.0E-72	AIR57635.1	EST_HUMAN	wk95g03_X1_NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN N.:contains AU repetitive element;
4113	9866	18805	0.89	9.0E-72	AIR57635.1	EST_HUMAN	wk95g03_X1_NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN N.:contains AU repetitive element;
4090	13298	22395	2.08	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4090	13298	22398	2.06	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4090	13298	22397	2.08	7.0E-72	4501868	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
6129	15313	24747	2.92	7.0E-72	S41684.1	NT	(pseudogene) PTMAP2=protymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
8964	17835		1.43	7.0E-72	F2629.1	EST_HUMAN	HSPD13870 HM3 Homo sapiens cDNA clone s4000051G02
6593	15789		2.97	8.0E-72	AL1823246.2	NT	Homo sapiens chromosome 21 segment HS21C046
65	9361	18484	1.3	5.0E-72	BF333707.1	EST_HUMAN	QVO-C50010-150900-398-e11 CS0010 Homo sapiens cDNA
65	9361	18485	1.3	5.0E-72	BF333707.1	EST_HUMAN	QVO-C50010-150900-398-e11 CS0010 Homo sapiens cDNA
66	9361	18484	9	5.0E-72	BF333707.1	EST_HUMAN	QVO-C50010-150900-398-e11 CS0010 Homo sapiens cDNA
66	9361	18485	9	5.0E-72	BF333707.1	EST_HUMAN	QVO-C50010-150900-398-e11 CS0010 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	10370		2.72	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6709	15904	25384	2.48	5.0E-72	AW161274.1	EST_HUMAN	eu80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to TR Q88785 Q88785 HYPOTHETICAL 32.4 KD PROTEIN; contains element MSIR1 repetitive element;
7765	16998	26502	3.23	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
7785	16998	26503	3.23	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-d05 BT0598 Homo sapiens cDNA
8523	18323		2.09	5.0E-72	BE928645.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
4939	14027		1.15	4.0E-72	11034844	NT	Homo sapiens hypothetical protein JJJ1057B20.2 (DJ1057B20.2), mRNA
8059	17184	26732	6.71	4.0E-72	H79421.1	EST_HUMAN	Y428a03.s1 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:235084 5'
8178	17310	26853	3.08	4.0E-72	T81910.1	EST_HUMAN	Y428a09.s1 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:108649 3'
8894	17788	23921	8.76	4.0E-72	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
20	9316	18418	1.29	3.0E-72	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (HBEF) mRNA
9113	10148		2.08	3.0E-72	AA723823.1	EST_HUMAN	ah63a06.s1 Soares_letsis_NH-T Homo sapiens cDNA clone 1310290 3'
1163	10385	19535	13.92	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1163	10385	19536	13.92	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1201	10421	19574	0.73	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1201	10421	19575	0.73	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1507	10720	18892	1.41	3.0E-72	BE242161.1	EST_HUMAN	TCAAPE1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Bay/fe-HSCC project-TCAA Homosapiens cDNA clone TCAAPE1252
3040	12277	21405	11.09	3.0E-72	AJ229043.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
3248	12478	21611	3.48	3.0E-72	8923548	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
3813	13031	22141	2.14	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha = T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4542	13737	22835	3.48	3.0E-72	11416196	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
5646	14869	24254	1.78	3.0E-72	AF073367.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
5846	14869	24255	1.78	3.0E-72	AF073367.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
5738	14957	24396	4.53	3.0E-72	AB028004.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
6738	14957	24357	4.53	3.0E-72	AB028004.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
5940	15158	24568	3.64	3.0E-72	4826987	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA
6327	15508		1.78	3.0E-72	U80017.1	NT	Human selenocysteine-rich protein 2 (SERPINA1) mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7326	16542	26031	2.65	2.0E-72 AA789277.1	EST_HUMAN	NT	aj22b08_31 Soares, testis_NHT Homo sapiens cDNA clone 1381609 3' similar to gb:X02067 Homo sapiens mRNA for 7SL RNA pseudogenes (HUMAN); Rattus norvegicus putative phosphate/phosphoenolpyruvate translocator mRNA, complete cds
8889	17784	23918	6.91	2.0E-72 AF182714.1	EST_HUMAN	NT	ai83d02_31 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1387395 3'
2043	11244	20453	0.89	1.0E-72 AA846225.1	EST_HUMAN	NT	Home sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
5559	14782	24151	4.02	1.0E-72 BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-902 HT0578 Homo sapiens cDNA	
6350	15530	24980	3.92	1.0E-72 BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-902 HT0578 Homo sapiens cDNA	
6350	15530	24981	3.92	1.0E-72 BE175434.1	EST_HUMAN	Home sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA	
6957	16135	25805	9.43	1.0E-72 AF222742.1	NT	Home sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds	
6957	16135	25806	9.43	1.0E-72 AF222742.1	NT	Home sapiens synaptic glycoprotein SC2 (SC2) mRNA, complete cds	
1458	10871	18843	1.08	9.0E-73 AW374968.1	EST_HUMAN	MR0-CT0063-071099-002-h11 CT0063 Homo sapiens cDNA	
7524	16729	3492	9.0E-73	11424089	NT	Home sapiens ribosomal protein L13a (RPL13A), mRNA	
1045	10270	19421	1.6	8.0E-73 AW071755.1	EST_HUMAN	ws55c08_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR-Q59050	
3262	12495	21625	0.82	8.0E-73	11435180	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656.
5912	16129	24538	5.01	8.0E-73	11426469	NT	Home sapiens lysosome homolog (LOC57151), mRNA
6493	15680	25155	3.2	8.0E-73 AF113129.1	NT	Home sapiens vacuolar ATPase isoform V-ATP8 mRNA, complete cds	
8949	17824	23904	5.07	8.0E-73	11418188	NT	Home sapiens thyroid autoantigen T00D (Ku antigen) (G22P1), mRNA
1142	10385	19516	0.74	7.0E-73	8923290	NT	Home sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3270	12503	21634	1.44	7.0E-73 AL163206.2	NT	Home sapiens chromosome 21 segment HS21C006	
4983	14150		1.27	7.0E-73 AL163282.2	NT	Home sapiens chromosome 21 segment HS21C082	
161	9443		2.72	6.0E-73 AL163218.2	NT	Home sapiens chromosome 21 segment HS21C013	
6152	15338	24773	3.59	6.0E-73 BE166574.1	EST_HUMAN	Q00-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA	
5303	14535	23539	2.11	4.0E-73	11422159	NT	Home sapiens HELG protein (FAMA11), mRNA
1830	11038	20234	1.22	3.0E-73	11435913	NT	Home sapiens heme-binding protein (HEBP), mRNA
1830	11038	20235	1.22	3.0E-73	11435913	NT	Home sapiens heme-binding protein (HEBP), mRNA
9185	17982		1.8	3.0E-73 AL163246.2	NT	Home sapiens chromosome 21 segment HS21C046	
9188	17984		1.4	3.0E-73 AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA	
861	10097	19239	3.36	2.0E-73 AF139897.1	NT	Home sapiens BASS1 (BASS1) mRNA, partial cds	
1915	11120		3.14	2.0E-73 AW898081.1	EST_HUMAN	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA	
2260	11455		1.58	2.0E-73 U01317.1	NT	Human beta globin region on chromosome 11	
3146	12381	21513	3.5	2.0E-73	4502582	NT	Home sapiens caspase-8, apoptosis-related cysteine protease (CASP8) mRNA
3525	12749	21880	0.94	2.0E-73	7689539	NT	Home sapiens Parkinson disease (autosomal recessive juvenile) 2, parkin (PARK2), transcript variant 3, mRNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3525	12749	21881	0.94	2.0E-73	7689539 NT	Homo sapiens mRNA	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3.
4428	13628	24405	2.51	2.0E-73 AL163283.2	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds	
5864	15822	24405	6.18	2.0E-73 AB048811.1	NT	Homo sapiens mRNA for galactosylceramidase (Krabbe disease) (GALC), mRNA	
7622	16825	26321	3.98	2.0E-73 4557612 NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA		
7622	16825	26322	3.98	2.0E-73 4557612 NT	Homo sapiens mRNA for KIAA1050 protein, partial cds		
7849	16849	28347	1.94	2.0E-73 AB028982.1	NT	Homo sapiens mRNA for KIAA1050 protein, partial cds	
8728	11120		2.68	2.0E-73 AW898081.1	EST_HUMAN	RC3-NN0066-270400-011-004 NN0066 Homo sapiens cDNA clone [MAMMA1000490 5'	
1763	10985	20150	2.16	1.0E-73 AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone [IMAGE:3617105 5'	
7886	16421	25908	3.76	1.0E-73 BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone [IMAGE:3617105 5'	
748	9889	19132	1.05	8.0E-74	4557426 NT	Homo sapiens CD39-like 4 (CD39L4) mRNA	
5623	14847	24228	2	8.0E-74 S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3428 nt]	
5623	14847	24229	2	8.0E-74 S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3428 nt]	
1919	11123	20318	4.93	7.0E-74 AJ001688.1	NT	Homo sapiens NK22D gene, exon 10	
3301	12532	21684	1.74	7.0E-74 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048	
8948	17823	23903	4.04	7.0E-74 BB286305.1	EST_HUMAN	601191827F1 NIH_MGC_7 Homo sapiens cDNA clone [IMAGE:3535855 5'	
1130	10354	19506	4.82	6.0E-74 AF09807.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds	
1604	10818	19983	1.07	6.0E-74 AW263177.1	EST_HUMAN	xn78g07-x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700336 3'	
2282	11477	20898	45.19	6.0E-74 BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603453 5'	
2282	11477	20899	45.19	6.0E-74 BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603453 5'	
2818	12055	21178	1.03	6.0E-74 AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-0-U1\$1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:27059365 3'	
2818	12055	21180	1.03	6.0E-74 AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-0-U1\$1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:27059365 3'	
3694	12914	22032	1.63	6.0E-74 BE048848.1	EST_HUMAN	hr54e11_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'	
3694	12914	22033	1.63	6.0E-74 BE048848.1	EST_HUMAN	hr54e11_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'	
5052	14234	23320	0.98	6.0E-74	4758 35 NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S_cerevisiae Chl-1-like helicase)	
5052	14234	23321	0.88	6.0E-74	4758 35 NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S_cerevisiae Chl-1-like helicase)	
5377	14608	23716	3.17	6.0E-74	11056013 NT	Homo sapiens actin filament associated protein (AFAP), mRNA	
915	10150	18310	2.7	5.0E-74 AW020986.1	EST_HUMAN	d117c09_y1 Martor Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'	
2663	11844		8.98	5.0E-74 AV382758.1	EST_HUMAN	PM0-CT0289-271099-001-H07 CT0289 Homo sapiens cDNA clone L (PIGL), mRNA	
5399	14827	23741	2.11	5.0E-74	11425417 NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA	
5558	14783	24168	12.05	5.0E-74 X89670.1	NT	H.sapiens mRNA for TPCR16 protein	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5567	14811	24185	7.5	5.0E-74	4507886	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
5620	14843	24221	1.93	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
5620	14843	24222	1.83	5.0E-74	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6038	15246	24668	3.76	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8476	19873	25144	3.84	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7521	16538	28028	2.02	5.0E-74	Y09420.1	NT	H_sapiens mRNA for HIF-1
7521	16538	28027	2.02	5.0E-74	Y09420.1	NT	H_sapiens mRNA for HIF-1
284	9558	18692	3.08	4.0E-74	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8812	10098	19260	4.6	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1832	11136	20331	2.56	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1832	11136	20332	2.56	4.0E-74	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
2040	11241	20449	8.89	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2040	11241	20450	8.89	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2102	11302	20516	1.2	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
3056	12292	21418	4.63	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene
3501	12725	21881	1.5	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4040	13250	22351	0.92	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4554	13749	22848	2.01	4.0E-74	7682133	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4816	13810	22801	0.75	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
6640	15835	2131	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37	
865	10198	18353	156.49	2.0E-74	7683491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
865	10198	18354	156.49	2.0E-74	7683491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1183	10404	16558	1.38	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T4/TD
1251	10467	18631	2.13	2.0E-74	AI950528.1	EST_HUMAN	wx51607_x1 NC_ CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SWGG95_HUMAN Q08379 GOLGIN-35; contains element MER22 repetitive element;
1576	10788	19963	1.77	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1575	10788	19964	1.77	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2562	11748	20988	11.6	2.0E-74	AI657280.1	EST_HUMAN	PT2.1_15_G11_r tumor2 Homo sapiens cDNA 3'
5030	14215	23289	2.54	2.0E-74	AI355092.1	NT	Novel human gene mapping to chromosome 22

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Table 4
Single Exon Probes Expressed in HEIA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5030	14215	23300	2.54	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5034	14219	23304	5.01	2.0E-74	J02963.1	NT	Human platelet glycoprotein IIb mRNA, 3' end
5571	18058	24169	1.84	2.0E-74	BE711134.1	EST_HUMAN	RC6-HT0878-220500-01-C03 HT0878 Homo sapiens cDNA
5613	18059	24212	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5613	18059	24213	2.23	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5638	18059	24212	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5638	18059	24213	2.91	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6871	16083	25581	11.56	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8664	17641		2.32	1	2.0E-74 AA198181.1	EST_HUMAN	ZP0830651 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:622018 3'
9223	18002	23868	1.34	2.0E-74	BF668568.1	EST_HUMAN	602121428F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278559 5'
55	8352	18468	1.67	1.0E-74	7657334	NT	Homo sapiens Missheaped NIK-related kinase (MINK), mRNA
3412	9810	18737	3.64	1.0E-74	AV816405.1	EST_HUMAN	QV4-ST0234-181199-03/-05 ST0234 Homo sapiens cDNA
506	9758	18885	0.96	1.0E-74	8822829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
513	9764	18890	17.5	1.0E-74	X0234.1	NT	Homo sapiens beta 2 gene
608	9855	18974	2.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 258 (ZNF258) mRNA
1007	10238	19380	1.74	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2183	11390	20613	4.9	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2X _M complete cds
3104	12339	21467	2.47	1.0E-74	4758897	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3945	13161	22277	6	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5228	14400	23483	1.28	1.0E-74	8858954	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
5228	14400	23484	1.29	1.0E-74	8858954	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
6719	15914	25374	2.79	1.0E-74	AF214562.1	NT	Homo sapiens trocheal epithelium enriched protein (PLUNC) gene, complete cds
8286	17401	26930	2.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8370	17457		4.1	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
8519	11390	20613	1.42	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2X _M , complete cds
9020	17872		1.62	1.0E-74	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2607	11791		3.57	8.0E-75	AF178228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
8688	17655		1.83	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C02
2287	11482	20703	3.62	6.0E-75	A1817415.1	EST_HUMAN	wk8688-x1 NCI_CGAP_P-22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); It31c12-x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242380 3' similar to TR:P7361 P97381
7144	16321	25802	4.05	5.0E-75	A16388623.1	EST_HUMAN	HYPOTHETICAL 20_1_KD PROTEIN
112	9400	16529	4.44	4.0E-75	BE081333.1	EST_HUMAN	QV1-BT08522-10200-019-002 BT0832 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
465	9718		0.83	4.0E-75	N38757.1	EST_HUMAN	y930t08_11 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:2690655' 5'	
1738	10848	20131	1.15	4.0E-75	AW887230.1	EST_HUMAN	CMD-NN0057-150400-335-e11 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'	
2801	12041	21182	5.28	4.0E-75	BE409464.1	EST_HUMAN	601303866f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'	
3474	12698	21834	1.02	4.0E-75	8922637 NT	Homo sapiens hypothetical protein FLJ10747 (FLJ10747). mRNA	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 ('10KD) (EIF3S8), mRNA	
5776	14894	24394	5.68	4.0E-75	55793457 NT	Homo sapiens NIPSNAP_C, elegans	Homo sapiens NIPSNAP_C, elegans, homolog 1 (NIPSNAP1), mRNA	
5983	15195	24612	2.08	4.0E-75	11417848 NT	Homo sapiens NIPSNAP_C, elegans	Homo sapiens NIPSNAP_C, elegans, homolog 1 (NIPSNAP1), mRNA	
5983	15195	24613	2.08	4.0E-75	11417848 NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA	
7277	18498	25988	8.7	4.0E-75	7868505 NT	Homo sapiens synaptosomal-associated protein 28kD (SNAP29), mRNA	Homo sapiens synaptosomal-associated protein, 28kD (SNAP29), mRNA	
8241	17370	26908	1.67	4.0E-75	AF039699.1	NT	Homo sapiens antigen NY-CO-37 (NY-CO-38) mRNA, complete cds	
1010	10241	18383	3.38	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds	
1011	10241	18383	2.18	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds	
1804	11013	20206	2.02	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds	
2082	11282	20498	28.14	3.0E-75	4507334 NT	Homo sapiens synaptotinin 1 (SYNJ1), mRNA	Homo sapiens synaptosomal-associated protein, 28kD (SNAP29), mRNA	
2387	11580	20797	5.08	3.0E-75	4759153 NT	Hom sapiens synaptosomal-associated protein, 28kD (SNAP29), mRNA	Hom sapiens synaptosomal-associated protein, 28kD (SNAP29), mRNA	
2986	12223	21358	0.91	3.0E-75	AL163201.2	NT	Hom sapiens chromosome 21 segment HS21C001	Hom sapiens chromosome 21 segment HS21C001
3152	12387	21519	1.02	3.0E-75	AB011153.1	NT	Hom sapiens mRNA for KIAA0581 protein, partial cds	Hom sapiens mRNA for KIAA0581 protein, partial cds
3324	12553	21688	1.08	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds
3324	12553	21689	1.08	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds
3720	12940	22057	0.89	3.0E-75	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds	Human calcium-dependent phospholipid-binding protein (PLA2), mRNA, complete cds
4150	13356	22459	3.01	3.0E-75	D87875.1	NT	Hom sapiens DNA for amyloid precursor protein, complete cds	Hom sapiens DNA for amyloid precursor protein, complete cds
4429	13629	22723	0.77	3.0E-75	7882421 NT	Hom sapiens KIAA0971 protein (KIAA0971), mRNA	Hom sapiens KIAA0971 protein (KIAA0971), mRNA	
5215	14390		0.98	3.0E-75	AL163209.2	NT	Hom sapiens chromosome 21 segment HS21C009	Hom sapiens chromosome 21 segment HS21C009
5986	15288	24694	1.62	3.0E-75	11526319 NT	Hom sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Hom sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	
5986	15288	24695	1.62	3.0E-75	11526319 NT	Hom sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	Hom sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA	
6134	15318	24751	4.68	3.0E-75	7682209 NT	Hom sapiens KIAA0623 gene product (KIAA0623), mRNA	Hom sapiens KIAA0623 gene product (KIAA0623), mRNA	
6134	15318	24752	4.66	3.0E-75	7682209 NT	Hom sapiens KIAA0623 gene product (KIAA0623), mRNA	Hom sapiens KIAA0623 gene product (KIAA0623), mRNA	
6344	15525	24972	2.76	3.0E-75	4885632 NT	Hom sapiens Oncogene TIM (TIM) mRNA	Hom sapiens Oncogene TIM (TIM) mRNA	
6344	15525	24973	2.76	3.0E-75	4885632 NT	Hom sapiens Oncogene TIM (TIM) mRNA	Hom sapiens Oncogene TIM (TIM) mRNA	
2267	11462	20682	11.09	1.0E-75	AW168135.1	EST_HUMAN	xg60d02_x1_NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2682707 3' similar to contains PTR7.1	
2897	12135	21272	3.26	1.0E-75	X52221.1	NT	PTR7 repetitive element;	
4698	13889	22989	1.48	1.0E-75	BE279301.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)	
							601157633f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6605	15801			7.18	1.0E-75 AA398270.1	EST_HUMAN	z57n03_s1 Scores_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13832 40S RIBOSOMAL PROTEIN S17 (HUMAN);
6887	16078	25547		5.15	1.0E-75 BF313645.1	EST_HUMAN	601900284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
6887	16078	25548		5.15	1.0E-75 BF313645.1	EST_HUMAN	601900284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
7460	16668			5.8	1.0E-75 AA64377.1	EST_HUMAN	ac77b08_s1 Strategene lung (#37210) Homo sapiens cDNA clone IMAGE:8686598 3'
7658	16858	28359		4.08	1.0E-75 AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8574	14503	23588		2.38	1.0E-75 BE834192.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
48	9343	18452		2.68	9.0E-76 AI652648.1	EST_HUMAN	wb30b10_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
48	9343	18453		2.68	9.0E-76 AI652648.1	EST_HUMAN	wb30b10_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1;
7041	16218	25683		55.5	9.0E-76 M12837.1	NT	Human ferritin Heavy subunit mRNA, complete cds
145	9427	18581		7.27	8.0E-76 AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
946	10179	19334		5.48	8.0E-76	4504374	Homo sapiens H factor 1 complement (HF1) mRNA
946	10179	19335		5.48	8.0E-76	4504374	Homo sapiens H factor 1 (complement) (HF1) mRNA
2862	12100	21231		1.47	8.0E-76	7708724	Human selenocysteine tRNA
5739	14958	24358		5.1	8.0E-76	11421442	Homo sapiens LIM domain kinase 1 (LIMK1) mRNA
7259	16479	25971		8.45	8.0E-76	10442821	Homo sapiens birc6lal IAP repeat-containing 6 (BIRC6) mRNA
8934	17815			1.97	8.0E-76	11417882	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
9030	18233	23702		1.41	8.0E-76 AI365515.1	NT	Novel human gene mapping to chromosome 22
785	10024	19174		1.91	7.0E-76	5016082	NT
3283	12488	21626		3.4	7.0E-76 AF056480.1	NT	Homo sapiens dihydrodipamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3289	12502	21633		8.15	7.0E-76	4505032	NT
4365	13567	22662		8.55	7.0E-76	4507184	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4365	13567	22663		6.55	7.0E-76	4507184	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1241	10457			8.89	8.0E-76 BE398253.1	EST_HUMAN	601312018F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36538157 5'
8001	16438	25923		3.25	8.0E-76 BE2273201.1	EST_HUMAN	601142283F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505029 5'
1912	11117	20312		11.44	5.0E-76 D63874.1	NT	Human mRNA for HMG-1, complete cds
1912	11117	20313		11.44	5.0E-76 D63874.1	NT	Human mRNA for HMG-1, complete cds
1912	11117	20314		11.44	5.0E-76 D63874.1	NT	Human mRNA for HMG-1, complete cds
3173	12408	21543		0.7	4.0E-76 BE814086.1	EST_HUMAN	QV3-BN0047-270700-283-g08 BN0047 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor		
7082	18259	25734	3.98	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFUjiwara) Homo sapiens cDNA clone GEN:178G01_5'		
7082	18259	25735	3.98	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (TFUjiwara) Homo sapiens cDNA clone GEN:178G01_5'		
63	9880	18003	1.54	3.0E-76	BF516262.1	EST_HUMAN	U1-H-BW1-5n2-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862_3'		
83	9880	18004	1.54	3.0E-76	BF516262.1	EST_HUMAN	U1-H-BW1-5n2-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862_3'		
1578	10792	198188	10.98	3.0E-76	450347.6	NT	Homo sapiens sukar potic translation elongation factor 1 beta 2 (EEF1B2) mRNA		
1579	10792	19969	10.99	3.0E-76	450347.6	NT	Homo sapiens sukar potic translation elongation factor 1 beta 2 (EEF1B2) mRNA		
3407	12633	21763	5.18	3.0E-76	BF3176689.1	EST_HUMAN	RC5-ST0300-180100-03-A03 ST0300 Homo sapiens cDNA		
3407	12633	21764	6.18	3.0E-76	BF3176689.1	EST_HUMAN	RC5-ST0300-180100-03-A03 ST0300 Homo sapiens cDNA		
5284	14483	28928	2.14	3.0E-76	Z41314.1	EST_HUMAN	HSC2QD042 normalized infant brain cDNA Homo sapiens cDNA clone c-zq04_3'		
5820	15037	24438	8.16	3.0E-76	AF288598.1	NT	Homo sapiens angiotatin binding protein 1 mRNA, complete cds		
6998	16174	25645	2.8	3.0E-76	AW289535.1	EST_HUMAN	xs4gho1.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009_3'		
8276	18148	23752	1.8	3.0E-76	AW987984.1	EST_HUMAN	EST36059 MAGE resequences. MAG1 Homo sapiens cDNA		
8382	18365	23592	4.03	3.0E-76	AW956455.1	EST_HUMAN	EST368525 MAGE resequences. MAG2 Homo sapiens cDNA		
286	9560	18694	1.1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds		
347	9815	18741	2.83	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds		
347	9815	18742	2.93	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds		
48	9720	1.48	2.0E-76	4557882	NT	Human sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA			
597	9844	18963	1.03	2.0E-76	4503944	NT	Human sapiens glucagon (GCG) mRNA		
1038	10284	18417	0.71	2.0E-76	4758053	NT	Human sapiens cAMP responsive element binding protein 1 (CREB1) mRNA		
1522	10736	19903	2.17	2.0E-76	4504028	NT	Human sapiens GM2 ganglioside activator protein (GM2A) mRNA		
1522	10736	18909	2.17	2.0E-76	4504028	NT	Human sapiens GM2 ganglioside activator protein (GM2A) mRNA		
1897	11104	20286	1.05	2.0E-76	AA253954.1	EST_HUMAN	zss60h11.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925_3'		
2794	12034	21158	3.2	2.0E-76	P23286	SWISSPROT	OLFACTOORY RECEPTOR-LIKE PROTEIN F5		
3266	12489	21630	1.85	2.0E-76	AA445992.1	EST_HUMAN	zw64e2.s1 Soares_tesis_NHT Homo sapiens cDNA clone IMAGE:780986_3' similar to SW:ITBS_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.		
3266	12489	21631	1.85	2.0E-76	AA445982.1	EST_HUMAN	zw64e2.s1 Soares_tesis_NHT Homo sapiens cDNA clone IMAGE:780986_3' similar to SW:ITBS_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR.		
4117	9560	18694	0.61	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds		
4495	13693	22787	1.14	2.0E-76	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5) mRNA		
4986	14153	23245	8.42	2.0E-76	AV817661.1	EST_HUMAN	CV3-Q0028-222303-132-511 OT0328 Homo sapiens cDNA		
5155	14334	23424	1.04	2.0E-76	5031560	NT	Homo sapiens EGFR-like repeats and discoidin I-like domains 3 (EDIL3) mRNA		
5550	14726	24086	5.67	2.0E-76	AB028604.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds		
7162	16339	25819	4.12	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63150), mRNA		
7495	16702	26187	2.68	2.0E-76	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA		

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4285	13488	22587	4.6	1.0E-76	D63974.1	NT	Human mRNA for HM/G-1, complete cds
4286	13488	22588	4.8	1.0E-76	D63974.1	NT	Human mRNA for HM/G-1, complete cds
5418	14646	23779	5.46	1.0E-76	BE798537.1	EST_HUMAN	601588986F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6053	15221	24840	4.38	9.0E-77	BE889525.1	EST_HUMAN	6015124336F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
8098	17814		1.36	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638753 5'
192	9471	18602	2.94	8.0E-77	R83144.1	EST_HUMAN	Yp11R02.1 Scores breast 3Nb4B1 Homo sapiens cDNA clone IMAGE:187155 5' similar to SP_ANKB_HUMAN Q01484 ANKYRIN BRAIN VARIANT 1
4522	13718	22813	1.3	8.0E-77	BF205181.1	EST_HUMAN	601886928F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5420	14648	23782	2.57	8.0E-77	4506230	NT	Hom sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
7925	17138	28669	2.71	8.0E-77	AA019770.1	EST_HUMAN	z662602.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
7925	17138	28670	2.71	8.0E-77	AA019770.1	EST_HUMAN	z662602.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
9078	17801	23801	8.5	8.0E-77	R00246.1	EST_HUMAN	y669f4.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element;
1898	11105	20297	2.31	7.0E-77	AA625755.1	EST_HUMAN	z481901.1 Scores basis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2374	11567	20788	12.68	7.0E-77	4505944	NT	Hom sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2374	11567	20789	12.68	7.0E-77	4505944	NT	Hom sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
267	9542	18872	8.02	8.0E-77	4504800	NT	Hom sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1150	10373	19524	0.7	8.0E-77	AW057753.1	EST_HUMAN	EST369823 MAGE sequences, MAGE Homo sapiens cDNA
1529	10743	18916	2.44	6.0E-77	A1204066.1	EST_HUMAN	q977h12.1 Scores fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
4949	14138	23229	0.72	6.0E-77	4557752	NT	Hom sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
4949	14136	23230	0.72	6.0E-77	4557752	NT	Hom sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
147	9429	18563	2.64	5.0E-77	AF154830.1	NT	Hom sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
147	9429	18564	2.64	5.0E-77	AF154830.1	NT	Hom sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
1243	10459	19818	1.8	5.0E-77	AF041016.1	NT	7 Homo sapiens glutathione S-transferase GCK1 gene, exon 2
1368	10582	19749	2.11	5.0E-77	4557250	NT	Hom sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2845	11828	21043	1.62	5.0E-77	AF162668.1	NT	Hom sapiens taurine-like kinase 1 (TLK1) mRNA, complete cds
2719	11838	21114	1.44	5.0E-77	4503160	NT	Hom sapiens cullin 1 (CUL1) mRNA
3495	12719	21856	1.39	5.0E-77	8394518	NT	Hom sapiens ubiquitin specific protease 18 (USP18) mRNA
4714	13905	23005	1.88	5.0E-77	5031680	NT	Hom sapiens EGFR-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4714	13905	23006	1.88	5.0E-77	5031680	NT	Hom sapiens EGFR-like repeats and discoidin-like domains 3 (EDIL3) mRNA
4958	14143	23236	2.29	5.0E-77	AL043953.1	EST_HUMAN	DKFZp43G1728_11_434 (synonym: Ites2) Homo sapiens cDNA clone DKFZp43G1728 5'
6220	15401	24842	10.02	5.0E-77	X98298.1	NT	H.sapiens mRNA for ubiquitin hydrolase
6947	16105	25571	4.08	5.0E-77	11421928	NT	Hom sapiens sorting nexin 5 (SNX5) mRNA

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6947	16105	26572	4.08	5.0E-77	11421628	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
3682	12803	22023	0.99	4.0E-77	AL449758	EST_HUMAN	AL449758 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
1842	11148	20345	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SE(MAR)) mRNA
1842	11148	20346	1.54	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SE(MAR)) mRNA
7462	16880	26149	4.66	3.0E-77	BF369917	EST_HUMAN	PM3-MT0078-08080-005-903 MT0078 Homo sapiens cDNA
1380	10575	18740	1.54	2.0E-77	AV784617	EST_HUMAN	AV784617 MDS Homo sapiens cDNA clone MDSBTTF10'5'
1435	10649	19823	8.06	2.0E-77	AV897712	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2060	11281	20475	1.8	2.0E-77	L41825	1	NT
2073	11273	20488	2.88	2.0E-77	7708315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2554	12019	20958	1.51	2.0E-77	AB037836	1	NT
2554	12019	20959	1.51	2.0E-77	AB037838	1	NT
4010	13222	22323	1.48	2.0E-77	BE044316	EST_HUMAN	hox3b05x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN;
4596	13790		1.9	2.0E-77	4504088	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (esparte aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4779	13968	23070	6.81	2.0E-77	AA653025	1	ns88g12.1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188838 similar to SW:RL29_HUMAN
5633	14881	24246	1.99	2.0E-77	BE298940	1	P47814_60S RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element;
5740	14959	24359	1.66	2.0E-77	BE787143	1	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:30294305'
6153	15337	24774	15.25	2.0E-77	AB833003	1	601476802F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38785056'
6928	16119	25588	4.1	2.0E-77	U50321	1	at74a09_x1 Barsteed colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720' similar to TR:Q13311
6928	16119	26587	4.1	2.0E-77	U50321	1	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
45	9341	16449	1	1.0E-77	AB033102	1	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
45	8341	18449	1	1.0E-77	AB033102	1	Hom sapiens mRNA for KIAA1276 protein, partial cds
27	9552	18683	3.78	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II Alzheimer disease) (APP), mRNA
27	9552	18684	3.78	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II Alzheimer disease) (APP), mRNA
885	11980	19284	6.39	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II Alzheimer disease) (APP), mRNA
886	11980	19285	6.39	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II Alzheimer disease) (APP), mRNA

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1895	11092	20283	1.21	1.0E-77	AW058119.1	EST_HUMAN	wv83e05_x1 Soenes_thymus_NHFT1 Homo sapiens cDNA clone IMAGE:25336160 3'
2407	11599	20820	2.84	1.0E-77	AE0296024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3010	12246	21375	2.85	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4346	13548	22640	3.77	1.0E-77	7706299	NT	Homo sapiens CGI-40 protein (LOC51826), mRNA
4523	13719	22814	20.84	1.0E-77	AJ228041.1	NT	Homo sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4852	13846	22837	2.38	1.0E-77	65562322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4702	13893	22892	1.01	1.0E-77	AJ273014.1	EST_HUMAN	qM0gg04_x1 NC1 CGAP_Kid8_Homo sapiens cDNA clone IMAGE:1981110 3'
4900	14088	23181	1.31	1.0E-77	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
5101	14281	23365	2.43	1.0E-77	76811849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5101	14281	23366	2.43	1.0E-77	76811849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5627	14851	24233	1.91	1.0E-77	AF086844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5627	14851	24234	1.91	1.0E-77	AF086844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5848	15065	24475	1.68	1.0E-77	4885192	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
6105	15199	24617	12.1	1.0E-77	58811412	NT	Homo sapiens elastin (supraventricular aortic stenosis, Williams-Bauren syndrome) (ELN), mRNA
5847	15064	24473	2.45	8.0E-78	AW947061.1	EST_HUMAN	RC22-ET0023-080500-012-805 ET0023 Homo sapiens cDNA
5847	15064	24474	2.45	8.0E-78	AW947061.1	EST_HUMAN	RC22-ET0023-080500-012-805 ET0023 Homo sapiens cDNA
85	9378	18508	1.94	8.0E-78	AU118789	EST_HUMAN	AU118789_HEMBA1 Homo sapiens cDNA clone HEMBA1004334 5'
85	9378	18509	1.94	8.0E-78	AU118789	EST_HUMAN	AU118789_HEMBA1 Homo sapiens cDNA clone HEMBA1004334 5'
3286	12517	21648	1.45	8.0E-78	BF344101.1	EST_HUMAN	6020169226F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152511 5'
5905	15122	21649	2.51	8.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRα1), mRNA
222	9501	18632	1.24	5.0E-78	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2528	11716	20933	8.37	5.0E-78	AW673424.1	EST_HUMAN	ba54h03_x3 NIH_MGCC_10 Homo sapiens cDNA clone IMAGE:28000405 5' similar to WPY49B6A 6 CE22121
3363	12591	21731	4.41	5.0E-78	M55586.1	NT	Human collagenase type IV (CLG4) gene, exon 6
5401	14629	23142	2.51	5.0E-78	AF038536.1	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
5478	14705	24059	10.31	5.0E-78	11416535	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFBI), mRNA
6143	15327	24763	2.23	5.0E-78	AW953120.1	EST_HUMAN	EST365190 MAGE resequences, MAGB_Homo sapiens cDNA
6797	15892	25450	8.12	5.0E-78	U508889.1	NT	Human lysosomal alpha-L-mannosidase (manB) gene, exon 7
6798	15893	25451	5.58	5.0E-78	BE860836.1	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931987 5'
1145	10368	19518	1.2	4.0E-78	AJ043314.2	EST_HUMAN	DKFZp64N0323_71 434 (synonym Hs33) Homo sapiens cDNA clone DKFZp64N0323 5'
1506	10719	19891	1.38	4.0E-78	AJ355684.1	NT	Novel human gene mapping to chromosome 22
2284	11479	20701	19.91	4.0E-78	AF07405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4313	13514	22607	1.61	4.0E-78	7686878	NT	Homo sapiens syncytin (LOC30816), mRNA
7194	16371	25851	2.19	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA

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Table 4
Single Exon Probes Expressed in HEA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7194	16371	25852	2.19	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	
7346	18562	26051	1.92	4.0E-78	11428610	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA	
7857	17096	26828	2.18	4.0E-78	AF168148.1	NT	Homo sapiens s-CaBP1 (CaBP1), mRNA, complete cds	
8092	17226	28763	3.42	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)	
8861	17833	23910	3.24	4.0E-78	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds	
164	9446	18576	2.52	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds	
164	9446	18577	2.52	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds	
2268	11463	20683	2.07	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3), mRNA	
2380	11573	20792	1.23	3.0E-78	7708705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA	
3748	12986			3.0E-78	AU14064	PLACE3 Homo sapiens cDNA clone PLACE3000373 5'		
3805	13023	22134	1.62	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'	
4082	13023	22134	0.77	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA	
5082	14282	23347	0.69	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA	
7168	16343			1.05	AF098810.1	NT	Homo sapiens neuregulin III/alpha gene, partial cds	
7554	16759	26253	6.59	3.0E-78	BE144758.1	EST_HUMAN	CMD-HT180-04/109-05-07 HT0180 Homo sapiens cDNA	
3085	12321			6.1	3.0E-78	BE156318.1	EST_HUMAN	QVO-HT10367-150/200-114-909 HT0367 Homo sapiens cDNA
3980	13204			5.97	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
6389	15559	25028	2.23	2.0E-78	AA1311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end	
6478	15675	25148	3.78	2.0E-78	BF889800.1	EST_HUMAN	602188529F-1 NIH_3T3 clone IMAGE4288599 5'	
6615	15811	25267	2.79	2.0E-78	AV1714177.1	EST_HUMAN	AV1714177 DCB Homo sapiens cDNA clone DCBAWF08 5'	
6615	15811	25268	2.8	2.0E-78	AJ57509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'	
7648	16846	26344	3.63	2.0E-78	AJ1197837.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'	
7684	16883	26391	6.13	2.0E-78	N68951.1	EST_HUMAN	q150h05.1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE1889861 3' similar to WP-R90.1	
5229	14403	23486	1.73	1.0E-78	4756843	NT	CE06325 PROTEIN_KINASE ;	
6333	14564	23638	3.18	1.0E-78	11417304	NT	Hom sapiens nucleoparin 155kD (NUP155) mRNA	
8452	17510	24019	1.3	1.0E-78	11430460	NT	Hom sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
8556	17578	23986	1.28	1.0E-78	11435903	NT	Hom sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA	
8920	18203	23692	1.72	1.0E-78	AJ650919.1	EST_HUMAN	wz20508_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE2288615 3'	
4709	13800	22999	4.24	8.0E-79	11525891	NT	Hom sapiens peptide YY (PYY), mRNA	
4880	14068	23164	3.22	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN074-090300-014-c12 BN0074 Homo sapiens cDNA	
5408	14536	23764	15.25	9.0E-79	AB0228070.1	NT	Hom sapiens mRNA for activator of S phase kinase, complete cds	

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon ORF SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5807	15024	24424	2.48	9.0E-79	54541451	NT	Homo sapiens ubiquitin-conjugating enzyme E2E_3 (homologous to yeast UBC4/5) (UBC4/5) mRNA
6792	15987	25447	4.89	9.0E-79	J02853.1	NT	Homo sapiens cassein kinase II alpha subunit mRNA, complete cds
6792	15987	25448	4.89	9.0E-79	J02853.1	NT	Homo sapiens cassein kinase II alpha subunit mRNA, complete cds
7635	16836	26332	1.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta mRNA, complete cds
8045	17181	28720	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA
8045	17181	28721	3.28	9.0E-79	11423827	NT	Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA
8093	17227	28764	3.83	9.0E-79	11417260	NT	Homo sapiens tRNA synthetase (TARS) mRNA
8093	17227	28765	3.83	9.0E-79	11417260	NT	Homo sapiens tRNA synthetase (TARS) mRNA
9170	17865	23985	1.48	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3723	12843	22010	0.82	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010 mRNA
4492	13690	22782	1.36	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4492	13690	22783	1.36	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
3219	12453	21586	20.38	7.0E-79	BEI19848.1	EST_HUMAN	60147276871 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:38756583' similar to z94ed4_s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4625588 3' similar to TR-Q1540B Q1540B NEUTRAL PROTEASE LARGE SUBUNIT
8301	17408		5.63	6.0E-79	AA399829.1	EST_HUMAN	TR-Q1540B Q1540B NEUTRAL PROTEASE LARGE SUBUNIT
8029	17186	28704	4.48	5.0E-79	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082 mRNA
3141	12376		1.06	4.0E-79	8922325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283) mRNA
3118	9559	18720	1.21	3.0E-79	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
985	10216	18372	3.68	3.0E-79	AF232708.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, partial cds
3064	12300	21424	2.34	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, complete cds
5149	14328	23417	0.78	3.0E-79	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
5149	14328	23418	0.78	3.0E-79	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
6374	14803	23712	4.61	3.0E-79	AF110322.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
5544	14768	24134	1.75	3.0E-79	AB020689.1	NT	Homo sapiens mRNA for KIAA00822 protein, partial cds
5560	14783	24152	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1) mRNA
5560	14783	24153	3.47	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1) mRNA
6108	15202	24619	3.01	3.0E-79	A8014620.1	NT	Homo sapiens mRNA for KIAA00620 protein, partial cds
6108	15202	24620	3.01	3.0E-79	A8014620.1	NT	Homo sapiens netrin 1 (NTN1) mRNA
7437	16846	26138	1.89	3.0E-79	A1249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
7437	16846	26139	1.89	3.0E-79	A1249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
292	9566		0.81	2.0E-79	H63128.1	EST_HUMAN	y48f03_s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:3511107 5'
640	9886	18011	1.14	2.0E-79	BE379928.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
936	10169	19326	1.04	2.0E-79	4757841	NT	Human sapiens BCL2-like_2 (BCL2L2) mRNA

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1042	10268			1.66	2.0E-79 AI523747.1	EST_HUMAN	Itt18h07.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2118685 3'
2116	11315	20531		5.52	2.0E-79 45365863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2116	11315	20532		5.52	2.0E-79 45365863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2159	11357	20575		3.99	2.0E-79 AI271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2279	11474	20687		3.2	2.0E-79 AI244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4051	13261	22364		1.07	2.0E-79 AI341536.1	EST_HUMAN	EST46988 Fetal kidney II Homo sapiens cDNA 5' end
4147	13353	22455		1.24	2.0E-79 AI271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4697	13888	22988		0.89	2.0E-79 AI163206.2	NT	Homo sapiens chromosome 21 segment HS21/C06
6149	15333	24770		2.41	2.0E-79 7362479	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP6), transcript variant 4, mRNA
6149	15333	24771		2.41	2.0E-79 7362479	NT	Homo sapiens Rho GTPase activating protein 8 (ARHGAP6), transcript variant 4, mRNA
6627	15823	25285		3.2	2.0E-79 11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
7598	18801	26293		4.84	2.0E-79 BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
7598	18801	26294		4.84	2.0E-79 BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
8339	14501	23586		2.95	2.0E-79 7682357	NT	Homo sapiens KIAA0379 protein (KIAA0379), mRNA
8425	17494	24011		4.83	2.0E-79 AI3020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
8868	17844	23976		3.11	2.0E-79 11418322	NT	Homo sapiens cadherin EGFLAG seven-pass G-type receptor 1 (CELSR1), mRNA
5925	18068			3.21	1.0E-79 BI363071.1	EST_HUMAN	MRO-NN0087-260600-Q17-b10 NN0087 Homo sapiens cDNA
8143	17275	26819		4.11	1.0E-79 BF087405.1	EST_HUMAN	QY2-HT0540-120500-358-a05 HT0540 Homo sapiens cDNA
8454	18289			1.35	1.0E-79 AI460115.1	EST_HUMAN	ar78ad4-x1 Barsdeed colon HPLR87 Homo sapiens cDNA clone IMAGE:2151438 3'
3111	12348	21473		15.25	9.0E-80 AI2725848.1	EST_HUMAN	ai23605_s1 Scores_tests_NHT Homo sapiens cDNA clone 1343648 3'
3111	12348	21474		15.25	9.0E-80 AI2725848.1	EST_HUMAN	ai23605_s1 Scores_tests_NHT Homo sapiens cDNA clone 1343648 3'
7615	16818			1.86	9.0E-80 AI498666.1	EST_HUMAN	tm47d08.x1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:2161283 3'
7825	17017	26532		12.17	9.0E-80 11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
7825	17017	26533		12.17	9.0E-80 11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 (SLC7A8), mRNA
3590	12802			4.51	8.0E-90 U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
6337	15517	24984		2.95	8.0E-90 11422687	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
6337	15517	24985		2.95	8.0E-90 11422687	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
4974	14161	23252		0.82	7.0E-90 HQ4618.1	EST_HUMAN	y49d02_x1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:152067 5'
910	10145	19306		2.29	9.0E-90 AI422197.1	EST_HUMAN	ff58d02_x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SWNUEM_HUMAN
							Q16785 NADH-LUBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1620	10833	20008	3.71	6.0E-80	U54898.1	NT	Homo sapiens NRD convertase mRNA, complete cds
2281	11456	20673	6.76	6.0E-80	6631034	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
2281	11456	20674	6.76	6.0E-80	6631034	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4270	13473	22968	2.1	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
4270	13473	22969	2.1	6.0E-80	AB032881.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6701	14920	24314	3.22	6.0E-80	A1404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
5784	14983	24382	3.97	6.0E-80	11436736	NT	Homo sapiens tubby-like protein 3 (TULP3), mRNA
7515	16720	26210	2.93	6.0E-80	11427386	NT	Homo sapiens briefdin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
7777	16872	26485	21.54	6.0E-80	AF-226730.1	NT	Homo sapiens Cyt19 mRNA, complete cds
8232	17361	28899	2.16	6.0E-80	AF-102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
8308	10145	19308	1.48	6.0E-80	A1422197.1	EST_HUMAN	tt58d02_x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
8436	18173		2.28	6.0E-80	AF-240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8648	17631		6.14	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for carboxylside sulfotransferase, exon 1, 2, 3, 4, 5
9166	18307		1.69	6.0E-80	AJ-133427.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
595	98442	189862	2.27	6.0E-80	4506228	NT	Homo sapiens protease (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3), mRNA
845	100882	19241	1.45	5.0E-80	AF-08830.1	NT	Homo sapiens serine-threonine protein kinase (MNHK) mRNA, complete cds
845	100882	19242	1.45	5.0E-80	AF-08830.1	NT	Homo sapiens serine-threonine protein kinase (MNHK) mRNA, complete cds
1197	10417		5.59	5.0E-80	X91647.1	NT	H. sapiens ncxt1 gene (exon 12)
1455	10868		2.61	5.0E-80	AL-163283.2	NT	Homo sapiens chromosome 21 segment HS21C033
2329	11522	20744	1	5.0E-80	U89358.1	NT	Human [3]mbt1 protein homolog mRNA, complete cds
2394	11587	20805	7.09	5.0E-80	AB037955.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2747	11928	21140	2.06	5.0E-80	4504222	NT	Homo sapiens H3 histone family, member J (H3F1) mRNA
4016	13228	22330	1.98	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4016	13228	22331	1.98	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4973	14160	23351	1.16	5.0E-80	AL-163268.2	NT	Homo sapiens chromosome 21 segment HS21C038
5237	14411	23491	2.78	5.0E-80	AL-163285.2	NT	Homo sapiens chromosome 21 segment HS21C035
6841	16046	25511	8.8	4.0E-80	F25915.1	EST_HUMAN	HSFD13155 HM3 Homo sapiens cDNA clone s400045F03
221	9500		17.47	3.0E-80	AL-163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4719	13910	23012	1.02	3.0E-80	BF085609.1	EST_HUMAN	PMG-GN0018-040900-002-E03 GN0018 Homo sapiens cDNA
4928	14117		12.26	3.0E-80	BE817465.1	EST_HUMAN	QVA-BR0263-040600-241-g10 BN0263 Homo sapiens cDNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{top}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5579	14803	24178	2	3.0E-80	AI091675.1	EST_HUMAN	co23612_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 5' similar to TR:O35780 O35780 PiGL-;
1767	10977	20168	6.28	2.0E-80	R35321.1	EST_HUMAN	Y665a08_x1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:380680 5'
1828	11038	20232	1.53	2.0E-80	AI44821.1	EST_HUMAN	RET4B subtracted retina cDNA library Homo sapiens cDNA clone RET4B7
2022	11223	20431	5.87	2.0E-80	AI043116.2	EST_HUMAN	DKFZp434D323_1 (synonym: hesc2) Homo sapiens cDNA clone DKFZp434D1323 5'
6818	16012	25478	2.2	2.0E-80	AV984270.1	EST_HUMAN	EST376342 MAGE resequences, MAGH Homo sapiens cDNA
7446	16654	26145	6.59	2.0E-80	AA393362.1	EST_HUMAN	#70112_x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315 G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN;
345	96131		2.45	1.0E-80	AI163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
809	10048	19189	1.37	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1824	11128		2.64	1.0E-80	AI732658.1	EST_HUMAN	nm011f12_x6 NCI_CGAP_Coe Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR_11 OFR repetitive element;
4456	13654	22748	1.38	1.0E-80	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4835	14024	23118	0.8	1.0E-80	NB9520.1	EST_HUMAN	Za39607_x1 Soares_fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:284972 5' similar to contains Ali repetitive element;
5350	14580		3.73	1.0E-80	BE386615.1	EST_HUMAN	60127405F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
5641	14865	24248	5.71	1.0E-80	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
6323	15504	24950	2.87	1.0E-80	AI948731.1	EST_HUMAN	wq25e05_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
6323	15504	24951	2.87	1.0E-80	AI948731.1	EST_HUMAN	wq25e05_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472298 3'
7245	16465	25955	2.04	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC641782) mRNA
7245	16465	25958	2.04	1.0E-80	11641278	NT	Homo sapiens similar to rat myomegalin (LOC641782) mRNA
8724	17676	23950	2.02	1.0E-80	11417801	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT) mRNA
7276	16485	25988	3.34	8.0E-81	AI251752.1	EST_HUMAN	qhg0g05_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
7276	16495	25987	3.34	8.0E-81	AI251752.1	EST_HUMAN	qhg0g05_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854296 3'
7713	16912	28420	6.83	8.0E-81	BE394525.1	EST_HUMAN	601310331F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							ZB21d10_x1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:3536335 5' similar to SW:KRHA_RABIT_Q02987 KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. [1] contains element MER22
2173	11370	20591	1.83	7.0E-81	AA011080.1	EST_HUMAN	repetitive element;
6188	15368	24808	2.88	7.0E-81	AI822115.1	EST_HUMAN	Za31G08_x5 Soares_fetal_lung_NbH19W Homo sapiens cDNA clone IMAGE:289818 3'
4381	13582	22683	5.13	6.0E-81	BE2536829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4381	13582	22684	5.13	6.0E-81	BE2536829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5316	14548	23617	1.74	6.0E-81	45011848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABC13), mRNA
5316	14548	23618	1.74	6.0E-81	45011848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABC13), mRNA
8867	17767	23937	1.88	6.0E-81	BF7879022.1	EST_HUMAN	602153868F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'

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Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{top}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8867 17767	23938		1.88	6.0E-81	BF679022.1	EST_HUMAN	602153666F_1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2183 11380	20804		4.15	5.0E-81	BE268042.1	EST_HUMAN	601125505F_1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8113 17247	26787		2.62	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
225 9504	18834		0.69	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
709 9951	18080		0.86	4.0E-81	A1521435.1	EST_HUMAN	th00e12_X1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85580 Q85580
3135 12370	21501		4.19	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
4142 13348	22447		2.53	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4142 13348	22448		2.53	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6554 15750	25211		2.36	4.0E-81	X06989.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
6638 15833	28294		3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6638 15833	28295		3.01	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
6835 16029	28494		3.59	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
7740 16936	28444		3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
7740 16936	28445		3.01	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8331 18239	23708		4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8331 18239	23707		4.54	4.0E-81	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8055 17887	23897		4.02	4.0E-81	11417874	NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1274 10489	19846		12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1274 10489	19847		12.21	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2339 11532	20755		11.44	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2948 12186	21318		6.63	3.0E-81	4506280	NT	Homo sapiens plakophilin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2948 12186	21319		6.63	3.0E-81	4506280	NT	Homo sapiens plakophilin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2786 12026	21152		2.43	2.0E-81	BE784636.1	EST_HUMAN	601474072F_1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2786 12028	21153		2.43	2.0E-81	BE784636.1	EST_HUMAN	601474072F_1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3175 12874	22090		0.83	2.0E-81	AV611542.1	EST_HUMAN	hg85c01_X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
4682 13874	22874		1.91	2.0E-81	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
9207 12974	22093		2.67	2.0E-81	AV611542.1	EST_HUMAN	hg85c01_X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2852384 3'
3632 12853	21972		1.31	1.0E-81	AV860658.1	EST_HUMAN	EST3172729 MAGE resequences, MAGF Homo sapiens cDNA
4516 13712	22805		2.89	1.0E-81	AA040370.1	EST_HUMAN	zK45h09.11 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to PIR:SS52437 SS2437 GDP-diacylglycerol synthase - fruit fly;
4646 13840	22830		7.9	1.0E-81	BE047896.1	EST_HUMAN	E45c04_Y1 NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291526 5'

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Table 4
Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5184	14343	23432	3.88	1.0E-81	9968844 NT		Human chromosome 12 open reading frame 3 (C12orf3), mRNA
5283	14482	26925	3.55	1.0E-81	U87828.1 NT		Human econazole hydrolase (ACO2) gene, exon 3
5367	14597	23674	3.93	1.0E-81	114329863 NT		Human sapiens polymerase (DNA directed), gamma (POLG), mRNA
5367	14597	23675	3.93	1.0E-81	114329865 NT		Human sapiens arm-repeat protein NRPAP/neurojungtin (CTNND2), mRNA, partial cds
5511	14756	24098	3.39	1.0E-81	U52351.1 NT		Human sapiens arm-repeat protein NRPAP/neurojungtin (CTNND2), mRNA, partial cds
5511	14756	24100	3.39	1.0E-81	U52351.1 NT		Human sapiens polymerase (DNA directed), gamma (POLG), mRNA
6403	15584	25041	7.33	1.0E-81	114329863 NT		Human sapiens polymerase (DNA directed), gamma (POLG), mRNA
7008	16188	25659	2.87	1.0E-81	BE958278.1 EST HUMAN	601645051 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3880228 5'	
7008	16188	25660	2.87	1.0E-81	BE958278.1 EST HUMAN	601645051 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3880228 5'	
7061	16238	25711	6.11	1.0E-81	BE564387.1 EST HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3885483 5'	
							ac14406 s1 Strategene HeLa cell s3 8372/16 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:yB36 YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.
7114	16281	25772	2.9	1.0E-81	AA630784.1 EST HUMAN		
7514	16719	26209	2.12	1.0E-81	8923698 NT		Human sapiens golgin-like protein (GLP), mRNA
7655	16855	28354	2.19	1.0E-81	AW844986.1 EST HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA	
7655	16855	28355	2.19	1.0E-81	AW844986.1 EST HUMAN	MRO-CT0006-250599-019 CT0006 Homo sapiens cDNA	
7821	12853	21972	3.15	1.0E-81	AW980658.1 EST HUMAN	EST37229 MAGE sequences, MAGF/Homo sapiens cDNA	
8054	17190	28730	2.23	1.0E-81	BF204263.1 EST HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110458 5'	
8550	17573	23994	3.86	1.0E-81	11418138 NT	Human sapiens phorbolin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA	
12	9308	18410	4.82	8.0E-82	AF161408.1 NT	Human sapiens HSPC228 mRNA, partial cds	
106	9308	18410	3.84	8.0E-82	AF161408.1 NT	Human sapiens HSPC228 mRNA, partial cds	
268	9543	18873	1.81	8.0E-82	U08988.1 NT	Human CRFB4 gene, partial cds	
824	10062	19214	2.49	8.0E-82	U08988.1 NT	Human CRFB4 gene, partial cds	
897	10132	19294	0.74	8.0E-82	U08988.1 NT	Human CRFB4 gene, partial cds	
1482	10685	19870	1.58	8.0E-82	AB037748.1 NT	Human sapiens mRNA for KIAA1327 protein, partial cds	
1633	10847	20028	1.59	8.0E-82	8715801 NT	Human sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA	
4229	13432	22526	0.76	8.0E-82	88223432 NT	Human sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA	
1451	10884		1.61	7.0E-82	BF035327.1 EST HUMAN	60145831F1 NIH_MGC_66 Homo sapiens cDNA clone HEMBA1000752 3'	
2722	11901	21117	1.57	7.0E-82	AU144050 EST HUMAN	AU144050 HEMBA1000752 3'	
4105	13312	22410	0.71	5.0E-82	AJ5156512.1 EST HUMAN	inf9e11_s1 NC_GAP_Co3 Homo sapiens cDNA clone IMAGE:925198 3'	
1846	10860	20041	59.84	4.0E-82	AT081484.1 NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	
8207	17338	26878	5.01	4.0E-82	AU837300.1 EST HUMAN	wp7569.x1 NC_GAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR:O75276	

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8807 17729			6.52	4.0E-82	AF028701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
282 9557	18690		20.38	3.0E-82	4502166	NT	Homo sapiens precursor beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
710 8952	18091		2.58	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-03-f02 BN0120 Homo sapiens cDNA
797 10036	18187		4.71	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
880 10116	19278		4.98	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1068 10294			38.43	3.0E-82	AA729548.1	EST_HUMAN	al23905.1 Soares, Isatis, NHT Homo sapiens cDNA clone 1543348 3'
1363 10578	19745		0.98	3.0E-82	AW075073.1	EST_HUMAN	RC8-PT0001-180100-021-B02 PT0001 Homo sapiens cDNA
1462 10675	19848		2.85	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1865 11072	20263		1.69	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-280700-018-004 BN01005 Homo sapiens cDNA
3239 12473			2.36	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2), mRNA
6505 15704	25170		2.69	3.0E-82	11425208	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
604 9851	18868		1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
604 9851	18970		1.37	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1661 10874	20058		1.4	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_1-434 (synonym: htes5) Homo sapiens cDNA clone DKFZp434M117 5'
2835 12137	21307		0.79	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3831 13048	22158		1.43	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3989 13212	22318		0.87	2.0E-82	U76833.1	NT	Human integral membrane serine protease Sereprase mRNA, complete cds
4219 13421	22516		0.89	2.0E-82	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4556 13750	22849		1.56	2.0E-82	AB029018.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4556 13750	22850		1.56	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
4888 14074	23172		2.13	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSCR1) and wbscr5 (WBSCR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5110 14280	23318		1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5110 14280	23317		1.23	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5427 14664	23781		2.59	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5741 14980	24360		5.35	2.0E-82	AF234882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
7824 17016	28531		1.74	2.0E-82	11471705	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR) mRNA
7858 17046	28564		5.19	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
7858 17046	28565		5.19	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8361 17452			2.21	2.0E-82	N94950.1	EST_HUMAN	2B31d10.1S1 Soares, Parathyroid tumor, NbHPA Homo sapiens cDNA clone IMAGE:3052033
8927 17810			3.89	2.0E-82	AA011278.1	EST_HUMAN	z10/g09.11 Soares, fetal liver, spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:426568
9241 18012			1.88	2.0E-82	11418097	NT	Homo sapiens SRY (sex determining region Y-box 10 (SOX10)) mRNA

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
599	8846	18964	1.63	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1218	10434		1.61	1.0E-82	BEE885106.1	EST_HUMAN	601510858F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1292	10507	18868	1.54	1.0E-82	BED84386.1	EST_HUMAN	RC4-BT0310-110 BT0310 Homo sapiens cDNA
1293	10508	18867	1.28	1.0E-82	ABD11110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
7331	16547	26037	2.65	1.0E-82	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21_C039
7578	16783	26276	1.95	1.0E-82	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21_C046
6885	15880	25339	4.85	9.0E-83	BFG72220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
1419	10831	19799	8.92	8.0E-83	BEE893973.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814362 5'
1656	11947	20052	10.45	8.0E-83	N88951.1	EST_HUMAN	2848112_s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:2958823 3'
1365	10580	19748	1.65	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271289-068-h11 LT0016 Homo sapiens cDNA
2817	12056		1.46	7.0E-83	AA584655.1	EST_HUMAN	nc12h101_s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element;
4830	14019		7.39	7.0E-83	BF221813.1	EST_HUMAN	7837a07_x1 NCI_CGAP_P_28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR_Q9Y316 Q9Y316
409	9862	18801	1.41	6.0E-83	M33320.1	NT	DJ207H1.1; Human platelet Glycoprotein IIb (GP1b) gene, exons 2-29
1757	10988	20153	2.7	6.0E-83	AW573088.1	EST_HUMAN	hf31h03_x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833525 3' similar to SW_YBEB_HAEIN P44471 HYPOTHETICAL PROTEIN H10034 ;
2882	12219	21354	0.72	6.0E-83	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
3016	12252		1.47	6.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3537	12780	21891	0.91	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5323	14555	23625	1.89	6.0E-83	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6291	15472	24913	1.99	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6884	16162	25633	3.82	6.0E-83	4505314	NT	Homo sapiens myosin (M-protein) 2 (165kD) (MYO12), mRNA
7007	16185	25657	3.15	6.0E-83	11430847	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
8062	17187		6.3	6.0E-83	AA486105.1	EST_HUMAN	ab14a10_s1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element;
8311	17418			4.28	8.0E-83	AF240786.1	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
954	10187			2.23	5.0E-83	U17883.1	Human succinate dehydrogenase iron-protein subunit (sdhb) gene, exon 5
2017	11950			19.94	5.0E-83	AFF008305.1	Homo sapiens 28S proteasome regulatory subunit (SUG2) mRNA, complete cds
3817	12838	21857		1.19	5.0E-83	AL133207.2	Novel human gene mapping to chromosome X
3884	13100	22217		0.67	5.0E-83	4885190	Homo sapiens deoxyribonuclease I (DNASE1), mRNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4425	13625	22720	0.69	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5109	14289	23374	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5109	14289	23375	12.48	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5177	14355	23442	1.07	5.0E-83	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
646	8892	18017	3.73	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1005	10236		4.72	3.0E-83	AA369311.1	EST_HUMAN	ESTT8542 Placenta Homo sapiens cDNA similar to endogenous retrovirus ERV9 np87cd7_s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR.i2 THR
2732	11911		1.22	3.0E-83	AA632654.1	EST_HUMAN	np87cd7_s1 NCI CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 3' similar to TR:Q92614 repetitive element:
1769	10979	20188	1.36	2.0E-83	AA893492.1	EST_HUMAN	Q92614 MYELOBLAST KIA0216..
1769	10979	20169	1.36	2.0E-83	AA893492.1	EST_HUMAN	Q92614 MYELOBLAST KIA0216..
1893	11100	20291	7.4	2.0E-83	N66951.1	EST_HUMAN	Q92614 MYELOBLAST KIA0216..
2803	12043	21164	1.24	2.0E-83	BE826894.1	EST_HUMAN	Q92614 MYELOBLAST KIA0216..
3236	12470		2.65	2.0E-83	11430834	NT	Q92614 MYELOBLAST KIA0216..
3756	12875		0.63	2.0E-83	AL163202.2	NT	Q92614 MYELOBLAST KIA0216..
4329	13530	22624	4.29	2.0E-83	AF202879.1	NT	Q92614 MYELOBLAST KIA0216..
4863	13B47	22838	5.69	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIA0216..
4863	13B47	22839	5.89	2.0E-83	7706398	NT	Q92614 MYELOBLAST KIA0216..
6266	15447	24886	5.44	2.0E-83	AF129533.1	NT	Q92614 MYELOBLAST KIA0216..
6565	15761	25223	3.51	2.0E-83	AF0111920.1	NT	Q92614 MYELOBLAST KIA0216..
6565	15761	25224	3.51	2.0E-83	AF0111920.1	NT	Q92614 MYELOBLAST KIA0216..
7426	16636	26129	4.43	2.0E-83	11436448	NT	Q92614 MYELOBLAST KIA0216..
7500	16707	26193	2.3	2.0E-83	AL134452.1	EST_HUMAN	DKFZp5471135_r1 547 (synonym: hftr1) Homo sapiens cDNA clone DKFZp5471135 5'
8986	17836	28194	2.3	2.0E-83	AL134452.1	EST_HUMAN	DKFZp5471135_r1 547 (synonym: hftr1) Homo sapiens cDNA clone DKFZp5471135 5'
1410	10929	19786	4.39	2.0E-83	AB0111399.1	NT	Homo sapiens gene for AF-B6, complete cds
1410	10929	19786	2.16	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thioesterase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1416	10629	19797	2.16	1.0E-83	4504326	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thioesterase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1887	11190	20400	1.81	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2618	11802	21019	1.72	1.0E-83	BE83690.1	EST_HUMAN	601507375F1 NIH MGIC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3850	13066	22180	5.44	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP80 mRNA, partial cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	13433	22527	3.15	1.0E-83	Z25822.1	NT	H_sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3
4908	14096	23189	2.7	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5963	15178	24595	1.87	1.0E-83	A1027614.1	EST_HUMAN	0x8808_x1 Soares_Tests_NHT_Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM
3779	12897	22113	4.49	7.0E-84	BE801209.1	EST_HUMAN	PROTEIN (HUMAN); 601676023F1 NIH MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1302	10517	19874	3.88	6.0E-84	BE838884.1	EST_HUMAN	RC2-FN0119-200600-011-805 FN0119 Homo sapiens cDNA
1302	10517	19875	3.88	8.0E-84	BE838884.1	EST_HUMAN	RC2-FN0119-200600-011-805 FN0119 Homo sapiens cDNA
2362	11555	20777	3.64	8.0E-84	AA7776574.1	EST_HUMAN	aa86603.s1 Strategene schizosaccharomyces pombe cDNA clone IMAGE:971020 3'
5296	14484		3.16	8.0E-84	AL042863.2	EST_HUMAN	DKFZp434H0322_1 r1 344 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0322 5'
5449	14675	23834	1.85	6.0E-84	AA897339.1	EST_HUMAN	al47603.s1 Soares_Tests_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338
6282	15463	24905	3.1	6.0E-84	BE810371.1	EST_HUMAN	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); PM0-LT0019-180600-004-F02 LT0019 Homo sapiens cDNA
6490	15687	25153	2.42	8.0E-84	BE770189.1	EST_HUMAN	PM4-FT0054-160600-004-#10 FT0054 Homo sapiens cDNA
8067	17202		2.15	8.0E-84	AW369812.1	EST_HUMAN	ILO-BT0168-091-199-139-#06 BT0168 Homo sapiens cDNA
721	88633	19102	3.3	5.0E-84	AA382811.1	EST_HUMAN	EST86094_Tests_I_Homo sapiens cDNA 5' end
2878	12213		2.48	5.0E-84	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
6078	17213	28745	2.34	5.0E-84	11428740	NT	Homo sapiens regulatory factor X_3 (influences HLA class II expression) (RFX3), mRNA
1415	10628	19795	3.31	4.0E-84	AI685321.1	EST_HUMAN	wa76c0_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_043847_NARDLYSN PRECURSOR
4969	14156	23248	1.1	4.0E-84	4505628	NT	Homo sapiens polymate (DNA-directed), alpha (TOKD) (POLA2), mRNA
4970	14157	23249	1.59	4.0E-84	AF059601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK), mRNA, complete cds
5775	14993	24393	2.02	4.0E-84	AF059650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
6355	15535	24989	14.25	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7492	16699	26184	5.84	4.0E-84	AB032856.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
321	9592	18723	1.54	3.0E-84	AF028200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1930	11134	20320	1.3	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
1975	11178	20386	2.89	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3588	12791	21917	1.11	3.0E-84	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
3730	12849	22087	5.34	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1), mRNA, complete cds
7455	16683		11.6	3.0E-84	AI983801.1	EST_HUMAN	wu20d05_x1 Soares_Ribosomal PROTEIN L18A (HUMAN); gb:105039_60S RIBOSOMAL PROTEIN L18A (HUMAN); CM1-BT0795-190600-212-b08 BT0795 Homo sapiens cDNA
2075	11275	20491	7.28	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-212-b08 BT0795 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HEK 293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2075	11275	20492	7.28	2.0E-84	BE695937.1	EST_HUMAN	CM1-BT0785-180600-272-b08 BT0795 Homo sapiens cDNA
2894	12132	21288	10.41	2.0E-84	AF036943.1	NT	Homo sapiens myelin transcription factor 1-like (MTTF1-) mRNA, complete cds
2818	12154	21289	1.58	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element nae30a022_x1 Lipski sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
8583	17595	24003	3.31	2.0E-84	BF448000.1	EST_HUMAN	TR-Q8UGS3 Q8UGS3 DJ756G23.1
8583	17595	24004	3.31	2.0E-84	BF448000.1	EST_HUMAN	nae30a022_x1 Lipski sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
3117	9589	18719	1.58	1.0E-84	AF114488.1	NT	nae30a022_x1 Lipski sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
556	9808	18931	12.69	1.0E-84	4507852	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
727	9889		1.24	1.0E-84	11427631	NT	Homo sapiens complement component 5 (C5), mRNA
1300	10515	18872	2.6	1.0E-84	AA984379.1	EST_HUMAN	am85b11.31 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:16228885 3'
2021	11222	20430	2.87	1.0E-84	BE392137.1	EST_HUMAN	601303006FT_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
2190	11387	20609	2.2	1.0E-84	11427197	NT	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3732	12852	220869	3.02	1.0E-84	AA720851.1	EST_HUMAN	nwi12601.51 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
4410	13610	22707	5.57	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4710	13901	23000	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZ43AN0323_11_434 (synonym: hies2) Homo sapiens cDNA clone DKFZ43AN0323 5'
4710	13901	23001	3.61	1.0E-84	AL043314.2	EST_HUMAN	DKFZ43AN0323_11_434 (synonym: hies2) Homo sapiens cDNA clone DKFZ43AN0323 5'
4833	13610	22707	3.37	1.0E-84	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
6124	15308	24741	2.57	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6334	15500	24945	2.39	1.0E-84	11430848	NT	Homo sapiens NGFI-A binding protein 1 (NAB1), mRNA
6831	16124		4.77	1.0E-84	5031894	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
7013	14492	23581	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7013	14492	23582	2.88	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
8453	17511		2.18	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
8573	17590	23898	4.24	1.0E-84	11418185	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
974	10206		1.55	9.0E-85	AL1632092	NT	Homo sapiens chromosome 21 segment HS21C009
1080	10305	19455	2.99	9.0E-85	U51432.1	NT	Homo sapiens chromosomal protein Skip mRNA, complete cds
1080	10305	19456	2.89	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1557	10771	19843	8.88	9.0E-85	M33282.1	NT	Human plasmminogen gene, exon 7
1557	10771	19844	8.68	9.0E-85	M33282.1	NT	Human plasmminogen gene, exon 7
1649	10863	20045	2.34	9.0E-85	7657020	NT	Hom sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
3785	13003	22118	1.05	9.0E-85	7019418	NT	Hom sapiens nucleolar GTPase (HUMAJANTIC), mRNA
4238	13441	22533	1.04	9.0E-85	AL16322802	NT	Hom sapiens chromosome 21 segment HS21C080

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4794	13983	23087	1.89	9.0E-85	M33764.1	NT	Human ornithine decarboxylase gene, complete cds
4794	13983	23098	1.89	9.0E-85	M33764.1	NT	Human ornithine decarboxylase gene, complete cds
4897	14085	23178	1.12	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4934	14121	23216	1.2	9.0E-85	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C0683
1144	10367	19518	10.12	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8158	17288		11.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
7954	17093	26623	3.24	8.0E-85	11438573	NT	Homo sapiens DEAD1 (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
7954	17093	26824	3.24	8.0E-85	11438573	NT	Homo sapiens DEAD1 (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2301	11495	20715	5.3	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5419	14847	23780	2.28	5.0E-85	BF035674.1	EST HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
5419	14847	23781	2.26	5.0E-85	BF035674.1	EST HUMAN	601458646F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862402 5'
7879	16878	26384	2.18	5.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9205	14497		3.22	5.0E-85	AF211158.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds
7220	16397		2.61	4.0E-85	BE0178263.1	EST HUMAN	RC1-BT0623-120200-01-07 BT0623 Homo sapiens cDNA
1303	10522	19681	0.77	3.0E-85	AF086157.1	NT	Homo sapiens protein phosphatase 2A_BR gamma subunit gene, exon 6
1750	10962	20144	35.52	3.0E-85	T97495.1	EST HUMAN	y653g091r Seares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121504 5'
4905	13506	22602	1.15	3.0E-85	BE287189.1	EST HUMAN	60118870dF2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4920	14108	23203	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4920	14108	23204	1.43	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4987	14174	23284	1.03	3.0E-85	7363442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5727	14945	24341	5.2	3.0E-85	7862308	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
5727	14945	24342	5.2	3.0E-85	7682309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6065	15255		7.81	3.0E-85	AJ404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6758	15953	25411	5.03	3.0E-85	11430889	NT	Homo sapiens phosphatase C, epsilon (PLCE), mRNA
8039	17175	28715	2.38	3.0E-85	5031680	NT	Homo sapiens EGFR-like repeats and discoidin I-like domains 3 (EDIL3), mRNA
8094	17810		3.91	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
970	10202	19358	0.84	2.0E-85	7657268	NT	Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1047	10273	19425	2.37	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1408	10621	19785	1.02	2.0E-85	7706205	NT	Homo sapiens CG1-201 protein (LOC51340), mRNA

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Single Exon Probes Expressed in HELa Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1424	10637	19806	10.87	2.0E-85	5174776	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1424	10637	19807	10.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2197	11394	20616	1.78	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2775	10560		7.76	2.0E-85	7857488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121), mRNA
2987	12224	21357	2.02	2.0E-85	M30988.1	NT	Human kru (p70/p80) subunit mRNA, complete cds
4926	13527	22621	6.55	2.0E-85	4505880	NT	Homo sapiens plasmalogen (PLG) mRNA
4932	14120	23215	1.04	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21(C084 w67n08_x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element MSR1 repetitive element;
6845	16034	25498	2.59	2.0E-85	A1760820.1	EST_HUMAN	
2251	11446		2.28	1.0E-85	BET94306.1	EST_HUMAN	601591416F1 NIH MGCG 7 Homo sapiens cDNA clone IMAGE:3945818 5'
2357	11550	20771	8.25	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH MGCG_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2357	11550	20772	8.25	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH MGCG_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7009	16187	25681	3.38	1.0E-85	BE257917.1	EST_HUMAN	601109738F1 NIH MGCG_16 Homo sapiens cDNA clone IMAGE:3356553 5'
7498	16705	26180	2.91	1.0E-85	AA778785.1	EST_HUMAN	244503.51 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
7498	16705	26191	2.91	1.0E-85	AA778785.1	EST_HUMAN	244503.51 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
7588	16773	26285	2.74	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH MGCG_19 Homo sapiens cDNA clone IMAGE:4126440 5'
7588	16773	28268	2.74	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH MGCG_19 Homo sapiens cDNA clone IMAGE:4126440 5'
7631	16832	26329	2.84	1.0E-85	Y00952.1	NT	Human mRNA for T-cell cyclophilin
8458	17679	23951	3.47	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8730	17679	23951	4.77	1.0E-85	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1432	10645		38.13	9.0E-86	BE274217.1	EST_HUMAN	601120777B1 NIH MGCG_20 Homo sapiens cDNA clone IMAGE:2867690 5'
5722	14940	24336	2.69	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
945	10178	19332	1.29	7.0E-86	AA860801.1	EST_HUMAN	aa88108.51 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
945	10178	19333	1.29	7.0E-86	AA860801.1	EST_HUMAN	aa88108.51 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1403559 3'
6076	14522	23565	6.39	7.0E-86	11421737	NT	Homo sapiens Tax (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1), mRNA
6698	15883	28354	3.63	7.0E-86	L38557.1	NT	Homo sapiens galactocerabrosidase (GALC) gene, exon 15
7533	16738	26228	2.69	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
7533	16738	26229	2.69	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
13011	10516	18673	3.14	6.0E-86	4505462	NT	Homo sapiens oxoglutarate dehydrogenase (lipoyamide) (OGDH) mRNA
216	8485	18628	1.86	4.0E-86	BE547173.1	EST_HUMAN	601072894F1 NIH MGCG_12 Homo sapiens cDNA clone IMAGE:3458830 5'
5615	14895	24287	11.54	4.0E-86	BE285843.1	EST_HUMAN	601176865F1 NIH MGCG_17 Homo sapiens cDNA clone IMAGE:3531953 5'
7783	9495	18629	1.86	4.0E-86	BE547173.1	EST_HUMAN	601072894F1 NIH MGCG_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4276	13479	22577	1.06	3.0E-86	BE8867703.1	EST_HUMAN	601443262F1 NIH MGCG_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5487	14713	24070	7.08	3.0E-86	AN340948.1	EST_HUMAN	x622h12X1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	16318	25800	2.86	3.0E-86	BE886479.1	EST_HUMAN	601509886F1 NIH_MGCC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7141	16318	25801	2.86	3.0E-86	BE886479.1	EST_HUMAN	601509886F1 NIH_MGCC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
7141	16318	25802	10.4	3.0E-86	AI859240.1	EST_HUMAN	h1B902_x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3636753 5'
7973	16408	25893	2.01	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGCC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
8427	18171		2.25	2.0E-86	AA303284.1	EST_HUMAN	EST177232 Jurkat T-cell VI Homo sapiens cDNA 5' end
2711	9548	18675	2.72	2.0E-86	AL182203.2	NT	Homo sapiens chromosome 21 segment HS21C003
420	9873		2.57	2.0E-86	NS977.1	EST_HUMAN	yZ-98d08_r1 Scores_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:283478 5'
1198	10418	18571	18.73	2.0E-86	9835487	NT	Human endogenous retrovirus, complete genome
2158	11356	20574	1.49	2.0E-86	AW868142.1	EST_HUMAN	EST378215 MAGE resequences, MAGI Homo sapiens cDNA
3363	12620	21751	3.14	2.0E-86	AF56776.1	NT	Homo sapiens lysophosphatidic acid acyltransferases-delta (LPAA1-delta) mRNA, complete cds
3727	12846	22063	3.14	2.0E-86	AF56776.1	NT	Homo sapiens lysophosphatidic acid acyltransferases-delta (LPAA1-delta) mRNA, complete cds
3727	12946	22064	3.14	2.0E-86	AF56776.1	NT	Homo sapiens lysophosphatidic acid acyltransferases-delta (LPAA1-delta) mRNA, complete cds
4017	13228		2.83	2.0E-86	AW515742.1	EST_HUMAN	hd87608_x1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916542 3'
4789	13988	23095	4.21	2.0E-86	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5093	14273	23396	0.94	2.0E-86	4505778	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PKHA1), mRNA
6848	15841	25301	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
6848	15841	25302	3.57	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
7196	16313	25854	3.67	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7196	16313	25855	3.67	2.0E-86	11545848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
7479	16687	28169	1.82	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S8 kinase, 80kD, polypeptide 5 (RPS8KA5) mRNA
8800	17793	23824	4.33	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
9077	17802		2.84	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
1577	10780	18968	2.82	1.0E-86	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUF51), mRNA
3126	12361	21490	1.41	1.0E-86	5453849	NT	Homo sapiens fibulin 5 (FBNL5) mRNA
3201	12436	21571	2.53	1.0E-86	LL20482.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3205	12498	21628	1.13	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3205	12498	21629	1.13	1.0E-86	AL163209.2	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3921	13137	22255	0.87	1.0E-86	7708161	NT	Human gamma-hypothetical protein (LOC51318), mRNA
3921	13137	22256	0.87	1.0E-86	7708161	NT	Human gamma-hypothetical protein (LOC51318), mRNA
4251	13454	22546	6.28	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4623	13817	22907	0.62	1.0E-86	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
4937	14124	23219	1.42	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKB23 isoform mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5468	14694	24047	3.81	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C034
8132	14694	24047	2.91	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C034
5370	14800		1.74	9.0E-87	AL150703.1	EST_HUMAN	qb77c09.x1 Soares fetal heart NbIIH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SWK1C1_MOUSE_P02535 KERATIN TYPE I CYTOSKELE TAL 10
6212	15452	24891	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
6212	15452	24892	2.05	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
488	9738	18871	78.74	8.0E-87	XG2245.1	NT	Oncoculus mRNA for elongation factor 1 epsilon
2238	11453	20871	2.01	7.0E-87	BFO63211.1	EST_HUMAN	7h85f0x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2238	11463	20872	2.01	7.0E-87	BFO63211.1	EST_HUMAN	7h85f0x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
7096	16273	25750	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_11434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434N0323 5'
7096	16273	25751	3.8	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_11434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434N0323 5'
7466	16874	28158	11.33	7.0E-87	KC03002.1	NT	Human mRNA from chromosome 15 gene with homology to MH-C-HLA-SB-1 intron A
7466	16874	28157	11.33	7.0E-87	KC03002.1	NT	Human mRNA from chromosome 15 gene with homology to MH-C-HLA-SB-1 intron A
3500	12724	21860	0.67	6.0E-87	7687213	NT	Human mRNA hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
7312	16530		8.07	6.0E-87	11424444	NT	Homo sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1166	16388	198539	6.71	5.0E-87	AJ382811.1	EST_HUMAN	EST68094 Testis Homo sapiens cDNA 5' end
8732	10388	198539	2.59	5.0E-87	AJ382811.1	EST_HUMAN	EST68094 Testis Homo sapiens cDNA 5' end
9173	10205	198560	1.04	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1180	10401	198554	18.34	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1889	112022	20413	2.08	4.0E-87	AB007925.1	NT	Homo sapiens mRNA for KIAA0456 protein, partial cds
2049	11250	20461	0.89	4.0E-87	R78133.1	EST_HUMAN	y80f10.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2049	11250	20462	0.99	4.0E-87	R78133.1	EST_HUMAN	y80f10.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element;
2386	11579	20795	1.87	4.0E-87	7706298	NT	Homo sapiens CG-80 protein (LOC51626), mRNA
2386	11579	20796	1.87	4.0E-87	7706298	NT	Homo sapiens CG-80 protein (LOC51626), mRNA
3441	12866	21800	1.43	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (MLLT4) mRNA
5418	14644	23776	6.4	4.0E-87	Q00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT 2)
5605	14805	24298	4.8	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBAP1E4051
7724	16823	26432	3.91	4.0E-87	ME60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
8253	17385	26918	3.1	4.0E-87	11417338	NT	Homo sapiens similar to heat shock 70kD protein 38 (mortalin-2) (H. sapiens) (LOC63184), mRNA

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8831	18223	23695	1.46	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8831	18223	23696	1.46	4.0E-87	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8994	17855	2193	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA	
2731	11910	21124	6.33	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMGA4), mRNA
2800	12138		1.12	2.0E-87	BG327920.1	EST_HUMAN	QVO-BN014B-050600-254-a03 BN014B Homo sapiens cDNA clone HEMBA10003075'
3767	12895	22101	0.7	2.0E-87	AU116895.1	EST_HUMAN	AU116895.1 Homo sapiens cDNA clone IMAGE:3843730 5'
5517	14742	24108	10.85	2.0E-87	BE734180.1	EST_HUMAN	601568041(F1 NIH_MGC_21) Homo sapiens cDNA clone IMAGE:3843730 5'
5517	14742	24109	10.85	2.0E-87	BE734180.1	EST_HUMAN	601568041(F1 NIH_MGC_21) Homo sapiens cDNA clone IMAGE:3843730 5'
5800	15017		5.29	2.0E-87	BE567193.1	EST_HUMAN	601341383(F1 NIH_MGC_53) Homo sapiens cDNA clone IMAGE:3883348 5'
6276	15456	24897	30.73	2.0E-87	N48128.1	EST_HUMAN	yy21e07.1 Soares fetal liver spleen 1NFL-S Homo sapiens cDNA clone IMAGE:243396 5'
6370	15550	25008	34.08	2.0E-87	N48128.1	EST_HUMAN	yy21e07.1 Soares fetal liver spleen 1NFL-S Homo sapiens cDNA clone IMAGE:243396 5'
6593	15794	25292	14.69	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
1180	11945		2.22	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1434	10847	19819	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-14(099-201-904 CT0265 Homo sapiens cDNA
1434	10847	19820	2.01	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-14(099-201-904 CT0265 Homo sapiens cDNA
3690	12911	22030	16.53	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3714	12834	22052	2.67	1.0E-87	4758827	NT	Homo sapiens neuregulin III (NRXN3), mRNA
5762	14981	24378	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6762	14981	24380	2	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
8499	15696	25180	12.4	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
6874	16152	25623	2.81	1.0E-87	BE18183.1	EST_HUMAN	RC6-BN0276-050700-012-E022 BN0276 Homo sapiens cDNA
6874	16152	25624	2.81	1.0E-87	BE18183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
7570	16775		1.88	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
7608	16811	26308	1.88	1.0E-87	5031680	NT	Homo sapiens EGFl-like repeats and discodin I-like domains 3 (EDIL3), mRNA
7608	16811	26307	1.86	1.0E-87	5031680	NT	Homo sapiens EGFl-like repeats and discodin I-like domains 3 (EDIL3), mRNA
8827	18371		1.87	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
1114	10338	19488	7.21	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1357	10572	19737	2.4	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1357	10572	19738	2.4	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2091	11291	20503	2.43	9.0E-88	7681701	NT	Homo sapiens DK7ZP58GP1522 protein (DKF2P58GP1522), mRNA
3608	12827	21947	1.22	9.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C099
4255	13458	22550	3.4	9.0E-88	X91929.1	NT	H.sapiens ECE-1 gene (exon 9)
4255	13458	22551	3.4	9.0E-88	X91928.1	NT	H.sapiens ECE-1 gene (exon 9)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5028	14213	23297	1.01	9.0E-88	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
1786	11005		3.42	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2863	11787	21008	6.14	5.0E-88	N88399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2958	12196	21330	0.78	5.0E-88	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
2972	12209	21348	1.02	5.0E-88	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
2972	12209	21347	1.02	5.0E-88	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
3387	12595		2.76	5.0E-88	AB693217.1	EST_HUMAN	wd8ch08.v1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Aliu repetitive element; contains element MER22 MER22 repetitive element;
3569	12733	21871	0.68	5.0E-88	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
4748	13939	23043	0.74	5.0E-88	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
5687	15269	24696	2.41	5.0E-88	HF1082.1	EST_HUMAN	ym05b10.1r Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5'
8672	11005		1.59	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
9214	11005		1.4	5.0E-88	7681887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1337	10552	18717	1.15	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA
1337	10552	19718	1.16	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-110 TN0028 Homo sapiens cDNA
6181	15363	24803	1.71	4.0E-88	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7484	16691	28174	1.8	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10) mRNA
8023	17160	26696	2.62	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8023	17160	26697	2.52	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
739	8880	18121	0.91	3.0E-88	115458010	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1781	10891		2.73	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2899	12137	21275	6.07	3.0E-88	N6851.1	EST_HUMAN	Z48112.s1 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:285623 3'
4228	13428	22520	0.91	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4228	13429	22521	0.91	3.0E-88	4601912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4474	13672		4.18	3.0E-88	1142830	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5328	14560	23632	2.81	3.0E-88	11428567	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5483	14709	24085	3.48	3.0E-88	9966888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5538	14762	24129	3.92	3.0E-88	11420897	NT	Homo sapiens v-ral simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA
6111	15205	24624	14.23	3.0E-88	AF278265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6308	15489	24934	6.98	3.0E-88	11436401	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
6432	15629	25094	15.11	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenic protein-1) (GDF5), mRNA

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
85598	17580			3.87	3.0E-88	11417974 NT	Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA
1043	10269	18419		1.37	2.0E-88	7305188 NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1801	10815	18891		1.56	2.0E-88	AF246219.1 NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1722	10834	20117		5.7	2.0E-88	AF246219.1 NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4417	13817	22713		2.0E-88	5031688 NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNA4), mRNA	
5621	14844	24223		5.34	1.0E-88	AVW139565.1 EST_HUMAN	U1-H-BII-see-d-04-0-LJLs1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5621	14844	24224		5.34	1.0E-88	AVW139565.1 EST_HUMAN	U1-H-BII-see-d-04-0-LJLs1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
5953	15169	24582		23.77	1.0E-88	AB007877.1 NT	Homo sapiens KIAA0417 mRNA, complete cds
5953	15169	24583		23.77	1.0E-88	AB007877.1 NT	Homo sapiens KIAA0417 mRNA, complete cds
6158	15341	24778		4.02	1.0E-88	AA488981.1 EST_HUMAN	AB54811.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP-B0272.2
6930	16128	25596		2.94	1.0E-88	AL043314.2 EST_HUMAN	DKFZp34N0323..1 r1434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N0323 5'
7881	16416	25903		3.87	1.0E-88	AA891479.1 EST_HUMAN	osf9103.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1612758 3 similar to gb-M16342
8790	17717			5.85	1.0E-88	AL163246.2 NT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN); Homo sapiens chromosome 21 segment HS21C046
7525	16730	26220		8.72	9.0E-89	11421238 NT	Homo sapiens transglutamin 2 (TAGLN2), mRNA
2682	11872	21087		0.98	8.0E-89	B2311557.1 EST_HUMAN	601142409F_1 NIH_3T3_G_14 Homo sapiens cDNA clone IMAGE:3506188 5'
4319	9693	18831		1.05	7.0E-89	7657213 NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4319	9693	18832		1.05	7.0E-89	7657213 NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4904	14092	23185		2.94	7.0E-89	4557300 NT	Homo sapiens complement component 8, beta polypeptide (C8B) mRNA
4951	14138	23232		6.21	7.0E-89	AL046748.1 EST_HUMAN	DKFZp34N0324..1 r1434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434N0324 5'
7791	16985	26500		2.86	7.0E-89	M59783.1 NT	Human aldose reductase (AR) gene, segment 2
9240	18011			1.76	7.0E-89	U37927.1 NT	Human sialic acid hydrolase (ACO2) gene, exon 2
1030	10256	18407		1.83	6.0E-89	5603114 NT	Homo sapiens inner membrane protein, mitochondrial (mitofillin) (MMT), mRNA
2180	11377	20599		4.97	6.0E-89	4506124 NT	Homo sapiens serine/threonine-protein kinase PRF4 homolog (PRP4), mRNA
2367	11590	20807		7.83	6.0E-89	4507788 NT	Homo sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3) mRNA
2367	11590	20808		7.83	6.0E-89	4507788 NT	Homo sapiens ubiquitin-conjugating enzyme E2L_3 (UBE2L3) mRNA
3458	12722	21858		0.65	6.0E-89	7661817 NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4478	13876	22785		1.37	6.0E-89	7661737 NT	Homo sapiens HSPCC18 protein (HSPCC18), mRNA
4639	13833	22821		3.22	6.0E-89	AB007868.2 NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4639	13833	22822		3.22	6.0E-89	AB007868.2 NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5214	14389	23474		1.53	6.0E-89	6806918 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5214	14389	23475		1.53	6.0E-89	6806918 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5105	14285	23369	2.93	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay/or-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5105	14285	23370	2.93	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Bay/or-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7700	18989	28408	1.84	4.0E-88	AI798672.1	EST_HUMAN	WE91C03.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2830	12069	21191	2.07	3.0E-89	AW976181.1	EST_HUMAN	EST382280 MAGE sequences, MAGN Homo sapiens cDNA
8935	17549	23886	2.42	3.0E-89	AV705749.1	EST_HUMAN	AV705749 ADB Homo sapiens cDNA clone ADDBGA01 5'
125	9887	18807	1.11	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
125	9887	18808	1.11	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
444	9887	18807	0.69	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
444	9887	18808	0.69	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
536	9787	18910	0.78	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2834	12073	21195	1.58	2.0E-89	AI222095.1	EST_HUMAN	qq86c08_x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J041311 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN) contains Alu repetitive element;
3527	12751	21983	0.64	2.0E-89	AA759149.1	EST_HUMAN	ah70803.s1 Scores_ntests_NHT Homo sapiens cDNA clone IMAGE:1320988 3'
3527	12751	21984	0.64	2.0E-89	AA759149.1	EST_HUMAN	ah70803.s1 Scores_ntests_NHT Homo sapiens cDNA clone IMAGE:1320988 3'
4127	13333	22431	1.26	2.0E-89	AF089897.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4135	13341	22441	5.58	2.0E-89	X58742.1	NT	H. sapiens HKC gene for tyrosine kinase (PTK), exons 10-11
4135	13341	22442	5.58	2.0E-89	X58742.1	NT	H. sapiens HKC gene for tyrosine kinase (PTK), exons 10-11
4342	13544	22635	1.7	2.0E-89	AI163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4500	13698	22782	1.09	2.0E-89	AJ007378.1	NT	Homo sapiens GGT gene, exon 5
5040	14224	23308	0.95	2.0E-89	11545821	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
5361	14591	58	2.0E-89	BE541744.1	EST_HUMAN	601055986F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'	
5432	14659	23798	2.85	2.0E-89	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
6384	15644	24699	4.77	2.0E-89	UB1004.1	NT	Human GT24 (GT24) mRNA, partial cds
6436	15633	25098	2.38	2.0E-89	11428801	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
7913	17128	26658	3.35	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
8104	17238	28776	5.65	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
8208	17339	26879	2.84	2.0E-89	UJ10692.1	NT	Human MAGE-7 antigen (MAGE7) pseudogene, complete cds
8259	17386		2.22	2.0E-89	11417260	NT	Human threonyl-tRNA synthetase (TARS), mRNA

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8107	17241	26780	6.89	1.0E-89	BF186052.1	EST_HUMAN	hr8/d09_x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR_O54778 O54778
8107	17241	26781	6.89	1.0E-89	BF186052.1	EST_HUMAN	hr8/d09_x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR_O54778 O54778
1070	10296	19445	2.31	8.0E-90	AL163246.2	NT	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN ;
1071	10296	19445	2.97	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21_C048
1338	11981	19719	3.38	8.0E-90	BE070581.1	EST_HUMAN	7638f08_x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1338	11981	19720	3.38	8.0E-90	BE070581.1	EST_HUMAN	7638f08_x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
848	10083			2.87	7.0E-90	AF223391.1	Hom sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3032	12268	21395	1.22	6.0E-90	X91926.1	NT	H sapiens ECE-1 gene (exon 6)
3032	12268	21398	1.22	6.0E-90	X91926.1	NT	H sapiens ECE-1 gene (exon 6)
4212	13415	22510	8.66	6.0E-90	89223388	NT	Hom sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4212	13415	22511	8.66	6.0E-90	89223388	NT	Hom sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
5647	14870	24258	3.59	6.0E-90	U77700.1	NT	Hom sapiens HsGCN1 mRNA, partial cds
5647	14870	24257	3.59	6.0E-90	U77700.1	NT	Hom sapiens HsGCN1 mRNA, partial cds
6570	15768	25227	6.84	6.0E-90	4504794	NT	Hom sapiens Inositol 1,4,5-triphosphate receptor type 3 (ITPR3) mRNA
6570	15768	25228	6.84	6.0E-90	4504794	NT	Hom sapiens Inositol 1,4,5-triphosphate receptor type 3 (ITPR3) mRNA
1553	9440			24.41	5.0E-90	AB035344.1	Hom sapiens TCL8 gene, exon 1-10b
1200	10420	19573	1.75	5.0E-90	UB0228.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
2521	11709	20925	1.83	5.0E-90	AF114487.1	NT	Hom sapiens intersectin long isoform (ITSN) mRNA, complete cds
4537	13732	22830	2.47	5.0E-90	4508354	NT	Hom sapiens pregnancy-zone protein (PZP) mRNA
4612	13808	22897	1.1	5.0E-90	AA705222.1	EST_HUMAN	282910_x1 Soares_fetal_liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:4614423
4612	13808	22898	1.1	5.0E-90	AA705222.1	EST_HUMAN	282910_x1 Soares_fetal_liver_spleen_INFSL_S1 Homo sapiens cDNA clone IMAGE:4614423
5486	14712	24069	3.24	5.0E-90	Z16411.1	NT	H sapiens mRNA encoding phospholipase C
5558	14712	24069	2.51	5.0E-90	Z16411.1	NT	H sapiens mRNA encoding phospholipase C
6171	15353	24781	2.22	5.0E-90	AF113708.1	NT	Hom sapiens angiopoietin 4 (ANG4) mRNA, partial cds
6171	15353	24782	2.22	5.0E-90	AF113708.1	NT	Hom sapiens angiopoietin 4 (ANG4) mRNA, partial cds
6318	15489	24944	7.67	5.0E-90	4557258	NT	Hom sapiens adenylylate cyclase 9 (ADCY9) mRNA
6557	15753	25216	4.76	5.0E-90	1134543	NT	Hom sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
7195	18372	25853	4.96	5.0E-90	11433721	NT	Hom sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9048	17921		1.36	5.0E-90	AB011398.1	NT	Hom sapiens gene for AF-6, complete cds
8085	17911		1.72	5.0E-90	AB23366.1	EST_HUMAN	ar78h05_x1 Bersteard sera HPLR86 Homo sapiens cDNA clone IMAGE:2128761 3'

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
307	9880	18712	1.78	4.0E-90	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
307	9880	18713	1.78	4.0E-90	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
1094	10318	19470	2.65	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MPT1), mRNA
1664	10877	20082	8.83	4.0E-90	X88033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2813	12053	21175	1.1	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2813	12053	21178	1.1	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12225	21358	1.5	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2888	12225	21359	1.5	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4659	13853	22850	4.47	4.0E-90	DB7675.1	NT	Homo sapiens amyloid precursor protein, complete cds
4809	13988	23104	1.63	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4833	14022	23116	1.9	4.0E-90	M95867.1	NT	Human prohormone converting enzyme (NEC2) gene, exon 8
5231	14405	23488	1.03	4.0E-90	572977	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
8984	12053	21175	1.35	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8984	12053	21178	1.35	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8148	17280	26825	52.24	3.0E-90	BE563833.1	EST HUMAN	801335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:36869147.5'
2118	9487	18631	3.74	2.0E-90	BE537913.1	EST HUMAN	801087378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:34538345'
1181	10402	18555	8.41	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGB7), mRNA
1181	10402	18558	8.41	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGB7), mRNA
3830	13047	22157	2.29	2.0E-90	A1138213.1	EST HUMAN	qc54c02_x1 Scores:placenta 8iceweeks_2NHP81tgW Homo sapiens cDNA clone IMAGE:1713410.3'
4894	13885	22988	1.12	2.0E-90	AB006627.4	NT	Homo sapiens mRNA for KIAA0288 gene, partial cds
4831	14119	23214	9.77	2.0E-90	5729855	NT	Homo sapiens GRB2-related adaptor protein (GRAF) mRNA
5566	14791	24163	4.95	2.0E-90	AW872686.1	EST HUMAN	HYPOTHETICAL 35.5 KD PROTEIN..
7012	16190	25663	6.27	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
7012	16190	25664	6.27	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
8006	16441	25929	3.86	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
281	9558	18689	4.74	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neprin-1, Alzheimer disease) (APP), mRNA
319	11939	18779	1.31	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
380	11839	18778	1.24	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
702	9944	19079	1.92	1.0E-90	A2317589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7012	9944	19080	1.82	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
737	9978	19118	11.4	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
737	9978	19119	11.4	1.0E-90	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1118	10342		1.49	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1313	10529	19690	3.36	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A, BR gamma subunit gene, exon 3
1313	10529	19691	3.36	1.0E-90	AF098154.1	NT	Homo sapiens protein phosphatase 2A, BR gamma subunit gene, exon 3
1643	10857		3.06	1.0E-90	BE378884.1	EST_HUMAN	60115863f2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3511118'5'
1968	11073	20284	2.95	1.0E-90	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like) (LOC57167'), mRNA
2865	12045	21167	6.75	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3835	13052	22163	1.47	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3835	13052	22164	1.47	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
4415	13615	22711	1.76	1.0E-90	AF167340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 8 and complete cds, alternatively spliced
5262	14435	23509	1.28	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5262	14435	23510	1.28	1.0E-90	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
5523	14748	24115	2.09	1.0E-90	AB014533.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
6365	15545	25000	2.58	1.0E-90	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6725	15920	25379	3.54	1.0E-90	11422086	NT	Homo sapiens brieflin A inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6859	16049	25514	2.42	1.0E-90	11422108	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
6859	16049	25515	2.42	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
8036	17880	23894	1.51	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XMI, complete cds
8036	17880	23895	1.51	1.0E-90	AB002059.1	NT	Homo sapiens DNA for Human P2XMI, complete cds
4178	13382	22483	5.53	8.0E-91	D12234.1	EST_HUMAN	HUM0015381 Liver HepG2 cell line, Homo sapiens cDNA clone s3813'
3451	12676	21811	1.9	5.0E-91	AA702794.1	EST_HUMAN	280b04.51 Seires, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE4480153'
4822	14011	23109	1.46	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4822	14011	23110	1.46	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
8068	17895		1.23	6.0E-91	Al193566.1	EST_HUMAN	q70f11_x1 Seires, fetal lung, NbHL19W Homo sapiens cDNA clone IMAGE1744365 3' similar to contains MIR_b2 MIR_MIR repetitive element;
3168	12401	21535	1.56	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
3168	12401	21536	1.56	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
7504	16711	26199	6.21	4.0E-91	AL163254.2	NT	Homo sapiens chromosome 21 segment HS21C0844 EST101579 Hippocampus, Strategene (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to
8509	17545	23983	2.28	4.0E-91	M7794.1	EST_HUMAN	Retrovirus-related gag polyprotein

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 Table 4
 Single Exon Probes Expressed in HEGLA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	17545	24031	2.28	4.0E-91	M77894.1	EST_HUMAN	EST01579 Hippocampus, Strengene (cat. #936205) Homo sapiens cDNA clone HHCMS60 similar to
1595	10809	19985	1.4	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1595	10809	19886	1.4	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3313	12543	21677	1.41	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3439	12684	21797	3.24	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3439	12684	21798	3.24	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3770	12988	22104	0.97	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4590	13784	22875	5.52	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4999	14186	23275	3.31	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4999	14188	23276	3.31	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5789	15006		3.05	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6), mRNA
5921	15138	24549	3.58	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
5921	15138	24550	3.58	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6351	15531	24982	4.48	3.0E-91	UB6959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
6351	15531	24983	4.48	3.0E-91	UB6959.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exons 10 and 11
8768	17704	23955	1.33	3.0E-91	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9124	14480	23535	4.48	3.0E-91	AF169665.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
9124	14490	23536	4.48	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
90	9347	18460	2.75	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1262	10468	19832	9.01	1.0E-91	AV449748.1	EST_HUMAN	U1-H-B13-akts-d-01-0-LJ1 s1 NCI_CGAP_Subs Homo sapiens cDNA clone IMAGE:2735280 3'
6015	15265	24689	1.89	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157804 5'
6015	15265	24690	1.89	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4157804 5'
8675	18308		1.69	1.0E-91	H15212.1	EST_HUMAN	Ym30603.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:49387 5'
1248	10465	19826	19.2	9.0E-92	AJ001689.1	NT	Homo sapiens NK2D gene, exon 10
1248	10465	19827	19.2	9.0E-92	AJ001689.1	NT	Homo sapiens NK2D gene, exon 10
5428	14053	23790	3.81	9.0E-92	J03007.1	NT	Human Na ⁺ /K ⁺ -ATPase alpha-subunit mRNA, partial cds
5493	14719	24076	1.9	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
5890	15088	24478	3.95	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6846	18035	25499	2.27	9.0E-92	11422086	NT	Homo sapiens briefdin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
92	8385	18514	3.46	8.0E-92	W26367.1	EST_HUMAN	263 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
280	9564	18697	6.09	8.0E-92	BE386368.1	EST_HUMAN	801273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614867 5'
1780	11000	20195	1.06	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
1780	11000	20198	1.06	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (80kD) (DGKG), mRNA
4207	13410	22504	0.94	8.0E-92	AA809157.1	EST_HUMAN	om36022.e1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.b2.L1 repetitive element;
5132	14310	23401	0.77	8.0E-92	AW157571.1	EST_HUMAN	au83n08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2752911 3' similar to TR_O60302_O60302_KIAA0555 PROTEIN :contains element MER22 repetitive element;
6603	15804	25280	4.9	8.0E-92	LD4183.1	NT	Human lens membrane protein (mp18) gene, exon 11
6608	15804	25281	4.9	8.0E-92	LD4183.1	NT	Human lens membrane protein (mp19) gene, exon 11
6791	15886	25446	3.26	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
7382	16597	26085	5.33	8.0E-92	AF074398.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
7900	17116	26848	2.27	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
8859	17762	23935	1.7	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
26	9322	18425	1.35	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
241	11953	18649	0.97	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
241	11953	18650	0.97	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
598	9845		1.47	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Sepressase truncated isoform mRNA, complete cds
1287	10502	19663	1.21	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2153	11351	20567	6.03	7.0E-92	5031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTTR2), mRNA
2153	11351	20568	6.03	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTTR2), mRNA
2530	11718	20935	9.05	7.0E-92	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2684	11868	21078	6.58	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (Q1S156E), mRNA
2709	11888	21105	2.57	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3319	14467	21681	0.74	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3319	14467	21682	0.74	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4586	13780	22872	1.34	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
4586	13780	22873	1.34	7.0E-92	S71824.1	NT	N-CAM=145 kda neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2860 nt]
5194	14370	23457	0.95	7.0E-92	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5305	14537	23541	5.59	7.0E-92	AA446208.1	EST_HUMAN	zmb6d12.r1 Soares_NHT_Homo sapiens cDNA clone IMAGE:781175 5'
1567	10780		1.21	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2721	11900	21116	2.78	3.0E-92 BE909714.1	EST_HUMAN	601501242F1_NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'	
5603	14827	24203	5.34	3.0E-92 AA378336.1	EST_HUMAN	EST91020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13	
7349	18565	26054	4.3	3.0E-92 X15804.1	NT	Human mRNA for alpha-actinin	
7349	18565	26055	4.3	3.0E-92 X15804.1	NT	Human mRNA for alpha-actinin	
27	9323	18428	1.34	2.0E-92	45019898 NT	Homo sapiens activin A receptor, type II B (ACVR2B) mRNA	
144	9426	18560	13.1	2.0E-92 AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds	
183	9462	18592	3.22	2.0E-92	11422948 NT	Homo sapiens hypothetical protein d4J62O23.2 (D4J62O23.2), mRNA	
183	9462	18593	3.22	2.0E-92	11422946 NT	Homo sapiens hypothetical protein d4J62O23.2 (D4J62O23.2), mRNA	
757	8888	18144	3.85	2.0E-92 BE289180.1	EST_HUMAN	601118337F1_NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'	
757	8888	18145	3.85	2.0E-92 BE289180.1	EST_HUMAN	601118337F1_NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'	
1689	10901		1.47	2.0E-92 S78853.1	NT	mrg-mas-related [Human, Genomic, 2416 nt]	
1805	11111	20305	1.45	2.0E-92 AIB18119.1	EST_HUMAN	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844	
1805	11111	20306	1.46	2.0E-92 AIB18119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;	
2015	11217	20428	6.58	2.0E-92	4506860 NT	wk27d07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844	
2021	11805	21022	24.83	2.0E-92	6512457 NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN ;	
2782	10844	20022	2.37	2.0E-92	11418424 NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	
2782	10844	20023	2.37	2.0E-92	11418424 NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA	
3581	12812	21932	1.28	2.0E-92 AF231918.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA	
3581	12812	21933	1.28	2.0E-92 AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA	
3868	12887	22008	5.14	2.0E-92	5803180 NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/hsp90-organizing protein) (STIP1), mRNA	
4274	13477	22574	1.37	2.0E-92 M10976.1	NT	Human endogenous retroviral DNA (4-4), complete retroviral segment	
4768	13955	23058	0.84	2.0E-92 AF136523.1	NT	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds	
5017	14204		3.73	2.0E-92 AL040437.1	EST_HUMAN	DKFZp434C0414_1^34 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'	
5248	14421		0.95	2.0E-92	4759169 NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA	
5941	15157	24569	2.81	2.0E-92 AB028891.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds	
7344	16560	28048	7.05	2.0E-92	1143490 NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA	
7703	16902	28410	1.75	2.0E-92 AW836290.1	EST_HUMAN	CN4-LT0028-161299-062-906 LT0028 Homo sapiens cDNA	
7703	16902	28411	1.75	2.0E-92 AW836290.1	EST_HUMAN	CN4-LT0028-161299-062-906 LT0028 Homo sapiens cDNA	
8878	17774	23943	2.73	2.0E-92 AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds	
8887	17791	23923	1.35	2.0E-92 AF108656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds	
9153	11805	21022	29.98	2.0E-92	6912457 NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA	

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Table 4
Single Exon Probes Expressed in HEK Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9269	18312	23600	1.48	2.0E-92	AF106858.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
1817	11025	20219	1.38	1.0E-92	R78678.1	EST_HUMAN	Y80808.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1817	11025	20220	1.38	1.0E-92	R78678.1	EST_HUMAN	Y80808.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2041	11242	20451	68.35	1.0E-92	45096688	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
1898	11201	20412	3.07	9.0E-93	AU121681.1	EST_HUMAN	AU121681.MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
							EST18844 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' and similar to ribosomal protein L29
2009	11212		43.7	9.0E-93	AA310723.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2609	11783		1.25	9.0E-93	AF223391.1	NT	601281887F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633832 5'
3593	12814	21935	1.06	9.0E-93	BE388571.1	EST_HUMAN	AU121681.MAMMA1000738 5'
4328	15229	22623	1.11	9.0E-93	AU121681.1	EST_HUMAN	AU121681.MAMMA1000738 5'
8157	17289		18.88	9.0E-93	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A) mRNA
5929	15145	24558	2.46	8.0E-93	B1703684.1	EST_HUMAN	601480521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863908 5'
250	9526	18856	7.52	7.0E-93	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3041	12278	21406	0.65	6.0E-93	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1), mRNA
1388	10802	19767	1.49	5.0E-93	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1411	10624	19789	11.81	5.0E-93	AI674184.1	EST_HUMAN	Wc09c08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2314670 3'
1411	10624	19790	11.81	5.0E-93	AI674184.1	EST_HUMAN	Wc09c08.x1 NCI_CGAP_Pt28 Homo sapiens cDNA clone IMAGE:2314670 3'
3199	12434	21569	5.83	5.0E-93	X02021.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
6382	15562	25018	3.42	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
6971	16149	25820	2.22	5.0E-93	AF2274883.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7402	16615	26105	2.18	5.0E-93	11439598	NT	Homo sapiens secretory pathway component Sec31B-1 (NUCE22), mRNA
8774	18037	23844	2.01	5.0E-93	11417877	NT	Z50e09.s1 Soares_testis_NH1 Homo sapiens cDNA clone IMAGE:795698 3' similar to SW:CLPA_RAT
87	8380		5.23	4.0E-93	AA445983.1	EST_HUMAN	P37397 CALPONIN, Acidic ISOFCRM:
4511	9704	18841	0.84	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
451	9704	18842	0.84	4.0E-93	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
781	10020	19169	3.31	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
781	10020	19170	3.31	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
1191	10411	19865	2.02	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731) mRNA
1948	11150	20352	4.6	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2209	11406	20630	1.21	4.0E-93	AF515747.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3542	12765	21898		0.92	4.0E-93	7705386	NT
4025	13238	22341		1.82	4.0E-93	4504654	NT
5047	12765	21898		0.65	4.0E-93	7705386	NT
5508	14733	24095		4.77	4.0E-93	T46864.1	EST_HUMAN
7693	16892	26401		18.41	4.0E-93	AV692051.1	EST_HUMAN
3631	12852	21970		15.84	3.0E-93	BF690830.1	EST_HUMAN
3631	12852	21971		15.84	3.0E-93	BF690830.1	EST_HUMAN
4220	13423			1.43	3.0E-93	AF226896.1	NT
5103	14283			1.05	3.0E-93	AF231981.1	NT
7379	16595	26082		5.39	3.0E-93	A1824839.1	EST_HUMAN
195	9476	18808		50.31	2.0E-93	AB0118610.1	NT
195	9475	18807		50.31	2.0E-93	AB0118610.1	NT
328	8589	18729		9.28	2.0E-93	AL163285.2	NT
329	8589	18729		8.05	2.0E-93	AL163285.2	NT
2100	11300	20514		2.1	2.0E-93	U40783.1	NT
2449	11640	20861		3.05	2.0E-93	BE252982.1	EST_HUMAN
5175	14353	23441		0.97	2.0E-93	BE253201.1	EST_HUMAN
5403	14631	23743		4.28	2.0E-93	AW094495.1	EST_HUMAN
8683	17640			1.69	2.0E-93	AA128735.1	EST_HUMAN
8749	17692			1.73	2.0E-93	L41825.1	NT
8925	17875			4.17	2.0E-93	BF035327.1	EST_HUMAN
103	8396	18525		2.48	1.0E-93	AF238997.1	NT
103	9398	18526		2.48	1.0E-93	AF238997.1	NT
524	9775	18900		11.32	1.0E-93	7857018	NT
607	9854	18973		4.39	1.0E-93	AI148755.1	EST_HUMAN
882	10118	18280		10.07	1.0E-93	D87675.1	NT
1244	10480	18619		8.18	1.0E-93	8923270	NT
1244	10480	18620		8.18	1.0E-93	8923270	NT
1353	10568	19732		2.25	1.0E-93	AF167708.1	NT

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2306	11500	20721	5.98	1.0E-93 AF231981.1	NT		Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2426	11617	20839	12.19	1.0E-83 AF055086.1	NT		Homo sapiens MHC class 1 region
2472	11663		2.57	1.0E-83 AL137200.1	NT		Novel human gene mapping to chromosome 1
2774	10518	18678	2.76	1.0E-93 BE297369.1	EST_HUMAN		601177886F NIH_MIGC_17 Homo sapiens cDNA clone IMAGE:35328865 5'
2774	10518	18877	2.75	1.0E-93 BE287369.1	EST_HUMAN		601177886F NIH_MIGC_17 Homo sapiens cDNA clone IMAGE:35328865 5'
2884	12122	21255	3.73	1.0E-93 DB7875.1	NT		Homo sapiens DNA for amyloid precursor protein, complete cds
3182	12417		2.24	1.0E-83 AF231981.1	NT		Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4421	13621	22716	3.48	1.0E-83 AL163284.2	NT		Homo sapiens chromosome 21 segment HS21C084
5474	14701	24055	1.97	1.0E-93 U78509.1	NT		Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5474	14701	24056	1.97	1.0E-93 U78509.1	NT		Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5824	14848	24230	10.31	1.0E-83	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
5994	15277	24707	2.01	1.0E-83	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6185	15367	24807	3.71	1.0E-83	D42072.1	NT	Human mRNA for NF-N-isofrom-exon11, complete cds
6847	15743	25204	2.45	1.0E-83	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6894	15800	25066	2.82	1.0E-83	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6954	16132	25600	4.68	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
6954	16132	25601	4.68	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
8312	18101	23807	2.74	1.0E-83	AB282922.1	EST_HUMAN	qm03c12.xt NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880758 3' similar to WP:T19B4.4 CE13742;
8830	17812		1.26	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
8918	17870		3.25	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
9200	18353		1.46	1.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
3839	13155	22272	2.41	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
9143	17949		1.5	6.0E-94	11418351	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5379	14608	23719	4.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5379	14608	23720	4.05	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5687	14907	24300	4.88	5.0E-94	AA722434.1	EST_HUMAN	Zg87908.s1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:409594 3'
6092	15283	24725	1.76	5.0E-94	AB015800.1	EST_HUMAN	ct83d05.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623369 3'
7544	18749	26242	2.23	5.0E-94	11423982	NT	Homo sapiens adenylyl kinase 2 (AK2), mRNA
7544	18749	26243	2.23	5.0E-94	11423982	NT	Homo sapiens adenylyl kinase 2 (AK2), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{Top}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8638	18356	23608	6.17	5.0E-94	TB8398.1	EST_HUMAN	yd98b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'
9227	18005		1.86	5.0E-94	9558724	NT	Homo sapiens cleavage and polyacetylation specific factor 1, 16kD subunit (CPNSF1), mRNA
1808	11018		17.14	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2619	11803	21020	1.98	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3662	12873	21981	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89112.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3652	12873	21982	1.02	4.0E-94	AW197851.1	EST_HUMAN	xn89112.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4729	13920	23023	4.08	4.0E-94	A1591312.1	EST_HUMAN	tw1110.x NCI_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2255403 3 similar to TR:Q15265 Q15265
5856	15074	24488	1.89	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
5856	15074	24487	1.89	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7689	16424	25911	1.68	4.0E-94	11545782	NT	Homo sapiens hypothalamic protein FLJ12455 (FLJ12455), mRNA
8117	9882	18982	1.1	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
728	8970	19108	0.9	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1713	10825	20109	2.41	3.0E-94	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds
1713	10925	20110	2.41	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein SS2 precursor, mRNA, complete cds
1742	10954	20137	3.37	3.0E-94	4575758	NT	Homo sapiens ET-1 binding protein p300 (EP300) mRNA
4171	13375	22474	0.66	3.0E-94	AA464805.1	EST_HUMAN	zw63g08.11 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone 1375163 3'
4308	13509	22604	1.2	3.0E-94	AA781836.1	EST_HUMAN	ei559h06.s1 Soares_tests_Nt-H Homo sapiens cDNA clone 1375163 3'
6526	14750	24117	3.33	3.0E-94	11496268	NT	Homo sapiens zinc finger protein 277/ZNF277, mRNA
5849	15066	24476	5.57	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6649	15844	25305	5.17	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0579 protein, partial cds
6958	16136	25607	3.97	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
7665	16864	26366	1.79	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
151	9433	18567	1.66	1.0E-94	BE295714.1	EST_HUMAN	601175162f_NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3054	12280	21415	2.17	1.0E-94	BE253433.1	EST_HUMAN	6011116896f_NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3054	12280	21416	2.17	1.0E-94	BE253433.1	EST_HUMAN	6011116896f_NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4352	13554	22650	1.54	1.0E-94	9506892	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
7010	16188	25682	2.51	1.0E-94	BE780478.1	EST_HUMAN	601468748f_NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872098 5'
7634	16835	26331	3.18	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
7864	17054	26575	2.47	1.0E-94	A1272244.1	EST_HUMAN	ap22602.x1 Schiller oligodendroglialoma Homo sapiens cDNA clone IMAGE:1956122 3 similar to TR:Q15265
							Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR ;

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8763	9433	18567	1.42	1.0E-94	BE2985714.1	EST_HUMAN	601175762Fl NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
9064	9433	18567	1.69	1.0E-94	BE285714.1	EST_HUMAN	601175762Fl NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1471	10684	19859	8.53	8.0E-85	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3119	12354	21482	1.11	8.0E-85	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3119	12354	21483	1.11	8.0E-85	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6544	15740	25201	2.68	9.0E-85	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
146	9428	18562	8.86	8.0E-85	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4533	13729	22825	1.87	8.0E-85	A1700988.1	EST_HUMAN	wed064_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:k00558
4533	13729	22826	1.87	8.0E-85	A1700988.1	EST_HUMAN	wed064_x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:k00558
6180	15362	24801	1.88	8.0E-85	11426529	NT	Homo sapiens prothrombin (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6180	15362	24802	1.88	8.0E-85	11426529	NT	Homo sapiens prothrombin (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
6528	15724	25189	2.69	8.0E-85	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
6869	16091	25558	2.63	8.0E-85	11420644	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
6869	16091	25559	2.63	8.0E-85	11420644	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
7024	16201	28679	2.45	8.0E-85	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
7033	16210	318	8.0E-85	AB037818.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds	
7302	16521	26012	1.85	8.0E-85	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGFR-like protein mRNA, complete cds
8018	17157	26683	2.51	8.0E-85	10864024	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZTF) mRNA
8386	17850		15.84	8.0E-85	AA628056.1	EST_HUMAN	z184b01_s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L111L1 repetitive element
280	9555	18887	9.96	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
280	9555	18888	9.96	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4360	13562	22658	7.94	7.0E-95	M65708.1	NT	Homo sapiens Ly-6-like protein (CD59) mRNA, complete cds
4407	13607		1.32	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7456	16684	26153	1.9	3.0E-95	R83180.1	EST_HUMAN	yp87g11_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:184468 5'
1621	10834	20009	3.28	2.0E-95	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1621	10834	20010	3.28	2.0E-95	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1910	11115	20311	3.87	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudodflammatory) (TIMP3) mRNA
1913	11118	20315	1.83	2.0E-95	BE383873.1	EST_HUMAN	601312161Fl NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36588862 5'
2390	11583	20800	1.13	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2390	11583	20801	1.13	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2428	11619	20840	3.71	2.0E-95	AF240786.1	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2479	11669	20887	11.4	2.0E-95	4768423	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3121	12356	21486	3.34	2.0E-95	AF015452.1	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3339	12762	21892	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3359	12762	21893	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3395	12816	21938	1.25	2.0E-95	AB0317807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
3731	12851	22068	0.85	2.0E-95	A1200264.1	EST_HUMAN	qm01c02_x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:18803463 similar to WIP:T23G7.4
4335	13557	22652	1.79	2.0E-95	7657189	NT	Homo sapiens hypothetical protein (HS522B1A), mRNA
5054	14244	23331	3.37	2.0E-95	7681978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5121	14300	23388	1.7	2.0E-95	AA447831.1	EST_HUMAN	2x11d07_r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:7861575'
5121	14300	23389	1.7	2.0E-95	AA447831.1	EST_HUMAN	2x11d07_r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:7861575'
5431	14658	23798	4.23	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5431	14658	23197	4.23	2.0E-95	7705764	NT	Homo sapiens-type phosphofructokinase (PFK-M) gene, exon 7
5731	14850	24349	4.34	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) mRNA, complete cds
5910	15127	24536	2.53	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA
6816	16010	25473	3.61	2.0E-95	11421785	NT	Homo sapiens ribophorin II (RPN2), mRNA
7311	16520	26020	2.34	2.0E-95	4767853	NT	Homo sapiens bone morphogenetic protein receptor type IA (BMPRA) mRNA
8735	17681	23953	2.2	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9154	17056	23884	5.88	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
							Z23n04_r1 Soares ovary tumor Nb-HOT Homo sapiens cDNA clone IMAGE:7140075' similar to TR:G1067084 G1067084 F55H12.6'
5498	14724	24082	7.75	1.0E-95	AA284651.1	EST_HUMAN	Z23n04_r1 Soares ovary tumor Nb-HOT Homo sapiens cDNA clone IMAGE:7140075' similar to TR:G1067084 G1067084 F55H12.6'
5498	14724	24083	7.75	1.0E-95	AA284651.1	EST_HUMAN	RC8-FN0019-280500-011-G11 FN0019 Homo sapiens cDNA
6226	15477	24919	3.3	1.0E-95	BF370000.1	EST_HUMAN	RC8-FN0019-280500-011-G11 FN0019 Homo sapiens cDNA
6226	15477	24920	3.3	1.0E-95	BF370000.1	EST_HUMAN	RC8-FN0019-280500-011-G11 FN0019 Homo sapiens cDNA
6527	15723	25188	2.63	8.0E-96	BE97259.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:38897615'
448	11987	18838	1.84	8.0E-96	BE97807.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:38897615'
448	11987	18839	1.84	8.0E-96	BE97807.1	EST_HUMAN	PM0-L70019-090300-002-d09 LT0019 Homo sapiens cDNA
5444	14870		2.59	8.0E-96	AW836047.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3887	13103	22220	0.88	7.0E-96	AF231920.1	NT	MRO-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA
2225	11421	20847	1.36	6.0E-96	BE171984.1	EST_HUMAN	MRO-HT0559-250200-002-d07 HT0559 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3280	12521	21652	0.88	6.0E-96	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3457	126882	21816	19.61	6.0E-96	M26873.1	NT	Human glyceradehyde-3-phosphate dehydrogenase pseudogene 3' end
8078	17214	28746	1.88	6.0E-96	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763). mRNA
8079	17214	28747	1.88	6.0E-96	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763). mRNA
8118	17252	28793	2.29	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MyH2). mRNA
325	9596	18725	2.91	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
832	10088	19248	3.55	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
852	10088	18249	3.55	5.0E-98	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2581	11767		6.37	5.0E-98	11416767	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A). mRNA
2862	12228	21361	0.85	5.0E-98	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5). mRNA
4925	14113		1.74	5.0E-98	X09812.1	NT	H.sapiens DNA for monocarboxyl oxidase type A (7) (partial)
5062	15274	24703	3.98	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1). mRNA
5062	15274	24704	3.98	5.0E-98	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1). mRNA
8485	15692	25156	2.69	5.0E-98	M58347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8485	18692	25157	2.69	5.0E-98	M58347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
4173	13377		18.09	3.0E-98	H88636.1	EST_HUMAN	y87h12.1 Soares fetal liver spleen cDNA clone IMAGE:212327.5'
421	9874		2.93	2.0E-98	4503038	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4). mRNA
755	9996	19141	2.39	2.0E-98	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4789	13958	23059	1.68	2.0E-98	BE148074.1	EST_HUMAN	RC3-HT0230-04500-110-g02 HT0230 Homo sapiens cDNA
6759	15654		6.71	2.0E-98	AV689461.1	EST_HUMAN	AV689461 GKC Homo sapiens cDNA clone GKCM0D7.5'
8416	17489		2.01	2.0E-98	AV249440.1	EST_HUMAN	2B18351 Ratmice NIH_3T3_Homo sapiens cDNA clone IMAGE:2819351.5'
6777	9821	18052	2.89	1.0E-98	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K) gag, pol and env genes
1751	10963	20145	3.39	1.0E-98	AW955054.1	EST_HUMAN	EST3612/124 MAGE resequences, MAGC Homo sapiens cDNA
1761	10963	20146	3.39	1.0E-98	AW955054.1	EST_HUMAN	EST3612/124 MAGE resequences, MAGC Homo sapiens cDNA
2231	11951	20853	1.03	1.0E-98	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
6686	15881	25340	28.75	1.0E-98	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214). mRNA
8403	14488	23533	1.38	1.0E-98	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM). mRNA
8403	14488	23534	1.38	1.0E-98	4826883	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM). mRNA
6315	15495		3.65	6.0E-97	BE141849.1	EST_HUMAN	I15-HT017-011098-04-D07 HT017 Homo sapiens cDNA
7944	17084	26613	2.09	6.0E-97	X5804.1	NT	Human mRNA for alpha-actinin
6467	15684	25135	2.41	5.0E-97	AL043314.2	EST_HUMAN	DKFZp734N0323_r1-434 (synonym: hts3) Homo sapiens cDNA clone DKFZp734N0323.5'
6508	15702	25168	13.07	5.0E-97	AA418026.1	EST_HUMAN	z97e12.61 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767758.3' similar to TR.G1304125
					G1304125 PMS4 mRNA;		

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6983	16161	25632	3.44	5.0E-97	BF154912.1	EST_HUMAN	RCO-BT0812-256300-032-a08 BT0812 Homo sapiens cDNA
8080	17215	26748	2.4	5.0E-97	BE148597.1	EST_HUMAN	MRO-HI0241-150500-010-b02 HI0241 Homo sapiens cDNA
8080	17215	26749	2.4	5.0E-97	BE148597.1	EST_HUMAN	MRO-HI0241-150500-010-b02 HI0241 Homo sapiens cDNA
947	10180	18336	1.69	4.0E-97	BE004426.1	EST_HUMAN	CMD-BN06-170300-293-a06 BN06-170300-293-a06 Homo sapiens cDNA
1874	11081	20271	1.08	4.0E-97	5453572	NT	Homo sapiens brefedin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6007	15257	24681	6.08	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GaINAC alpha-2, 6-sialyltransferase I, long form
6007	15257	24682	6.08	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GaINAC alpha-2, 6-sialyltransferase I, long form
7722	16921	26429	1.74	4.0E-97	11883122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
7722	16921	26430	1.74	4.0E-97	11883122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8606	17604	6	4.0E-97	114183	18	NT	Homo sapiens G-2 and S-phase expressed 1 (GSE1), mRNA
247	9524	18654	0.98	3.0E-97	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
884	10120	18282	8.01	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
884	10120	19283	8.01	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1443	11995	19832	2.27	3.0E-97	4758819	NT	Homo sapiens N-myc (and STAT) interactor (NM), mRNA
2402	11952	20813	3.91	3.0E-97	U36255.1	NT	Human beta-prime-actinin (BAN22) gene, exon 7
3227	12461	21583	1.34	3.0E-97	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
4789	13978	23082	31.26	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA
5840	15057	24484	2.48	1.0E-97	BE568486.1	EST_HUMAN	601338520F1 NIH MG-53 Homo sapiens cDNA clone IMAGE:3581821 5'
7294	16513	28005	4.29	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
7294	16513	28006	4.29	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
7857	17047	28566	3.58	1.0E-97	AA553761.1	EST_HUMAN	hk29g02.s1.NCI_CGAP_Co11 Homo sapiens cDNA clone IMAGE:10149623
8004	18439	25926	18.38	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
8004	18439	25927	18.38	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
911	10146	18307	3.5	9.0E-98	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1283	10488	18658	0.87	9.0E-98	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
5247	14420	23497	1.46	9.0E-98	11419594	NT	Homo sapiens FSH primary response (LRPR1, rat) homolog 1 (FSHPRH1), mRNA
6434	15631	25098	11.48	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
6434	15631	25097	11.48	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7574	16779	26273	2.68	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
7574	16779	26274	2.68	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8621	10146	18307	2.6	9.0E-98	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA

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25	9321			1.5	8.0E-98 AJ251158.1	NT	Human sapiens partial MLCB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1701	10913	20100		3.45	8.0E-98 AB017007.1	NT	Human sapiens PMS2L16 mRNA, partial cds
1701	10913	20101		3.45	8.0E-98 AB017007.1	NT	Human sapiens PMS2L16 mRNA, partial cds
3778	12996	22112		7.09	8.0E-98 J04489.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2144	11342	20560		1.34	3.0E-98 AJ403124.1	EST_HUMAN	Al403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2598	11753	20973		3.5	3.0E-98 AB014607.1	NT	Human sapiens mRNA for KIAA0707 protein, partial cds
2706	11885			0.49	3.0E-98 AJ077498.1	EST_HUMAN	7B1BH01 Chromosome 7_Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
6082	15252	24675		1.94	3.0E-98	11419210 NT	Human sapiens activator of S phase kinase (ASK), mRNA
6082	15252	24676		1.94	3.0E-98	11419210 NT	Human sapiens activator of S phase kinase (ASK), mRNA
7035	16212	25688		2.7	3.0E-98 AJ403124.1	EST_HUMAN	Al403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
7035	16212	25689		2.7	3.0E-98 AJ403124.1	EST_HUMAN	Al403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
7526	16731	26221		2.58	3.0E-98 U56309.1	NT	Human fumurate precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9213	17894			3.36	3.0E-98	11418177 NT	Human sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
743	9884	19127		0.75	2.0E-98 BE261694.1	EST_HUMAN	601149486F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE3502245 5'
2047	11248	20458		3.98	2.0E-98 BE284281.1	EST_HUMAN	601172658F1 NIH MGIC_17 Homo sapiens cDNA clone IMAGE3528134 5'
2204	11401	20926		2.69	2.0E-98 AL163202.2	NT	Human sapiens chromosome 21 segment HS21C02
2342	11535	20758		0.91	2.0E-98 AF248540.1	NT	Human sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
2342	11535	20759		0.91	2.0E-98 AF248540.1	NT	Human sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
3098	12332	21458		1.3	2.0E-98 AB032377.1	NT	Human sapiens hCHK1 gene for checkpoint kinase, exon 2
3098	12332	21459		1.3	2.0E-98 AB032377.1	NT	Human sapiens hCHK1 gene for checkpoint kinase, exon 2
4084	13293	22392		1.45	2.0E-98	8923308 NT	Human sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4284	13487	22586		0.64	2.0E-98 AF032897.1	NT	Human sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4333	13534	22825		3.89	2.0E-98	4758331 NT	Human sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4), mRNA
4843	14032	23123		1.04	2.0E-98 AF218802.1	NT	Human sapiens attractin precursor (ATRN) gene, exon 16
4843	14032	23124		1.04	2.0E-98 AF218802.1	NT	Human sapiens attractin precursor (ATRN) gene, exon 16
5384	14613	23726		5.47	2.0E-98	7706512 NT	Human sapiens PDZ domain-containing glutamine nucleotide exchange factor 1 (LOC51735), mRNA
6658	15853	25312		3.8	2.0E-98	11428813 NT	Human sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
6658	15853	25313		3.8	2.0E-98	11428813 NT	Human sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8629	17619	23971		4.83	2.0E-98	11435947 NT	Human sapiens chromosome 12 open reading frame 3 (C12orf3), mRNA
411	9664	18804		50.73	1.0E-98 AJ862007.1	EST_HUMAN	Iw36b04_X1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE2281743 3 similar to SW_RL2B_HUMAN
461	9714	18849		2.19	1.0E-98 AW988811.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A
							PM0-BN0065-100300-001-006 BN0065 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1768	10976	20185	45.72	1.0E-98	IN49818.1	EST_HUMAN	y23105.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:SS6204 SS6204 ribosomal protein L29 - human;
5342	14572	23648	3.57	1.0E-98	AA195654.1	EST_HUMAN	XP98009.11 Streptogene muscle 931209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:GB065622
6784	15959	25413	3.58	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
6784	15959	25414	3.58	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5680	14900	24284	4.01	9.0E-98	AW068635.1	EST_HUMAN	EST380711 MAGE sequences, MAGU Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW_BID_HUMAN
7682	16881	26388	2.79	9.0E-98	A1479829.1	EST_HUMAN	Im69n07_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW_BID_HUMAN
7682	16881	26389	2.79	9.0E-98	A1479829.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST
7682	16881	26390	2.79	9.0E-98	A1479829.1	EST_HUMAN	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST
7952	17091	26621	2.22	9.0E-98	AA134604.1	EST_HUMAN	Zn80d02_r1 Strategelung carcinoma 931218 Homo sapiens cDNA clone IMAGE:565443 5' similar to TR:G662994 G662994 GPI-ANCHORED PROTEIN P137.;
5585	14809	24183	9.29	7.0E-99	AF005808.1	NT	Homo sapiens oscillin (hLn) gene, linker region exon 5
8134	17287	26811	2.64	7.0E-99	AF001888.1	NT	Homo sapiens NK-receptor (KIR-G2) gene, partial cds
478	9730	18884	0.66	U10981.1	NT	Human G2 protein mRNA, partial cds	
2087	11297	20509	2.73	6.0E-99	11430555.1	NT	Homo sapiens cysteine-rich repeat-containing protein Ss2 precursor, (LOC51232), mRNA
2087	11297	20510	2.73	6.0E-99	11430555.1	NT	Homo sapiens cysteine-rich repeat-containing protein Ss2 precursor, (LOC51232), mRNA
4780	13951	23052	1.05	6.0E-99	4502660.1	NT	Homo sapiens CD34 antigen (CD34) mRNA
5228	14402	23485	0.95	6.0E-99	8923244.1	NT	Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA
6705	15900	25361	2.55	6.0E-99	AB036428.1	NT	Homo sapiens NDST4 mRNA for N-deacetylasparaginyltransferase 4, complete cds
6735	15930	25389	4.2	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
6735	15930	25390	4.2	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
7307	18525	26016	4.46	6.0E-99	11526290.1	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
929	10163	19319	0.59	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
929	10163	19320	0.59	5.0E-99	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
1934	11138	20334	1.39	5.0E-99	Y11365.1	NT	H.sapiens MPA gene, exon 8
4562	13798	22854	1.41	5.0E-99	AF009690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV12S2 region
8837	17628		2.18	5.0E-99	BE890177.1	EST_HUMAN	6011513157F1 NIH MGC_71 Homo sapiens cDNA clone IMAGE:3914391_5'
6568	15765		8.7	3.0E-99	M85586.1	NT	Human E2A/HLF fusion protein (E2AHLF) mRNA, complete cds
1246	10463		13.38	2.0E-99	AW274792.1	EST_HUMAN	XP09608_x1 NCI_CGAP_HMG Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYO SIN LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
3225	12459	21592	1.56	2.0E-99	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4498	13698	22789	0.82	2.0E-99	BE612554.1	EST_HUMAN	6014520677F1 NIH MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4498	13698	22780	0.82	2.0E-99	BE612554.1	EST_HUMAN	60145206771 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5' Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
4540	13735	22833	2.2	2.0E-99	AF095703.1	NT	Zp46d06.r1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:3066635 5' similar to 9bM15i182 BETAGLUCURONIDASE PRECURSOR (HUMAN);
6683	15878	26337	2.24	2.0E-99	W23507.1	EST_HUMAN	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
7670	16869	26372	4.48	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
320	9591	18722	1.48	1.0E-99	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
384	8848	18783	0.88	1.0E-99	11526150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1425	10838	19808	5	1.0E-99	M50938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1541	10754	19827	1.5	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1541	10754	19928	1.5	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, and translated products
1895	11102	20293	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1895	11102	20284	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3050	12286	21412	1.22	1.0E-99	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4374	13576	22672	2.53	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4374	13576	22673	2.53	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6922	16115	25581	2.58	1.0E-99	AW340174.1	EST_HUMAN	TR02102.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:002711
7741	16937	28446	1.78	1.0E-99	5901979	NT	Human heat shock transcription factor 2 binding protein (HSF2BP), mRNA
7918	17131	26681	2.7	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
8268	17393	28923	1.78	1.0E-99	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8387	17458		4.43	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	9298	18401	2.49	1.0E-100	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	9299	18401	4.78	1.0E-100	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
68	8363	18487	1.69	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XXKRY), mRNA
68	8363	18488	1.69	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XXKRY), mRNA
88	9379	18510	0.69	1.0E-100	AW275237.1	EST_HUMAN	x778611.x1 NCI_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
172	9453	18584	0.83	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C046
322	9583	18724	1.06	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
348	9816	18743	2.37	1.0E-100	T05087.1	EST_HUMAN	EST02975 Fetal brain, Strategene (cat#308208) Homo sapiens cDNA clone HFBCR32
443	9897		1.92	1.0E-100	AF003528.1	NT	Homo sapiens X-linked arthritrophic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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Table 4
Single Exon Probes Expressed in HEA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
496 9749			8.33	1.0E-100	X89631.1	NT	G gorilla DNA for ZNF80 gene homolog
518 9787	18893		1.08	1.0E-100	BE180609.1	EST HUMAN	RC3-HT0625-040500-022-b09 HT0625 Homo sapiens cDNA
1026 10252	19402		2.26	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1026 10252	19403		2.28	1.0E-100	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1532 10746			1.38	1.0E-100	AW207555.1	EST HUMAN	UI-H-B11-afk-c-07-0-U1-s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW.CYT_COTJA
1538 10749	10922		1.28	1.0E-100	A1200857.1	EST HUMAN	P81061 CYSTATIN :
2207 11404			1.09	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2401 11594	20812		0.99	1.0E-100	X62468.1	NT	H sapiens mRNA for IFN-gamma (IFC-Q)
2667 11848	21063		1.09	1.0E-100	11418978	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2983 12220			5.64	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4193 13397	22497		1.68	1.0E-100	AF057354.1	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
4221 13424	22517		2.1	1.0E-100	4503762	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5123 14302	23390		3.15	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5123 14302	23391		3.15	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5319 14551	23621		1.73	1.0E-100	BF244218.1	EST HUMAN	6011863184F1 NIH_MCG_57 Homo sapiens cDNA clone IMAGE:4080969 5'
5536 14760	24127		1.88	1.0E-100	AU118182.1	EST HUMAN	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
5875 15093	24506		5.22	1.0E-100	AU140214.1	EST HUMAN	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
6037 15245	24687		5.68	1.0E-100	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
6831 15827	25289		10.17	1.0E-100	BF103853.1	EST HUMAN	601647357F1 NIH_MCG_61 Homo sapiens cDNA clone IMAGE:3931310 5'
6843 15838			8.14	1.0E-100	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21(C003
6837 16031	25498		2.53	1.0E-100	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
6952 16130	25598		2.8	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
6952 16130	25599		2.8	1.0E-100	AB046846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7343 16559	26047		8.66	1.0E-100	BF327292.1	EST HUMAN	MRO-BN0070-270300-008-111 BN0070 Homo sapiens cDNA
7834 17028	26542		3.69	1.0E-100	X94633.1	NT	H sapiens CD97 gene exon 4
7834 17028	26543		3.59	1.0E-100	X94633.1	NT	H sapiens CD97 gene exon 4
7893 17109	26638		4.35	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; end unknown gene
7893 17109	26639		4.35	1.0E-100	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; end unknown gene
7822 9289	18401		2.41	1.0E-100	AL183247.2	NT	Homo sapiens chromosomal S-transferase theta 2 (GSTT2) gene, complete cds
8179 17311			2.07	1.0E-100	AF288285.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
8309 17414	26936		8.55	1.0E-100	AF240786.1	NT	

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 Table 4
 Single Exon Probes Expressed in HEGLA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8439	18237			1.33	1.0E-100	BF448549.1	EST_HUMAN
8627	17820	23972		2.51	1.0E-100	11545732	NT
8875	17772	23941		1.51	1.0E-100	11418123	NT
9262	18029	23854		4.18	1.0E-100	11417874	NT
77	9371	18500		0.89	1.0E-101	7110714	NT
77	9371	18501		0.89	1.0E-101	7110714	NT
6833	9936	19066		1.7	1.0E-101	AB007815.2	NT
7111	9953	19092		5.91	1.0E-101	7110734	NT
7111	9953	19093		5.91	1.0E-101	7110734	NT
780	10019	19168		2.81	1.0E-101	7857454	NT
883	10099	19261		2.61	1.0E-101	4503914	NT
934	10167	19324		1	1.0E-101	220656.1	NT
982	10223	19380		8.49	1.0E-101	BF881218.1	EST_HUMAN
1059	10285	19435		1.86	1.0E-101	AI221818.1	EST_HUMAN
1582	10776	19851		1.09	1.0E-101	5821460	NT
1582	10776	19852		1.09	1.0E-101	5821460	NT
1914	11119	20316		2.15	1.0E-101	4502866	NT
2023	11224	20432		5.82	1.0E-101	BF884307.1	EST_HUMAN
2318	12015	20732		1.12	1.0E-101	5729882	NT
2577	11763	20984		6.68	1.0E-101	X72983.1	NT
2700	11879	21094		12.23	1.0E-101	AJ1237744.1	NT
2700	11879	21095		12.23	1.0E-101	AJ1237744.1	NT
2868	12146			15.41	1.0E-101	AJ252312.1	NT
3167	12402	21537		2.87	1.0E-101	4885270	NT
3207	12441			2.4	1.0E-101	BF035927.1	EST_HUMAN
3359	12587	21728		1.72	1.0E-101	AW985556.1	EST_HUMAN
3378	11879	21094		3.41	1.0E-101	AJ1237744.1	NT
3378	11879	21095		3.41	1.0E-101	AJ1237744.1	NT
3858	13074	22189		5.17	1.0E-101	AB022785.1	NT
5058	14238	23327		1.2	1.0E-101	5821460	NT
5058	14238	23328		1.2	1.0E-101	5821460	NT
5170	14349	23437		0.73	1.0E-101	BE012554.1	EST_HUMAN
							601452067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'

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Table 4

Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5170	14349	23438	0.73	1.0E-101	BE612554.1	EST_HUMAN	6014520-67F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761' 5'
5854	14877	24265	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
5854	14877	24266	4.27	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6218	15389	24840	4.91	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6218	15389	24841	4.91	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
6283	15464	24908	4.88	1.0E-101	AW008475.1	EST_HUMAN	wf5f12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487' 3'
6324	15505	25022	1.73	1.0E-101	BE257384.1	EST_HUMAN	6011082117F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349801' 5'
6386	15585	25022	6.59	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-2207004-018-f12_BT0313 Homo sapiens cDNA
6483	15680	25149	4.94	1.0E-101	BF029174.1	EST_HUMAN	601784886F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3988837' 5'
6898	15805	25070	25.34	1.0E-101	X68069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6899	15605	25071	25.34	1.0E-101	X68069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
6904	16081	25528	16.67	1.0E-101	9845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7003	16181	25653	4.98	1.0E-101	BE619837.1	EST_HUMAN	60147280817 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953' 3'
7003	16181	25654	4.98	1.0E-101	BE619667.1	EST_HUMAN	60147280817 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953' 3'
7188	16385	25845	2.7	1.0E-101	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
7182	16389	25848	4.46	1.0E-101	AI670283.1	EST_HUMAN	to77d11.x1 NCI_CGAP_Gasa Homo sapiens cDNA clone IMAGE:2184309' 3' similar to gb:M26326
7192	16389	25849	4.46	1.0E-101	AI670283.1	EST_HUMAN	KERATIN_TYPE I CYTOSKELE TAL 18 (HUMAN); to77d11.x1 NCI_CGAP_Gasa Homo sapiens cDNA clone IMAGE:2184309' 3' similar to gb:M26326
8805	17798	5.23	1.0E-101	AW039051.1	EST_HUMAN	QV1-DT0068-240200-085-e01 DT0068 Homo sapiens cDNA	
41	8337	18444	0.9	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
346	9614	18740	3.75	1.0E-102	AL163303.2	NT	Home sapiens chromosome 21 segment HS21C103
628	8871	18983	1.28	1.0E-102	BE252470.1	EST_HUMAN	601108292F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326' 5'
784	10023	19173	1.51	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1125	10349	19500	2.13	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (+4), complete retroviral segment
1275	10490	19848	1.28	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1275	10490	19849	1.28	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1423	10636	19805	387.84	1.0E-102	BE408447.1	EST_HUMAN	60129882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628901' 5'
2276	11470	20691	4.62	1.0E-102	A1124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:15399854' 3' similar to SW:GG95_HUMAN Q08379 GOLIN-95;
2275	11470	20692	4.52	1.0E-102	A1124689.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:15399854' 3' similar to SW:GG95_HUMAN Q08379 GOLIN-95;
3029	12265	21383	1.65	1.0E-102	7681979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3098	12334	21460	3.08	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650' 5'

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3098	12334	21461	3.08	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4217	13420	22515	1.84	1.0E-102	AL168207.2	NT	Homo sapiens chromosome 21 segment HS21C017
4406	13608	22705	1.98	1.0E-102	BE251310.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
6145	14324	23416	0.97	1.0E-102	R88488.1	EST_HUMAN	y32c04_r1 Soares placenta Nb24P Homo sapiens cDNA clone IMAGE:140834 5'
5550	14774		5.79	1.0E-102	AB034851.1	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5587	14792	24164	3.16	1.0E-102	770538.1	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5587	14792	24165	3.16	1.0E-102	770538	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5753	15001	24404	2.82	1.0E-102	AL459825.1	EST_HUMAN	er22f09_x1 Barstead cloned HPLB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
6233	15414	24855	8.1	1.0E-102	A1238894.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
6345	16526	24974	2.87	1.0E-102	A7710738.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CUAAKD03 5'
6880	16050	25516	2.68	1.0E-102	T70393.1	EST_HUMAN	jd13d07_r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:67021 5'
6880	16050	25517	2.68	1.0E-102	T70393.1	EST_HUMAN	jd13d07_r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:67021 5'
6882	16073	25642	3.85	1.0E-102	AU124629.1	EST_HUMAN	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
7205	16382	25862	3.09	1.0E-102	AB05037.1	EST_HUMAN	RC-BT074-260499-014 BT074-Homo sapiens cDNA
7205	16382	25863	3.09	1.0E-102	AB05037.1	EST_HUMAN	RC-BT074-260499-014 BT074-Homo sapiens cDNA
7640	16840	26337	2.15	1.0E-102	45078322	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
7640	16840	26338	2.15	1.0E-102	45078322	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
7942	17082	26610	3.51	1.0E-102	BT359243.1	EST_HUMAN	RCG-E1072-150600-011-F01 ET072-Homo sapiens cDNA
8200	17332	28875	4.71	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
8315	17419		3.74	1.0E-102	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C030
8890	17786	23919	5.19	1.0E-102	AW300862.1	EST_HUMAN	xk07c12_x1 NCI CGAP_Co20 Homo sapiens cDNA clone IMAGE:2668038 3'
89	9364	18489	3.08	1.0E-103	BE908158.1	EST_HUMAN	6011600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
69	9364	18490	3.08	1.0E-103	BE908158.1	EST_HUMAN	6011600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
100	9393	18522	9.97	1.0E-103	DB7078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
213	9493	18625	3.06	1.0E-103	5453763	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
988	10219	18633	0.89	1.0E-103	A1276348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPP-E gene)
1250	10468	18630	7.51	1.0E-103	BE877541.1	EST_HUMAN	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1578	10789	18685	2.39	1.0E-103	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (PI4K230) mRNA, complete cds
1879	11086	20276	1.08	1.0E-103	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP) mRNA
1944	11148	20348	1.12	1.0E-103	4502428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
1944	11148	20349	1.12	1.0E-103	4502428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA
2270	11465	20866	2.26	1.0E-103	AU134991.1	EST_HUMAN	AU134991 PLACE1 Homo sapiens cDNA clone PLACE1000965 5'

Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2414	11605	20827	1.88	1.0E-103	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2583	11769	20989	2.7	1.0E-103	N32770.1	EST_HUMAN	yw91d08_s1 Soares placenta_8t6weeks_2NbHPtgc8W Homo sapiens cDNA clone IMAGE:259599 3'
3033	12269		2.84	1.0E-103	BE744722.1	EST_HUMAN	6015731137f NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3358	12588	21725	3.16	1.0E-103	AW288245.1	EST_HUMAN	U1-H-BW0-ajt-h-11-0-U1_s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3418	12643	21772	1.28	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1458 protein, partial cds
3737	12957		24.88	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3776	12994	22110	1.05	1.0E-103	AA485663.1	EST_HUMAN	ab10di12_s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element;
3980	13194	22302	2.68	1.0E-103	T23683.1	EST_HUMAN	seq340_b4HB3MA-Cot108+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109-10-Bio 7-3'
4838	14025	23119	0.83	1.0E-103	BE900203.1	EST_HUMAN	601673135f NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
5972	15186	24604	1.63	1.0E-103	AIS90071.1	EST_HUMAN	tm58b05_s1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS;
5972	15186	24605	1.63	1.0E-103	AIS90071.1	EST_HUMAN	tm58b05_s1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS;
6017	14507	23575	1.82	1.0E-103	5032282 NT		Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6017	14507	23576	1.62	1.0E-103	5032282 NT		Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
6224	15405	24846	3.42	1.0E-103	BE748158.1	EST_HUMAN	601571537f NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3836545 5'
8404	15585	25042	3.78	1.0E-103	AIS90071.1	EST_HUMAN	tm58b05_s1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS;
8404	15585	25043	3.78	1.0E-103	AIS90071.1	EST_HUMAN	tm58b05_s1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769 Q13769 ANONYMOUS;
8809	16004	25464	3.8	1.0E-103	6005921 NT		Homo sapiens triple functional domain (PTPRF interacting) (TR10), mRNA
8809	16004	25465	3.8	1.0E-103	6005921 NT		Homo sapiens triple functional domain (PTPRF interacting) (TR10), mRNA
7093	16270	25747	2.45	1.0E-103	Z37876.1	NT	H_sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7112	16289	25770	2.96	1.0E-103	AW063367.1	EST_HUMAN	EST375749 MAGE genes, MAGH Homo sapiens cDNA
7146	16323	25805	14.27	1.0E-103	AIR78956.1	EST_HUMAN	eu51g04_s1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O62084 Q62084
7319	16538	26024	7.29	1.0E-103	A1792759.1	EST_HUMAN	00206_v6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:O62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7410	16822	28115	1.75	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA	
7410	16822	28116	1.75	1.0E-103	11424061	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA	
7421	16632	28124	2.88	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	
7421	16632	28125	2.88	1.0E-103	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	
7814	17129	28659	2.68	1.0E-103	AU136283.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE103823 5'	
7982	18417	25904	5.33	1.0E-103	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30	
8230	17359	26898	3.38	1.0E-103	BE844611.1	EST_HUMAN	7668a10_xr Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE3287610 3' similar to contains MER28 13 MER28 repetitive element;	
8310	17415		2.27	1.0E-103	AF224668.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds	
8340	17437		2.53	1.0E-103	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA	
8546	17571	23892	2.58	1.0E-103	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds	
239	9518	18847	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp584H1072_r1_584 (synonym: fibr2) Homo sapiens cDNA clone DKFZp584H1072 5'	
239	9518	18848	2.5	1.0E-104	AL037549.3	EST_HUMAN	DKFZp584H1072_r1_584 (synonym: fibr2) Homo sapiens cDNA clone DKFZp584H1072 5'	
1853	11050	20251	1.92	1.0E-104	4502428	NT	Homo sapiens bone morphogenic protein 8 (osteogenic protein 2) (BMP8) mRNA	
2160	11358	20576	23.83	1.0E-104	AA132875.1	EST_HUMAN	x022c06_s1 Strategene clone (#867204) Homo sapiens cDNA clone IMAGE387626 3' similar to gb:Z14146_m11_CDS Glycoprotein PRECURSOR (HUMAN);	
2170	11367	20588	10.72	1.0E-104	BE744628.1	EST_HUMAN	601577480F1 NIH_MCC_9 Homo sapiens cDNA clone IMAGE3826438 5'	
2337	11530	20752	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-1110900-214-f12 CT0249 Homo sapiens cDNA	
2337	11530	20753	10.57	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-1110900-214-f12 CT0249 Homo sapiens cDNA	
2400	11693	20811	7.19	1.0E-104	6031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA	
2467	11658	20878	4.12	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	
2467	11658	20879	4.12	1.0E-104	7662125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA	
2823	12092	21185	13.3	1.0E-104	M34871.1	NT	Human lymphocytic antigen CD56/MEM43 mRNA, complete cds	
2867	12105		2.28	1.0E-104	Y11151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II	
3230	12464	21598	1.01	1.0E-104	AU138926.1	EST_HUMAN	AU138926 OVARC1 Homo sapiens cDNA clone OVARC10000536 5'	
3368	12596		2.12	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end	
3579	12801	21827	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds	
3579	12801	21828	0.91	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds	
3918	13134	22251	1.03	1.0E-104	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds	
4112	13319	22419	0.85	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31607	
4371	13573	22689	4.33	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)	
4610	13804	22894	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA	
4610	13804	22895	0.94	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5855	15073	24484	8.42	1.0E-104	A1768797.1	EST_HUMAN	wj03b12_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
5855	15073	24485	8.42	1.0E-104	A1768797.1	EST_HUMAN	KIAA0132 PROTEIN .contains element LTR repetitive element;
5949	15281	24713	2.3	1.0E-104	BE314182.1	EST_HUMAN	wj03b12_x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145
5949	15281	24714	2.3	1.0E-104	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN .contains element LTR repetitive element;
6176	15358	24798	1.82	1.0E-104	11425572	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6858	16048	25512	7.16	1.0E-104	AF091395.1	NT	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6858	16048	25513	7.16	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
6890	15593	25059	5.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080800-248-F07 HT0619 Homo sapiens cDNA
6890	15593	25080	5.48	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080800-248-F07 HT0619 Homo sapiens cDNA
7108	16283	25763	5.13	1.0E-104	BE791713.1	EST_HUMAN	6011581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7108	16283	25764	5.13	1.0E-104	BE791713.1	EST_HUMAN	6011581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
7193	16370	25850	4.72	1.0E-104	AU130765.NT2RP3	Hom sapiens cDNA clone NT2RP30013698 5'	Hom sapiens AU130765.NT2RP3 Homo sapiens cDNA clone NT2RP30013698 5'
7218	16395	25879	5.56	1.0E-104	U68535.1	NT	Human beta4-integrin (ITGB4) gene, exons 19-20; 21, 22, 23-24 and 25
7844	17036	26551	1.89	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0385-310700-021-B09 HT0885 Homo sapiens cDNA
7844	17038	26552	1.89	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0385-310700-021-B09 HT0885 Homo sapiens cDNA
7872	17081	28585	5.29	1.0E-104	BF684288.1	EST_HUMAN	602141215F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4302507 5'
9159	17953		1.43	1.0E-104	BE363892.1	EST_HUMAN	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36598676 5'
283	11937	18691	4.46	1.0E-105	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (prolease nexin-II, Alzheimer disease) (APP), mRNA
431	9298	18398	17.77	1.0E-105	4505150	NT	Hom sapiens Mais1 (mouse) homolog (MEIS1) mRNA
601	9848	18966	8.49	1.0E-105	AF032897.1	NT	Hom sapiens potassium channel subunit (HERG-3) mRNA, complete cds
601	9848	18967	8.49	1.0E-105	AF032897.1	NT	Hom sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1654	10888		3.22	1.0E-105	AB020981.1	NT	Hom sapiens mRNA for cyclin B2, complete cds
1789	10999	20194	1.68	1.0E-105	AL163280.2	NT	Hom sapiens chromosome 21 segment HS21C080
1894	11101	20292	2.64	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds
2290	11354	20572	5.87	1.0E-105	AA318369.1	EST_HUMAN	EST20609 Spleen Homo sapiens cDNA 5' end similar to autoimmune antigen Ku, p70/p50 subunit
2290	11485		0.92	1.0E-105	BE891766.1	EST_HUMAN	601434491F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918511 5'
2680	11862		0.89	1.0E-105	AA584808.1	EST_HUMAN	h010d05:s1 NCI_OGAP_Phe1 Homo sapiens cDNA clone IMAGE:1102653
2680	12204		3.44	1.0E-105	AJ228041.1	NT	Hom sapiens 859 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3289	12530	21661	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158143 5'
3289	12530	21662	1.73	1.0E-105	BF347753.1	EST_HUMAN	602022595F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158143 5'
3325	12554	21690	1.01	1.0E-105	7304922	NT	Hom sapiens bromodomain adjacent to zinc finger domain 2B (BAZ2B), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3325	12554	21691	1.01	1.0E-105	7304822	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4075	13285	22383	2.88	1.0E-105	AW7861688.1	EST_HUMAN	EST373781 MAGE resequences, MAGG Homo sapiens cDNA
4755	13946	23046	0.64	1.0E-105	BE888881.1	EST_HUMAN	601445823F NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850156 5'
4755	13948	23047	0.84	1.0E-105	BE888881.1	EST_HUMAN	601445823F NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3850156 5'
4957	14144		5.22	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5137	14315	23406	0.98	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0798 protein, partial cds
5195	14371	23458	0.69	1.0E-105	AW0686015.1	EST_HUMAN	EST378088 MAGE resequences, MAGI Homo sapiens cDNA
6079	14525	23546	3.33	1.0E-105	1141919.8	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6079	14525	23547	3.33	1.0E-105	1141919.8	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6473	15670	25141	8.43	1.0E-105	T05087.1	EST_HUMAN	EST02875 Fetal brain, Strategene (Cat#336206) Homo sapiens cDNA clone HFBCR32
6785	16880	25440	3.95	1.0E-105	AW016878.1	EST_HUMAN	U1-H-B10p-ab1-b12-q-11 s1 NCI CGAP Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
7508	16712	26200	6.62	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
7782	16977	26490	2.18	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(N) collagen, exon 31.
7830	17022	26537	2.28	1.0E-105	7705638	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
8115	17249	26789	2.41	1.0E-105	AW027554.1	EST_HUMAN	wu74f07_x1 Seares_thymus_NHFTt Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR_P87892
154	9438		1.85	1.0E-106	AW503208.1	EST_HUMAN	U1-H-B10p-ab1-q-7-q-11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
210	9490	18623	1.58	1.0E-106	A1685085.1	EST_HUMAN	tu78c01_x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
548	9769	18924	1.98	1.0E-106	AW965556.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
8111	9858	18977	1.87	1.0E-106	J0146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
8112	9858	18977	2.89	1.0E-106	J0146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1511	10725	18987	1.01	1.0E-106	AF148712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1676	10888	20074	4.47	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1694	10806	20092	1.72	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1772	10982	20172	5.79	1.0E-106	AA527446.1	EST_HUMAN	ng41cd5_s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
1772	10982	20173	5.79	1.0E-106	AA527446.1	EST_HUMAN	ng41cd5_s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
2283	11478	20700	7.27	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2469	11660	20881	4.02	1.0E-106	AF003528.1	NT	Homo sapiens X-linked arachidic acid/dihydroxy acid/dysplasia protein gene (EDA), exon 2 and ranking repeat regions
2561	11747	20987	1.21	1.0E-106	U64875.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2563	11749	20969	1.18	1.0E-106	BE260201.1	EST_HUMAN	601149783F NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502461 5'
2713	11892	21110	9.2	1.0E-106	AI276526.1	EST_HUMAN	q176h10_x1 Seares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1878307 3'

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2777 10648		19821	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2777 10648		19822	2.45	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2828 12067		21188	2.2	1.0E-106	BE384296.1	EST_HUMAN	601272675F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:36138185
2892 12129		21263	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
2892 12129		21264	6.26	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3145 12380		21511	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3145 12380		21512	2.8	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3352 12580		21720	0.65	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type II B, complete cds
3790 13008		22123	0.99	1.0E-106	AF001445.1	NT	Homo sapiens core binding factor alpha 1 subunit (CBFA1) gene, exon 2
4015 13227		22328	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE sequences, MAGN Homo sapiens cDNA
4015 13227		22329	10.33	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE sequences, MAGN Homo sapiens cDNA
4034 13244		22347	1.34	1.0E-106	5729729	NT	Homo sapiens API5-like 1 (APISL1), mRNA
4601 13795		22885	0.73	1.0E-106	BE14286.1	EST_HUMAN	MRO-HT065-1420200-008-010 HT065 Homo sapiens cDNA
4918 14106		232200	1.48	1.0E-106	U31520.1	NT	Human alpha mannosidase II mRNA, complete cds
5381 14610		23722	2.35	1.0E-106	AA781155.1	EST_HUMAN	aj24b09_st Soares_teslis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN PHPS1_2 (HUMAN);
5708 14927		24322	14.75	1.0E-106	BF679574.1	EST_HUMAN	602154012F1 NIH MGC_83 Homo sapiens cDNA clone IMAGE:42950675
5836 15053		24460	18.72	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (X72), mRNA
5836 15053		24461	18.72	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (X72), mRNA
6243 15424		24865	4.9	1.0E-106	AA663779.1	EST_HUMAN	ae72e07_s1 Striagene schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X655873 KINESIN HEAVY CHAIN (HUMAN);
6281 15442		24881	4.59	1.0E-106	11428617	NT	Homo sapiens XPMC2 protein (LOC57109), mRNA
6341 15521		24968	8.36	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
6341 15521		24969	8.36	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
6458 15655		25125	6.43	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5' ar68a07_x1 Barsleed aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X06233 CALGRANULIN B (HUMAN);
6458 15655		25126	6.43	1.0E-106	BE741408.1	EST_HUMAN	ty62a05_x1 NCI CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:CA6_HUMAN Q05084_69 KDIISLET CELL AUTOANTIGEN_1;
6517 15713		25178	2.23	1.0E-106	A1523066.1	EST_HUMAN	6816 15011 25474 2.41 1.0E-106 AA825307.1 EST_HUMAN oc67e08_s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
6682 15877		25336	2.64	1.0E-106	AA1654123.1	EST_HUMAN	6816 15011 25475 2.41 1.0E-106 AA825307.1 EST_HUMAN oc67e08_s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
7148 16325		25808	6.74	1.0E-106	AA804417.1	EST_HUMAN	7148 16325 25808 6.74 1.0E-106 AA804417.1 EST_HUMAN np57b10_s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
7148 16325		25809	6.74	1.0E-106	AA804417.1	EST_HUMAN	7148 16325 25809 6.74 1.0E-106 AA804417.1 EST_HUMAN np57b10_s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7165	16342	25821	2.68	1.0E-108	AW363269.1	EST_HUMAN	RC0-CT0318-201199-031-a11 CT0318 Homo sapiens cDNA
7221	16398	25882	2.79	1.0E-108	AL168202.2	NT	Homo sapiens chromosome 21 segment HS21C012
7472	16880	26162	6.77	1.0E-108	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857368 5'
7472	16880	26163	6.77	1.0E-108	BF032755.1	EST_HUMAN	601453481F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857368 5'
7639	16830	26927	2.56	1.0E-108	J05200.1	NT	Homo sapiens cDNA clone IMAGE:3857368 5'
7639	16830	26928	2.56	1.0E-108	J05200.1	NT	Homo sapiens cDNA clone IMAGE:3857368 5'
7946	17086	26815	2.41	1.0E-108	BE257385.1	EST_HUMAN	601109219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
8077	17212	26743	1.82	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8077	17212	26744	1.82	1.0E-108	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
8334	18151		4.43	1.0E-108	AW410405.1	EST_HUMAN	mg5n1_x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
8618	17615	23968	2.49	1.0E-108	BS894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916524 5'
8618	17615	23969	2.49	1.0E-108	BS894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916524 5'
8843	17752		5.27	1.0E-108	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
240	9519		3.88	1.0E-107	A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
269	9544		1.37	1.0E-107	X804459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
636	9881	18005	1.88	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN 26 antigen mRNA, partial cds
823	10081	19213	1.06	1.0E-107	X804459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
896	10131	19293	1.89	1.0E-107	X804459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
976	10208	19363	11.69	1.0E-107	AF154121.1	NT	
1285	10590	19861	1.31	1.0E-107	AB032253.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1550	10764	18838	4.8	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120500-358-a05 HT0540 Homo sapiens cDNA
1724	10936	20119	5.69	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
2175	11372	20594	1.07	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2330	11523	20745	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2330	11523	20746	10.58	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2500	11689	20809	2.56	1.0E-107	BE732460.1	EST_HUMAN	6015657619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2500	11689	20810	2.56	1.0E-107	BE732460.1	EST_HUMAN	6015657619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2867	12205	21340	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
2867	12205	21341	3.76	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-180100-001-d03 CN0031 Homo sapiens cDNA
3065	12301	21425	3.94	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2), mRNA
3818	13034	22145	4.53	1.0E-107	AF020671.1	NT	Hom sapiens myotubularin (MTM1) gene, exon 9
5597	14821	24198	2.68	1.0E-107	BE867489.1	EST_HUMAN	601442658F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3848494 5'
6239	15420	24860	1.82	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-af-c-08-0-U1_r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078310 5'

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6239	15420	24861	1.82	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BND-alp-s-0B-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:30798310 5'
7293	16512	26004	3.78	1.0E-107	A1392850.1	EST_HUMAN	Ig10606_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICDI
7520	16725	28216	1.91	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
7531	16736	28228	2.86	1.0E-107	BF686511.1	EST_HUMAN	602129865F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
7898	17058	28579	4.19	1.0E-107	BE540550.1	EST_HUMAN	601066881F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
7831	16407	25891	4.65	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
7831	16407	25892	4.65	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
8450	18283		5.84	1.0E-107	AA001415.1	EST_HUMAN	z845601_s1 Soares retina N254H Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR,b1
8478	18147		1.52	1.0E-107	11418318	NT	THR repetitive element
181	9481		1.35	1.0E-108	AA341834.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1(GTSE1), mRNA
9812	10195	19350	1.46	1.0E-108	BE296042.1	EST_HUMAN	EST47383 Fetal muscle Homo sapiens cDNA 5' end
1272	10487	19645	3.83	1.0E-108	Y18600.1	NT	Homo sapiens NF2 gene
20468	11247	20457	2.49	1.0E-108	BF026728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
							b626b10_x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:283859 3' similar to gb:X53777 60S
2391	11584	20802	107.38	1.0E-108	BE208694.1	EST_HUMAN	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3323	12552	21688	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3323	12552	21687	0.71	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3802	13020	22132	1.04	1.0E-108	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4139	13345	22445	1.37	1.0E-108	AW584438.1	EST_HUMAN	h12a11_x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE
4525	13721	22816	6.72	1.0E-108	U72861.1	NT	P55194 SH3-BINDING PROTEIN 3BP-1;
4525	13721	22817	6.72	1.0E-108	U72861.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4818	14007	23107	3.11	1.0E-108	7681979	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4839	14126	23222	0.77	1.0E-108	AW504789.1	EST_HUMAN	U1-HF-BND-ain-e-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
4968	14155	23247	2.17	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5185	14344	23433	0.98	1.0E-108	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5187	14373	23460	1.08	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
5454	14680	23840	3.03	1.0E-108	BB868016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5454	14680	23841	3.03	1.0E-108	BB868016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5729	14948	24346	5.76	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5729	14948	24347	5.76	1.0E-108	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds	
6146	15330	24766	5.4	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPRC5B), mRNA	
6269	15449	24888	2.13	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS2) mRNA	
6485	15682		2.74	1.0E-108	AF03500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds	
7260	15591	25052	2.23	1.0E-108	BE535227.1	EST_HUMAN	60118622172 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'	
7404	14373	23460	1.9	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)	
7632	16833	26330	1.64	1.0E-108	AF2223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-9 and partial cds, alternatively spliced	
7820	17013	26527	5.69	1.0E-108	AW/866185.1	EST_HUMAN	EST378238 MAGE resequences, MAGI Homo sapiens cDNA	
7810	17125		2.41	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA	
7866	17145	26879	1.7	1.0E-108	D63539.1	NT	Homo sapiens COL4A6 gene for a(V) collagen, exon 23	
8833	17623	23973	3.18	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00337 protein, partial cds	
8040	17882		6.89	1.0E-108	BF346356.1	EST_HUMAN	60201857171 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4154297 5'	
44	9340	18447	1.37	1.0E-109	AW803116.1	EST_HUMAN	IL2UM0772-260400-079-D06 UM077 Homo sapiens cDNA	
67	9352	18486	2.74	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds	
223	9502	18633	0.83	1.0E-109	11422488	NT	Homo sapiens hypothetical protein FLJ111316 (FLJ111316), mRNA	
232	9510	18638	6.14	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA	
473	9726	18858	3.14	1.0E-109	4507712	NT	Homo sapiens tetraspaninypeptide repeat domain 2 (TTC2) mRNA	
605	9852	18971	16.2	1.0E-109	AB023218.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds	
605	9852	18972	16.2	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds	
1210	10429	19585	41.98	1.0E-109	M28659.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	
1211	10429	19585	22.4	1.0E-109	M28659.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds	
1528	10742	19914	1.35	1.0E-109	BE283673.1	EST_HUMAN	601186222172 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:28595363 5'	
1528	10742	19915	1.35	1.0E-109	BE283673.1	EST_HUMAN	601186222172 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:28595363 5'	
1840	11048	20238	5.02	1.0E-109	D13843.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds	
2206	11403	20628	4.37	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
2215	11412	20836	2.87	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6	
2585	11771	20891	3.53	1.0E-109	AI022328.1	EST_HUMAN	ow8sa01.x1 Soares_fetal_liver_spleen INFSL_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197_002197 CIRCULATING CATHODIC ANTIGEN;	
2585	11771	20892	3.53	1.0E-109	AI022328.1	EST_HUMAN	ow8sa01.x1 Soares_fetal_liver_spleen INFSL_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197_002197 CIRCULATING CATHODIC ANTIGEN;	
2586	11772	20983	2.16	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retin)(GUCA1A) mRNA	

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3023	12259	21387	1.32	1.0E-109	N85180_1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3366	12594	21733	1.33	1.0E-109	AV1893192_1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3366	12594	21734	1.33	1.0E-109	AV1893192_1	EST_HUMAN	CM3-NN0009-190400-150-110 NN0009 Homo sapiens cDNA
3491	12715	21851	1.1	1.0E-109	AF2406598_1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3828	13046		1.43	1.0E-109	BE146144_1	EST_HUMAN	MRO-HT0209-110400-108-ab4 HT0209 Homo sapiens cDNA MRO-HT0209-110400-108-ab4 HT0209 Homo sapiens cDNA
4128	13335	22434	4.35	1.0E-109	AI855417_1	EST_HUMAN	ts985016_x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WP:F53A2.8 CE1610_1;
4144	13350	22450	1.02	1.0E-109	AA662274_1	EST_HUMAN	nu88c12.51 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW_GTTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;
4144	13350	22451	1.02	1.0E-109	AA662274_1	EST_HUMAN	nu88c12.51 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1218262 3' similar to SW_GTTT2_HUMAN P30712 GLUTHATHIONE S-TRANSFERASE THETA 2;
4398	13599	22700	2.55	1.0E-109	4504208_1	NT	Homo sapiens glutamylate cyclase activator 1A (retina) (GUCA1A) mRNA
4600	13794	22884	1.28	1.0E-109	7882053_1	EST_HUMAN	nu88c12.51 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2859636 5'
5084	14264	23350	0.72	1.0E-109	BE283673_1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5084	14264	23351	0.72	1.0E-109	BE283673_1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859636 5'
5340	14570	23645	3.5	1.0E-109	5174822_1	NT	Homo sapiens placental protein 11 (serine protease) (P11) mRNA
6319	156501	24846	3.53	1.0E-109	11432574_1	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
6320	15502	24947	5.4	1.0E-109	BF182707_1	EST_HUMAN	601809485F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6320	15502	24948	5.4	1.0E-109	BF182707_1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
6692	15887	25346	12.39	1.0E-109	BE1787540_1	EST_HUMAN	601479417F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3882124 5'
6692	15887	25347	12.39	1.0E-109	BE1787540_1	EST_HUMAN	601479417F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3882124 5'
7385	16589	26087	25.47	1.0E-109	BF694483_1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
7539	16744	28237	2.35	1.0E-109	7662279_1	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744), mRNA
7539	16744	28238	2.35	1.0E-109	7662279_1	NT	Homo sapiens KIAA0744 gene product histone deacetylase 7 (KIAA0744), mRNA
7885	16884	28392	1.97	1.0E-109	AU121370_1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone IMAGE:301439 5' similar to
7909	17124	28655	2.23	1.0E-109	4502838_1	NT	z008b12.11 Scarce_fetal_lung_NblL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:S:33869_S43869_p54-Delta stress-activated protein kinases rat;
7945	17085	28614	6.23	1.0E-109	W18510_1	EST_HUMAN	Homo sapiens SNF5/N11 gene, exon 6
8529	11412	20636	2.3	1.0E-109	Y17123_1	NT	Homo sapiens SNF5/N11 gene, exon 6
8761	11412	20636	1.98	1.0E-109	Y17123_1	NT	Homo sapiens gene for AF-6, complete cds
8883	17778	23944	3.23	1.0E-109	AB011389_1	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
3	9300	18402	1.41	1.0E-110	7549804_1	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
39	9335	18441	4.02	1.0E-110	5803073_1	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
39	9335	18442	4.02	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
109	9300	18402	1.41	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
289	9572	18705	0.65	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
533	9784	18907	0.95	1.0E-110	0845501	NT	Human dihydrobrevin (DTN) gene, exon 20
1188	10409	19563	0.6	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCR) mRNA
1286	10501	19662	2.39	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1889	11096	20287	1.11	1.0E-110	BE379477.1	EST_HUMAN	6011237545F_NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2025	11226		1.68	1.0E-110	BF503896.1	EST_HUMAN	U1-H-B14-as-p-O-U..S1_NCL_CGAP_Sub8_Homo sapiens cDNA clone IMAGE:3085784 3'
2793	12033		0.97	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
2898	10501	19662	1.14	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3052	12288		1.19	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
3158	12393	21527	2.68	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3158	12393	21528	2.68	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4185	13389	22488	2.18	1.0E-110	M15918.1	NT	Homo sapiens antigen small nuclear ribonucleoprotein E pseudogene
4636	13830	22917	2.23	1.0E-110	A0171213.1	EST_HUMAN	OU32B10.x1_Soares_NFL_T_GBC_S1_Homo sapiens cDNA clone IMAGE:1627963 3' similar to SWuN121_RAT_P52591_NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN PCM 121 ; AUJ117812_HEMBA1_Homo sapiens cDNA clone HEMBA1002241 5'
4656	13850	22945	2.83	1.0E-110	AU117812.1	EST_HUMAN	Homologous gene
4983	14180		1.54	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5324	14556	23626	2.32	1.0E-110	BE299406.1	EST_HUMAN	601118710F1_NIH_MGC_17_Homo sapiens cDNA clone IMAGE:3028538 5'
5548	14772	24139	7.74	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5548	14772	24140	7.74	1.0E-110	11419323	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5971	18068	24603	4.49	1.0E-110	M655112.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
6262	15443	24882	9.01	1.0E-110	AV714276.1	EST_HUMAN	AV714276_DCB_Homo sapiens cDNA clone DCBCGE01 5'
6262	15443	24883	9.01	1.0E-110	AV714276.1	EST_HUMAN	AV714276_DCB_Homo sapiens cDNA clone DCBCGE01 5'
6278	15458	24899	2.8	1.0E-110	AB020675.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
6949	16127	25595	3.81	1.0E-110	AW838394.1	EST_HUMAN	QV2-LT0053-D20400-119-ed4_LT0053_Homo sapiens cDNA clone GALK2, mRNA
7176	16353	25831	4.98	1.0E-110	11432732	NT	H.sapiens mRNA for myotonic dystrophy protein kinase like protein
7333	16549	26039	4.23	1.0E-110	YI12337.1	NT	60115656045F1_NIH_MGC_21_Homo sapiens cDNA clone IMAGE:3840433 5'
7538	16743	26235	4.26	1.0E-110	BT734357.1	EST_HUMAN	ZW679021_NIH_MGC_21_Homo sapiens cDNA clone IMAGE:3840433 5'
7538	16743	26236	4.26	1.0E-110	BET34357.1	EST_HUMAN	60115656045F1_NIH_MGC_21_Homo sapiens cDNA clone IMAGE:3840433 5'
7979	16414	25901	2.82	1.0E-110	AA446529.1	EST_HUMAN	G1145816_FKBPS4 :
8342	17439		3.73	1.0E-110	BB897218.1	EST_HUMAN	6011439784F1_NIH_MGC_72_Homo sapiens cDNA clone IMAGE:3924548 5'

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8469	17522		8.6	1.0E-110	AV062258.1	EST_HUMAN	IL0-BT0163-040899-094-910 BT0163 Homo sapiens cDNA
8725	17677		2.84	1.0E-110	AB011389.1	NT	Homo sapiens gene for AF-6, complete cds
8866	18305		3.72	1.0E-110	BF384546.1	EST_HUMAN	PM3-NN1082-140900-008-112 NN1082 Homo sapiens cDNA
9158	11226		1.83	1.0E-110	BF508896.1	EST_HUMAN	U1-H-B14-aes-b-05-U1-s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
178	9458		27.48	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
201	8481	18814	0.78	1.0E-111	4758807	NT	Homo sapiens GTPase activating protein-like (GAP) mRNA
742	9983		2.19	1.0E-111	BF035327.1	EST_HUMAN	60145833-171 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882086 5'
751	9992	19136	4.09	1.0E-111	83983092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
835	10168	19325	3.26	1.0E-111	M25142.1	NT	Human cardiac alpha-1 myosin heavy chain (MYH6) gene, exons 32 to 34
3678	12898	22019	0.83	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3678	12898	22020	0.83	1.0E-111	6912641	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4153	13359	22460	1.88	1.0E-111	7661569	NT	Human protein DKFZP44A156 protein (DKFZP44D156), mRNA
4321	13522	22617	4.54	1.0E-111	K02268.1	NT	Human enkephalin B (enkB) gene, exon 4 and 3' flank and complete cds
4752	13943	23045	1.01	1.0E-111	4605778	NT	Homo sapiens phosphorylase kinase, alpha 1 (muscle) (PHKKA1), mRNA
6271	15451	24890	2.83	1.0E-111	BF386228.1	EST_HUMAN	IL2-NT0101-280700-114-EG3 NT0101 Homo sapiens cDNA
6538	15734	25198	3.4	1.0E-111	U66533.1	NT	Human beta-4 integrin (ITGB4) gene, exon 13
6720	15915		8.85	1.0E-111	BF214802.1	EST_HUMAN	601847132F NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
6740	15935	25395	18.91	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
6740	15935	25396	18.91	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
6800	16985	25453	4.59	1.0E-111	AF091395.1	NT	Homo sapiens Tio isoform mRNA, complete cds
7124	16301	25782	2.56	1.0E-111	AA504160.1	EST_HUMAN	aa589251 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:8525170 3' similar to gbl_002335
7158	16335	25818	7.75	1.0E-111	AA131248.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN); 231101-11 Scores: pregnant uterus Nb-HPV Homo sapiens cDNA clone IMAGE:503545 5'
7613	16816	26312	5.35	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
8299	17407	26932	4.68	1.0E-111	11417901	NT	Homo sapiens megalomina (disrupted in balanced translocation) 1 (MN1), mRNA
8880	17763	23936	1.5	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAOB08 5'
8982	18086	23804	2.08	1.0E-111	W22582.1	EST_HUMAN	72C9 Human retina cDNA Tsp509(-)-cleaved sublibrary Homo sapiens cDNA not directional
9128	14505	23589	1.53	1.0E-111	AB035358.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
614	9859	18978	0.98	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
618	9861	18980	6.43	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
618	9861	18981	6.43	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (StAR) gene, exon 5
638	9883	19007	1.7	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-aes-g-04-0-U1-s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
638	9883	19008	1.7	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-aes-g-04-0-U1-s1 NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1009	10240	18392	3.97	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1089	10295	19444	1.67	1.0E-112	P52712	SWISSPROT	ZINC FINGER PROTEIN 135
1659	10872	20054	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1858	10872	20055	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	11684	20883	3.23	1.0E-112	BE066859.1	EST_HUMAN	601442614F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3846858 5'
3043	12280		0.82	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3211	12445	21577	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-509 BT0642 Homo sapiens cDNA
3211	12445	21578	1.35	1.0E-112	BE083092.1	EST_HUMAN	RC2-BT0642-030400-021-509 BT0642 Homo sapiens cDNA
3346	12565	21703	0.61	1.0E-112	A026511.1	EST_HUMAN	wk45b12_X1 NCI_CGAP_Pt22 Homo sapiens cDNA clone IMAGE:2418335 3' similar to gbm:MS1650_mer1
3853	13079	22195	0.78	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0598-090300-113-009 BT0598 Homo sapiens cDNA PRECURSOR (HUMAN);
4604	13768	22888	0.62	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4793	13953	23053	5	1.0E-112	A0937832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4793	13953	23054	5	1.0E-112	A0937832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5521	14748	24114	37.86	1.0E-112	N46046.1	EST_HUMAN	y65d07_r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273229 5'
6526	15722	25187	3.4	1.0E-112	AU18051.1	EST_HUMAN	AU18051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
6796	15951	25408	3.08	1.0E-112	BE887683.1	EST_HUMAN	601443151F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847285 5'
6796	15951	25409	3.08	1.0E-112	BE887683.1	EST_HUMAN	601443151F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:3847285 5'
7359	16575	26067	2.68	1.0E-112	AW863327.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SH0009 Homo sapiens cDNA
7522	16127	26218	5.43	1.0E-112	A249890.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
7682	16862	26364	1.98	1.0E-112	BE280479.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138898 5'
7739	16835	28443	4.66	1.0E-112	AW377670.1	EST_HUMAN	PM0-C70237-141058-001-h02 CT0237 Homo sapiens cDNA
8850	17757		1.37	1.0E-112	Af106856.1	NT	Homo sapiens adenylyl/succinate lyase gene, complete cds
750	9891	19134	5.03	1.0E-113	A1365588.1	EST_HUMAN	bc85f0_X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
750	9891	19135	5.03	1.0E-113	A1365588.1	EST_HUMAN	bc85f0_X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
950	10183	19339	17.13	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1527	10741	19813	3.48	1.0E-113	A1365588.1	EST_HUMAN	bc85f0_X1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1868	11948	20309	1.11	1.0E-113	Af240775.1	NT	Homo sapiens eIF4E transporter mRNA, complete cds
2084	11265	20478	0.98	1.0E-113	BF15218.1	EST_HUMAN	UI-H-BW1-anif-f-03-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3094	12330	21456	1.75	1.0E-113	A1223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
6301	18134		3.33	1.0E-113	BE780888.1	EST_HUMAN	601469455F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5439	14666	23819	6.09	1.0E-113	AU127214	EST_HUMAN	AU127214 NT2RP21 Homo sapiens cDNA clone NT2RP2000807 5'
5625	14849	24231	4.06	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE200274 5'
5698	14818	24312	2.38	1.0E-113		NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database & Source	Top Hit Descriptor
6803	159988	254568	3.64	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
6803	159989	254567	3.64	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
7883	16882	26390	1.75	1.0E-113	AV500519.1	EST_HUMAN	U1-HF-BN0-akib-12-01.U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
7881	16880	26397	3.01	1.0E-113	AV630291.1	EST_HUMAN	hh81a05.y1 NCI_CGAP_GUT_Homo sapiens cDNA clone IMAGE:2989176 5' similar to TR:O60327 O60327
7891	16890	26398	3.01	1.0E-113	AV630291.1	EST_HUMAN	KIAA0584 PROTEIN:
7812	17005	26518	3.6	1.0E-113	BE292968.1	EST_HUMAN	hh81a05.y1 NCI_CGAP_GUT_Homo sapiens cDNA clone IMAGE:2989366 5'
8031	17168	26708	3.34	1.0E-113	AA580720.1	EST_HUMAN	nc80b03.11 NCI_CGAP_GCT_Homo sapiens cDNA clone IMAGE:787059 5' similar to SW.FEN1_HUMAN
8031	17168	26707	3.34	1.0E-113	AA580720.1	EST_HUMAN	P39748 FLAP ENDONUCLEASE-1:
60	9356	18474	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9356	18475	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	9356	18476	1.21	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
651	9887	19023	8.43	1.0E-114	770551.1	EST_HUMAN	yd15dn.s1 Staras fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:1082688 3' similar to gb:A21187 ALPHAGLOBULIN PRECURSOR (HUMAN).contains Alu repetitive element;
1078	10303	19454	1.39	1.0E-114	8823067	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080).mRNA
1320	10535	19899	4.23	1.0E-114	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1).mRNA
1619	10832	20007	4.87	1.0E-114	6631054	NT	Homo sapiens minichromosome maintenance deficient (S_cerevisiae) 3 (MCM3).mRNA
1847	10881	20042	8.45	1.0E-114	6678073	NT	Homo sapiens nucleopore-like protein 1 (NLP_1).mRNA
2220	11417	20842	1.26	1.0E-114	AB002374.1	NT	Human mRNA for KIAA0376 gene. partial cds
2758	9342	18450	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2758	9342	18451	1.22	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3085	12331	21457	2.27	1.0E-114	X04086.1	NT	Human gene for catalase (EC:1.11.1.6) exon 2 mapping to chromosome 11, band p13
3136	12371	21502	1.26	1.0E-114	BF206374.1	EST_HUMAN	60186932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3862	13206	22312	1.54	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4385	13586	22688	0.77	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec).mRNA, complete cds
5198	14347	23435	1.03	1.0E-114	BE275324.1	EST_HUMAN	60112273F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5'
5206	14381	23487	0.94	1.0E-114	AF004849.1	NT	Human PKY protein kinase mRNA, complete cds
6201	15382	24823	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6201	15382	24824	9.02	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
6425	15822	25086	2.57	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2).mRNA

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Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6680	15875	25334	4.26	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
6706	15901	25362	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6706	15901	25363	7.86	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
6884	16075		10.62	1.0E-114	AW327455.1	EST_HUMAN	dQ03705_x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 S
6900	15606	25072	4.01	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
7368	16584		15.17	1.0E-114	BE302666.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN), gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE)
7745	16941	26452	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cdABA08S'
7745	16941	28453	3.76	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cDNA Homo sapiens cDNA clone cdABA08S'
8767	18368		2.74	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
9033	17878	23891	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ042K10.2), mRNA
9033	17878	23892	3.22	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ042K10.2), mRNA
23	9319	18423	5.81	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
127	9410	18544	2.5	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POTR2A) mRNA
131	9414		16.52	1.0E-115	4557887	NT	Homo sapiens keratin 10 (KRT10) mRNA
297	9570	18702	2.23	1.0E-115	AV8604759.1	EST_HUMAN	Q164JUM094-30300-156-b08 JMU094 Homo sapiens cDNA
542	9793	18916	0.6	1.0E-115	A1339206.1	EST_HUMAN	Q106101_x1 NCL_CGAP_GCA_Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:000536 000536
542	9793	18917	0.6	1.0E-115	A1339206.1	EST_HUMAN	TTF-I INTERACTING PEPTIDE 5;
796	10035	19185	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAK1), mRNA
796	10035	19186	1.09	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAK1), mRNA
798	10037	19188	349.13	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTTH1) mRNA
1808	11017	20210	1.36	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2048	11249	20459	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 S'
2048	11249	20460	1.05	1.0E-115	BE745469.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 S'
2054	11253	20468	0.94	1.0E-115	AB007902.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2264	11459	20678	1.92	1.0E-115	AF23124.1	NT	Homo sapiens testicar-1 mRNA, complete cds
3079	12315	21437	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBAB gene)
3079	12315	21438	5.51	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBAB gene)
3449	12674	21809	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4019	13231	22334	3.93	1.0E-115	AB0023348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4283	13456	22548	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4305	13598	22697	3.42	1.0E-115	6912659	NT	Homo sapiens siRNA-3 (SIRT3), mRNA
4428	13628	22722	4.3	1.0E-115	4758278	NT	Homo sapiens EphA4 (EPHA4), mRNA
4591	13785	22878	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
4591	13785	22877	1.84	1.0E-115	8922435	NT	Homo sapiens hypothetical protein FLJ10468 (FLJ10468), mRNA
4679	13872	22971	2.9	1.0E-115	AL0968857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4679	13872	22972	2.9	1.0E-115	AL0968857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4927	14115	23210	3.92	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4927	14115	23211	3.92	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5303	14593	23870	1.74	1.0E-115	AW970335.1	EST_HUMAN	EST382418 MAGE resequences, MAGK Homo sapiens cDNA
5463	14689	24040	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
5463	14689	24041	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC83433), mRNA
5828	15045	24449	14.79	1.0E-115	11426038	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC83438), mRNA
5880	15107	24517	1.88	1.0E-115	78611833	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
5880	15107	24518	1.88	1.0E-115	78611833	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6225	15438	24875	7.4	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0595 protein, partial cds
6511	15107	25172	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6511	15107	25173	6.99	1.0E-115	BE830187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
6722	15917	25376	9.48	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
7305	16523	26014	3.52	1.0E-116	AW571544.1	EST_HUMAN	x032f08_x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2839239 3' similar to SW:CAVP_CANFA P10483 CALCYPHOSINE
7836	17076	26804	2.64	1.0E-115	4502538	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
8232	17380	26914	4.28	1.0E-115	BF361984.1	EST_HUMAN	QV2-NN0044-210800-308-e10 NN0044 Homo sapiens cDNA
8324	17425			1.76	1.0E-115	AF240786.1	NT
579	9828	16847	0.93	1.0E-116	BBE275502.1	EST_HUMAN	601121347F1 NIH MGIC_20 Homo sapiens cDNA clone IMAGE:2888875 5'
810	10049	19200	1.33	1.0E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
869	10105		0.8	1.0E-116	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
1868	11170	20375	2.57	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1996	11170	23376	2.57	1.0E-116	5174478	NT	Homo sapiens pericentrin (PCNT), mRNA
1995	11198	20408	1.19	1.0E-116	AU133080.1	EST_HUMAN	AU133080 NT2EP4 Homo sapiens cDNA clone NT2EP4001228 5'
2087	12009	20480	1	1.0E-116	M18824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2087	12009	20481	1	1.0E-116	M18824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2273	11468	20889	1.85	1.0E-116	5453941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1), mRNA

Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2398	11503			4.25	1.0E-116	U78308.1	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor psuedo olfr17-01 (OR17-01) pseudogene, complete cds
2419	11610	20832		2.52	1.0E-116	AEO18833.1	Homo sapiens mRNA for KIAA0780 protein, partial cds
2691	11956	21086		6.81	1.0E-116	BE588925B.1	EST_HUMAN 60151337/F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3130	12365			6.84	1.0E-116	T07515.1	EST_HUMAN EST05405 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFBEK28 similar to EST containing L1 repeat
3139	12374	21504		6.18	1.0E-116	L77570.1	EST_HUMAN Homo sapiens DiGeorge syndrome critical region, centromeric end
3139	12374	21505		6.18	1.0E-116	L77570.1	EST_HUMAN Homo sapiens DiGeorge syndrome critical region, centromeric end
4372	13574	22870		2.17	1.0E-116	5031634	NT Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4470	13668	22759		1.39	1.0E-116	AB026898.1	NT Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4872	14060	23154		1.55	1.0E-116	AB0707088.1	EST_HUMAN PM-BT135-070486-016 BT135 Homo sapiens cDNA
5644	14867	24252		2.81	1.0E-116	W42822.1	EST_HUMAN xx24d07.1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW_MDHM_MOLECULAR_P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
5757	14976	24374		1.87	1.0E-116	AB048656.1	NT Homo sapiens mRNA for KIAA1638 protein, partial cds
5757	14976	24375		1.87	1.0E-116	AB048656.1	NT Homo sapiens mRNA for KIAA1638 protein, partial cds
5881	15098			2.13	1.0E-116	BE15833.1	EST_HUMAN MR2-HT0378-210200-102-504 HT0379 Homo sapiens cDNA
6080	15250	24672		1.77	1.0E-116	C02844.1	EST_HUMAN C02844 Human heart cDNA (Y Nakamura) Homo sapiens cDNA clones 3NHC0567
6167	15349	24787		8.61	1.0E-116	A7716314	EST_HUMAN AV716314 DCB Homo sapiens cDNA clone DCBBG06 5'
6586	15782	25242		2.88	1.0E-116	A354256.1	EST_HUMAN EST62885 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
6586	15782	25243		2.68	1.0E-116	A354256.1	EST_HUMAN EST62885 Jurkat T-cells V Homo sapiens cDNA 5' end similar to keratin 2
6805	16000	25459		6.64	1.0E-116	A1216352.1	EST_HUMAN q09805.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to db X53741_m1 FBILIN-1, ISOFORM A PRECURSOR (HUMAN);
7279	16498	26890		4.18	1.0E-116	BF335849.1	EST_HUMAN CN2-C70482-300800-349-608 CT0482 Homo sapiens cDNA
7695	16894	26403		3.79	1.0E-116	A1367140.1	EST_HUMAN qq41e04.x1 Soares_NiHMPu_S1 Homo sapiens cDNA clone IMAGE:1835102 3' similar to WP-B0495.7 CEO1785 ;
8233	17381	26915		3.84	1.0E-116	D44816.1	EST_HUMAN HUMSFY287 Human brain cDNA Homo sapiens cDNA clone NF187-S
8890	18361			1.69	1.0E-116	BE258569.1	EST_HUMAN 601108350F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:344580 5'
9031	18225			2.02	1.0E-116	AI134889.1	EST_HUMAN DKFZp762_1110_1762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762_1110_5'
5685	9815	18637		1.67	1.0E-117	4826636	NT Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1085	11985	19462		2.51	1.0E-117	AF124393.1	NT Mus musculus fragile-X-related protein 1 (Fxr1) gene, exons 13a through 15
1725	10837	20120		1.74	1.0E-117	AF123320.1	NT Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1799	11008	20201		2.17	1.0E-117	M19816.1	NT Human apolipoprotein B-100 (apoB) gene, exon 10

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2178	11375	20597	3.14	1.0E-117	AW957699.1	EST_HUMAN	EST369769 MAGE resequences, MAGE Homo sapiens cDNA Human alpha-5 collagen type IV gene, exon 5
2672	11757	20977	4.99	1.0E-117	ME3468.1	NT	op32c11_s1 Scores NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1576548 3'
3235	12469	21601	2.35	1.0E-117	AA978114.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to ribosomal protein L29
3868	13183	22283	10.3	1.0E-117	AA316723.1	EST_HUMAN	EST34C1120_f1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1120_5'
4000	13213	22317	0.69	1.0E-117	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4337	13538	22629	3.11	1.0E-117	8859584	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4575	13769	22884	2.19	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_f1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1120_5'
4736	13927	23030	0.89	1.0E-117	X89870.1	NT	H_sapiens mRNA for TPCR16 protein
4736	13927	23031	0.89	1.0E-117	X89870.1	NT	H_sapiens mRNA for TPCR16 protein
4824	14013	23112	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scat2 (SCAR2) gene, partial cds
4824	14013	23113	10.37	1.0E-117	AF134304.2	NT	Homo sapiens Scat2 (SCAR2) gene, partial cds
4885	14073	23170	1.62	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4885	14073	23171	1.62	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4958	14145	23237	3.13	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5274	14446	23518	0.81	1.0E-117	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; actinin receptor interacting protein 1 (KIAA0705), mRNA
5285	14456	23525	16.42	1.0E-117	6997248	NT	Homo sapiens eel (Oreosoma)like 1 (SALL1), mRNA
5364	14594	23671	3.1	1.0E-117	BE730508.1	EST_HUMAN	601562657f1_NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6273	15453	24893	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (sip) gene, 3' end of cds
6273	15453	24894	5.21	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (sip) gene, 3' end of cds
6311	15492	24937	4.74	1.0E-117	AV717788	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6311	15492	24938	4.74	1.0E-117	AV717788	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
6454	15651	25119	6.33	1.0E-117	AB950145.1	EST_HUMAN	wp86607_x1_NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2488628 3' similar to TR:075065 O75065_KIAA0477 PROTEIN_;
7434	16643	26135	1.68	1.0E-117	D83776.1	NT	Human mRNA for KIAA0191 gene, partial cds
7822	17014	28528	2.73	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
7822	17014	28629	2.73	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
7832	17072	327	32.7	1.0E-117	BE269856.1	EST_HUMAN	601186203f1_NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'
8121	17255	26798	2.27	1.0E-117	4501848	NT	Homo sapiens A1 P-binding cassette, sub-family A (ABC1), member 3 (ABC1), mRNA
8121	17255	26797	2.27	1.0E-117	4501848	NT	Homo sapiens A1 P-binding cassette, sub-family A (ABC1), member 3 (ABC1), mRNA
8567	18304		1.98	1.0E-117	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9277	11985	19462	1.98	1.0E-117	AF124383.1	NT	Mus musculus fragile-X-related protein 1 (Fxrl1) gene, exons 13a through 15

Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
70	9365	18491	3.8	1.0E-118 AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds	
95	9368	18517	0.68	1.0E-118 AL045854.1	EST_HUMAN	DKEZp434056_r1_434 (synonym: hesc) Homo sapiens cDNA clone DKFZp434056_5'	
523	9174	18859	7.45	1.0E-118	7657016 NT	Homo sapiens hypothetical protein (D32BE19.C1.1), mRNA	
924	11881	19316	0.92	1.0E-118	5174680 NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA	
2189	11396	20618	4.13	1.0E-118 BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019_5'	
2189	11398	20619	4.13	1.0E-118 BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019_5'	
2189	11396	20620	4.13	1.0E-118 BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3804019_5'	
2298	11493		12.88	1.0E-118 AW957729.1	EST_HUMAN	EST383199 IMAGE sequences, MAGGB Homo sapiens cDNA	
2697	11877	21081	4.25	1.0E-118 U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
2697	11877	21082	4.25	1.0E-118 U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
3068	12304		4.86	1.0E-118 Y13932.1	NT	Human breakpoint cluster region (BCR) gene, complete cds	
3159	12384	21528	5.35	1.0E-118 A1347694.1	EST_HUMAN	qpo1105_x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1916769_3'	
3159	12384	21530	5.35	1.0E-118 A1347694.1	EST_HUMAN	qpo1105_x1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1916769_3'	
3925	13141	22258	1.12	1.0E-118 AB024469.1	NT	Pongo pygmaeus DNA, similar to pdt gene of HERV-W and MSRV, isolate:ORW3-3	
4064	13274	22374	7.45	1.0E-118 D28660.1	NT	Human mRNA for ribosomal protein, complete cds	
4718	13809	23011	1.6	1.0E-118	11425783 NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA	
5405	14633	23744	1.89	1.0E-118 AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3	
5405	14633	23745	1.89	1.0E-118 AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3	
5834	14858	24241	1.65	1.0E-118	11420764 NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	
6333	15614	24981	4.89	1.0E-118	11431050 NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA	
6592	15798	25247	7.57	1.0E-118 BE028355.1	EST_HUMAN	QV0-BT0263-080200-097-h03_B10283 Homo sapiens cDNA	
6592	15798	25248	7.57	1.0E-118 BE028355.1	EST_HUMAN	QV0-BT0263-080200-097-h03_B10283 Homo sapiens cDNA	
6595	15791	25249	3.03	1.0E-118 AA443024.1	EST_HUMAN	268807_r1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:811789_5'	
6595	15791	25250	3.03	1.0E-118 AA443024.1	EST_HUMAN	268807_r1 Soares_NihMPU_S1 Homo sapiens cDNA clone IMAGE:811789_5'	
6775	15970	25426	3.19	1.0E-118 BE283134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502_5'	
7828	17018	26534	5.5	1.0E-118 AA315007.1	EST_HUMAN	EST18814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynain, light chain 1, cytoplasmic	
8086	17230	28768	1.71	1.0E-118 BF093687.1	EST_HUMAN	QV0-UM0091-120900-3855-b12 UM0091 Homo sapiens cDNA	
8098	17230	28769	1.71	1.0E-118 BF093687.1	EST_HUMAN	QV0-UM0091-120900-3855-b12 UM0091 Homo sapiens cDNA	
8219	17349		1.97	1.0E-118	63252465 NT	Homo sapiens flap structure-specific endonuclease 1 (FEN1), mRNA	
785	10005	19154	0.77	1.0E-119 AF170492.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds	
1044	11884	19420	1.68	1.0E-119	7705607 NT	Homo sapiens CGI-105 protein (LOC51011), mRNA	
1902	11108	20301	2.49	1.0E-119 AB023147.1	NT	Homo sapiens mRNA for KIAA0890 protein, partial cds	

Table 4

Single Exon Probes Expressed In HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3206	12440		0.74	1.0E-119 AA916760.1	EST_HUMAN	CE01214;	cn10b05.s1 NCI_CGAP_LuS Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:ED4F6.2
3929	13145	22262	0.87	1.0E-119	4504116 NT		Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5357	14587	23884	2.81	1.0E-119 AU133899.1	EST_HUMAN	AU133899 NT2RP4 Homo sapiens cDNA clone NT2RP4001891 5'	
5365	14595	23672	10.88	1.0E-119 M88914.1	NT	Homo sapiens fibromin (NF1) gene, complete cds	
5368	14598	23676	3.46	1.0E-119 BE336121.1	EST_HUMAN	RC1-NHG073-250800-018-q08 NIH_73 Homo sapiens cDNA	
5409	14637	23765	1.8	1.0E-119 AV693731.1	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDHB03 5'	
5723	14841	24337	6.85	1.0E-119 AI150703.1	EST_HUMAN	cb77509_x1 Seares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW_K1CJ_MOUSE_P02535 KERATIN_TYPE I CYTOSKELETAL 10;	
5852	15070	24480	2.4	1.0E-119 X062892.1	NT	Human c-fos/fos proto-oncogene	
5858	15076	24489	4.25	1.0E-119 AW974193.1	EST_HUMAN	EST386296 MAGE sequences, MAGM Homo sapiens cDNA clone IMAGE:814977 5'	
7150	16327	25810	3.05	1.0E-119 AA485124.1	EST_HUMAN	aa32105.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'	
7225	18402	25887	5.18	1.0E-119 AB032261.1	NT	Homo sapiens Scd mRNA for steroid-C4A desaturase, complete cds	
7755	18651		11.06	1.0E-119 BFF69571.1	EST_HUMAN	6021186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310533 5'	
8624	18291		7.48	1.0E-119 AW847519.1	EST_HUMAN	RC3-CT0212-240969-011-f03 CT0212 Homo sapiens cDNA	
306	9879	18711	0.7	1.0E-120	4507334 NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA	
1048	10274	19426	5.48	1.0E-120 AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	
1048	10274	19427	5.48	1.0E-120 AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds	
1429	10642	19813	3.03	1.0E-120 NA44873.1	EST_HUMAN	yy40g12.1 Soares melanocyte 2Nb61 Homo sapiens cDNA clone IMAGE:273768 5'	
1581	10794	18671	4.28	1.0E-120 AF67706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds	
1775	10885	20177	1.78	1.0E-120	4557250 NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA	
2077	11277	20483	1.44	1.0E-120 AB011399.1	NT	Homo sapiens gene for AF-8, complete cds	
2077	11277	20494	1.44	1.0E-120 AB011399.1	NT	Homo sapiens gene for AF-8, complete cds	
3278	9579	18711	0.85	1.0E-120	4507334 NT	Homo sapiens synaptotagmin 1 (SYN1), mRNA	
4351	13553	22648	1.8	1.0E-120 AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds	
4351	13553	22649	1.8	1.0E-120 AF056490.1	EST_HUMAN	CM-BT043-090289-075 B1043 Homo sapiens cDNA	
4666	13860	22980	1.74	1.0E-120 AF098483.1	NT	EST_HUMAN	
4666	13880	22981	1.74	1.0E-120 AF098483.1	NT	EST_HUMAN	
5178	14356		0.69	1.0E-120 BE289720.1	EST_HUMAN	600944382F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860414 5'	
5200	14376	23483	1.38	1.0E-120 AB04151.1	EST_HUMAN	CM-BT043-090289-075 B1043 Homo sapiens cDNA	
5545	14769	24135	13.47	1.0E-120 BF588222.1	EST_HUMAN	6021183984F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'	
5545	14769	24136	13.47	1.0E-120 BF588222.1	EST_HUMAN	6021183984F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'	
6426	15623	25087	2.58	1.0E-120 Y00087.1	NT	Human gene for neurofilament subunit M (NF-M)	
6426	15623	25088	2.58	1.0E-120 Y00087.1	NT	Human gene for neurofilament subunit M (NF-M)	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6573	15768	25232	2.78	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4183333 5'
6603	15768	25256	2.72	1.0E-120	AB007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6803	15798	25257	2.72	1.0E-120	AB007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
6911	16098	25685	6.03	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH MGIC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
6911	16098	25598	6.03	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH MGIC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
7000	16178	25649	3.59	1.0E-120	BF308541.1	EST_HUMAN	601888956F1 NIH MGIC_17 Homo sapiens cDNA clone IMAGE:41722876 5'
7004	16182	25655	12.1	1.0E-120	AU13205	EST_HUMAN	AU13205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
7089	16276	25756	2.58	1.0E-120	AB028900.1	NT	Homo sapiens mRNA for KIAA0777 protein, partial cds
7688	16885	28393	10.02	1.0E-120	BE296387.1	EST_HUMAN	601178727F1 NIH MGIC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
7884	17100	28830	1.7	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
7884	17100	28831	1.7	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
8782	17711	23957	1.24	1.0E-120	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
73	9367	18405	1.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
383	9847	18752	1.32	1.0E-121	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
731	11915	19111	1.23	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1), mRNA
1935	11139	20335	0.86	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1935	11139	20336	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2072	11272	20487	1.12	1.0E-121	L76831.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta), mRNA, complete cds
2540	11278	20945	1.42	1.0E-121	BF344318.1	EST_HUMAN	602014755F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5'
2540	11278	20946	1.42	1.0E-121	BF344318.1	EST_HUMAN	602014755F1 NCI CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150286 5'
3046	12282	21409	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hb3 gene for hair keratin, exons 1 to 9
3046	12282	21410	4.5	1.0E-121	Y19208.1	NT	Homo sapiens hb3 gene for hair keratin, exons 1 to 9
3510	12734	218172	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3510	12734	21873	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3657	12878	21898	8.82	1.0E-121	AF155158.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3704	12924	22043	0.74	1.0E-121	A1904151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
4322	13523	22618	15.63	1.0E-121	A1263294.1	EST_HUMAN	Φ67901.x1 NCI CGAP_Pant Homo sapiens cDNA clone IMAGE:2005417 3'
4986	14183	23271	3.41	1.0E-121	X91837.1	NT	H sapiens ECE-1 gene (exon 1)
5139	14318	23409	1.18	1.0E-121	A1904151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
6437	15634	25098	2.45	1.0E-121	11438217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
6438	15635	25100	2.34	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
6438	15635	25101	2.34	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7357	16573	28065	3.21	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
7364	16580	28071	2.22	1.0E-121	AF084200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4-E458 allele, complete cds
7540	16745	28239	4.58	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4), mRNA
7587	16772	28284	1.92	1.0E-121	N59624.1	EST_HUMAN	y746c01_s1_Scares fetal liver spleen 1NF1_S Homo sapiens cDNA clone IMAGE:248448_3'
2722	9547	18878	1.18	1.0E-122	11626176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
341	9609	18738	3.68	1.0E-122	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
363	9629	18761	1.23	1.0E-122	11826176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
892	10127	18280	3.5	1.0E-122	AF114488.1	NT	Homo sapiens intersect short isoform (ITSN) mRNA, complete cds
1227	10445	18601	4.46	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1688	10881	20085	3.77	1.0E-122	AF18708.1	NT	Homo sapiens cysteine-rich repeat-containing protein 552 precursor, mRNA, complete cds
1887	10889	20087	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1887	10889	20088	2.46	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1783	10983	20189	6.26	1.0E-122	BE908024.1	EST_HUMAN	601497032F_NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2454	11645	20885	22.45	1.0E-122	BF3:16170.1	EST_HUMAN	601898173F_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129234 5'
2454	11645	20886	22.45	1.0E-122	BF3:16170.1	EST_HUMAN	601898173F_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129234 5'
2792	12032	21157	1.26	1.0E-122	AF284717.1	NT	Homo sapiens FV/E domain-containing dual specificity protein phosphatase FV/E-DSP2 mRNA, complete cds
4863	14051	23145	3.37	1.0E-122	4502168	NT	Homo sapiens arylidid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5011	14198		1.3	1.0E-122	AW504845.1	EST_HUMAN	UI-HF-BND-ell-a-03-0-U_1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'
5682	14700	24054	6.1	1.0E-122	BE256039.1	EST_HUMAN	601113567F_NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6382	17453		3.75	1.0E-122	11418187	NT	Homo sapiens phosphomannomutase 1 (PMN1), mRNA
777	10018	19164	1.53	1.0E-123	BF3452274.1	EST_HUMAN	602018058F_NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
777	10018	19185	1.53	1.0E-123	BF3452274.1	EST_HUMAN	602018058F_NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
1020	10248	19399	6.17	1.0E-123	AL1683249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1029	10255	19408	3.73	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofillin) (NMNT), mRNA
1245	10461	18621	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1245	10461	18622	4.94	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2069	11269	20483	2.16	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2069	11269	20484	2.16	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2069	11269	20485	2.16	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2281	11476		3.66	1.0E-123	7705682	NT	Homo sapiens RAS9-like protein (LOC51209), mRNA
5417	14645	23777	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5417	14645	23778	1.83	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
8857	15075	24488	1.97	1.0E-123	AU116435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
6357	15537	24991	1.92	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3509162 5'
6870	16092	25560	3.52	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
6912	16100	25567	31.08	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabfil2) mRNA, complete cds
8211	17342	26881	5.75	1.0E-123	BF677292.1	EST_HUMAN	602086781F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4250879 5'
8211	17342	26882	5.75	1.0E-123	BF677292.1	EST_HUMAN	602086781F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE4250879 5'
273	9548	18677	1.3	1.0E-124	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	9548	18678	1.3	1.0E-124	D87675.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
279	9554		1.47	1.0E-124	450750	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
492	9745	18876	2.86	1.0E-124	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21CO46
698	9940	19073	4.88	1.0E-124	AA397551.1	EST_HUMAN	ZB1804_11 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE728719 5' similar to TR_G300482
698	9940	19074	4.88	1.0E-124	AA397551.1	EST_HUMAN	ZB1804_11 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE728719 5' similar to TR_G300482
766	10006	19155	6.95	1.0E-124	AF155654.1	NT	Human putative ribosomal protein S11 mRNA
818	10058	19209	1.35	1.0E-124	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
914	10149	19309	1.76	1.0E-124	7705446	NT	Homo sapiens hypothetical protein (HSPC058), mRNA
1354	10569	19733	7.35	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1354	10569	19734	7.35	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1784	10894	20190	4.41	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (nHL61 gene)
2029	11230	20438	1.29	1.0E-124	BE878524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE3893954 5'
2420	11611	20833	2.18	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3341	12570	21709	0.6	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3465	12690	21828	0.73	1.0E-124	S7884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/B/R1) gene, exon
3465	12690	21827	0.73	1.0E-124	S7884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/B/R1) gene, exon
3628	12849	21968	3.42	1.0E-124	X13794.1	NT	H.sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (end joined CDS)
3876	13092	22208	0.7	1.0E-124	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4044	13254	22358	0.6	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4053	13263	22363	0.98	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4757	13948	23049	1.91	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
5327	14559	23631	9.25	1.0E-124	89222337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5609	14833	24208	6.87	1.0E-124	BF696135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6094	15294	24727	3.05	1.0E-124	Y11717.1	NT	Mus musculus mRNA for hoxa3 gene
6545	15741	25202	12.38	1.0E-124	45066554	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
6909	16097	25563	2.65	1.0E-124	AV645633	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6909	16097	25564	2.65	1.0E-124	AV645633	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
6967	16145	25615	9.53	1.0E-124	AT67133.1	EST_HUMAN	wi93f02.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2400591 3'
6967	16145	25616	9.53	1.0E-124	AT67133.1	EST_HUMAN	wi93f02.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2400591 3'
7877	17085	26589	3.49	1.0E-124	AV665663.1	EST_HUMAN	hj05c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:298096 3'
8008	16443	25932	3.27	1.0E-124	AI446455.1	EST_HUMAN	l19e03.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:241980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
8008	16443	25933	3.27	1.0E-124	AI446455.1	EST_HUMAN	l19e03.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:241980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
8437	9940	19073	5.82	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene Schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
8437	9940	19074	5.82	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stratagene Schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
8885	17789	23922	1.72	1.0E-124	AB028016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
9164	18238	23704	1.62	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9164	18238	23705	1.62	1.0E-124	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
153	9435	18569	3.63	1.0E-125	BE219510.1	EST_HUMAN	hv53a08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLINA ;
153	9435	18570	3.63	1.0E-125	BE219510.1	EST_HUMAN	hv53a08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058 FIBROPELLINA ;
324	9595	9595	9.19	1.0E-125	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
432	9297	18399	5.95	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3925685 5'
650	9896	19021	4.06	1.0E-125	AH11656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
650	9896	19022	4.06	1.0E-125	AH11656.1	EST_HUMAN	HA0086 Human fetal liver cDNA library Homo sapiens cDNA
735	9976	19115	1.92	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
870	10106	19268	1.99	1.0E-125	AA042813.1	EST_HUMAN	zK53c07.st Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65887_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1006	10237	19389	1.04	1.0E-125	AL165210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1162	10384	19534	1.97	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA

Table 4

Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1780	10990	20185		2.74	1.0E-125 AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1780	10990	20186		2.74	1.0E-125 AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2326	11519	20739		4.04	1.0E-125 AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal liver_spine_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2468	11659	20880		3.16	1.0E-125 AA042813.1	EST_HUMAN	zk5607.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2556	11743	20961		2.42	1.0E-125 4504656	NT	Homo sapiens Inhibin_alpha (INHA) mRNA
2556	11743	20962		2.42	1.0E-125 4504656	NT	Homo sapiens Inhibin_alpha (INHA) mRNA
2971	14464	21345		1.26	1.0E-125 BE018009.1	EST_HUMAN	bb74f06.v1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:Q955604 Q955604
3841	13058	22173		1.21	1.0E-125 AA042813.1	EST_HUMAN	zk53c07.s1 Soares_pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
4547	13742	22842		2.2	1.0E-125 11425114	NT	Homo sapiens Zinc finger protein ZNF287 (ZNF287), mRNA
4619	13813	22903		1.18	1.0E-125 BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5056	9435	18569		1.71	1.0E-125 BE219510.1	EST_HUMAN	hv53a08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058
5056	9435	18570		1.71	1.0E-125 BE219510.1	EST_HUMAN	hv53a08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3177686 3' similar to TR:Q25058 Q25058
5629	14853	24236		3.41	1.0E-125 BE892660.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
5919	15136	24546		4.5	1.0E-125 BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3659790 5'
5919	15136	24547		4.5	1.0E-125 BE562526.1	EST_HUMAN	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3659790 5'
6109	15203	24621		4.08	1.0E-125 X03427.1	NT	Homo sapiens IgF-II gene, exon 5
6109	15203	24622		4.08	1.0E-125 X03427.1	NT	Homo sapiens IgF-II gene, exon 5
6812	16007	25468		12.48	1.0E-125 BE181640.1	EST_HUMAN	QVI-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
6812	16007	25469		12.48	1.0E-125 BE181640.1	EST_HUMAN	QVI-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
7274	16493	25985		3.47	1.0E-125 AF043458.1	NT	Homo sapiens I-REL gene, exon 5
7696	16895	26404		4.49	1.0E-125 AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
7837	17029	26545		1.76	1.0E-125 7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
7842	17034	26550		5.99	1.0E-125 AF026029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
7939	17079	26807		3.23	1.0E-125 AW812899.1	EST_HUMAN	RC3-ST0186-250200-018-c11 S70186 Homo sapiens cDNA
8035	17171	26709		5.52	1.0E-125 BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
8035	17171	26710		5.52	1.0E-125 BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
783	10022	19172		1.06	1.0E-126 4758007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
786	10025	19175		1.61	1.0E-126 M61936.1	NT	Human laminin B1 chain gene, exon 20

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2313	11507	20728	1.65	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2557	11744	20983	6.17	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3037	12274	21403	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072603.1 Strategene pancreas (AA37208) Homo sapiens cDNA clone IMAGE:592420 5'
3037	12274	21404	11.07	1.0E-126	AA160709.1	EST_HUMAN	z072603.1 Strategene pancreas (AA37208) Homo sapiens cDNA clone IMAGE:592420 5'
3607	12828	21948	0.94	1.0E-126	X33841.1	NT	H.sapiens DNA for liver cytochrome b5 pseudogene
3655	12856	21975	1.42	1.0E-126	7657058	NT	Homo sapiens death receptor 6 (DR6), mRNA
4757	15988	23091	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4797	15986	23092	1.09	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4851	14040	23133	1.81	1.0E-126	NA3078.1	EST_HUMAN	y78c06.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:267850 5'
5164	14360	23446	0.81	1.0E-126	BE143922.1	EST_HUMAN	601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
5767	14986	24386	4.09	1.0E-126	AA460075.1	EST_HUMAN	z066e03.1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:798444 5' similar to TR:G1145880 G1145880 TITIN
5781	14899	24401	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
5781	14899	24402	3.92	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
6439	15656	25127	3.09	1.0E-126	X16609.1	NT	Human mRNA for ankyrin (variant 2.1)
7455	16844	26136	3.63	1.0E-126	BF683175.1	EST_HUMAN	602139138F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4298240 5'
8049	17185	26724	2.23	1.0E-126	BE261960.1	EST_HUMAN	6011149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
8933	14360	23446	5.06	1.0E-126	BE143922.1	EST_HUMAN	601577881F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
175	9458	18588	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
175	9458	18589	7.09	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	9458	18588	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
176	9458	18589	6.74	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
2178	9553	18685	1.51	1.0E-127	DB1675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2178	9553	18686	1.51	1.0E-127	DB1675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
891	10126	19289	0.9	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
926	10160	18318	1.07	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1686	10879	20063	2.02	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2033	11234	20441	2.82	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2033	11234	20442	2.82	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2166	11384	20583	85.3	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2310	11504	20725	2.49	1.0E-127	AF245505.1	NT	Homo sapiens adican mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2569	11754	20874	40.25	1.0E-127 X12881.1	NT		Human mRNA for cyclotinin 18
3670	12891	22012	0.63	1.0E-127 AF114498.1	NT		Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3789	13017	22130	1.23	1.0E-127 AW161297.1	EST_HUMAN		au80e06 y1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2702594 5' similar to TRQ15170 Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element;
4094	13302	22402	0.68	1.0E-127 AF135168.1	NT		Homo sapiens delayed rectifier potassium channel subunit IsK mRNA, complete cds
4241	13444	22534	22.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4241	13444	22535	22.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4498	13697	22781	0.82	1.0E-127 AF262287.1	NT		Homo sapiens cytochrome P450 reductase-metabolizing protein P450RA1-2 mRNA, complete cds
4603	13797	22887	4.81	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4635	13829		2.81	1.0E-127 AL163268.2	NT		Homo sapiens chromosome 21 segment HS21C068
4676	13870	22869	0.88	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYP), mRNA
5186	14382	23447	0.88	1.0E-127 AF105989.1	NT		Homo sapiens acetylcholine receptor epsilon subunit (CHRN) gene, complete cds
6186	14382	23448	0.88	1.0E-127 AF105989.1	NT		Homo sapiens acetylcholine receptor epsilon subunit (CHRN) gene, complete cds
5186	14382	23449	0.88	1.0E-127 AF105989.1	NT		Homo sapiens acetylcholine receptor epsilon subunit (CHRN) gene, complete cds
							za01a10 r1 Scores melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIP8_RAT P10888 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5539	14783	24130	2.03	1.0E-127 W03547.1	EST_HUMAN		
5573	14797	24171	4.34	1.0E-127 X85784.1	NT		H.sapiens NOS2 gene, exon 8
5737	14956	24355	2.24	1.0E-127 X84060.1	NT		H.sapiens TCF11 gene, exon 3-6
5798	15015	24418	6.1	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6978	16158	25827	4.37	1.0E-127 AF274863.1	NT		Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
6978	16158	25828	4.37	1.0E-127 AF274863.1	NT		Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7179	16356	25834	3.58	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
7718	16917	26424	6.51	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (LOC53184), mRNA
7718	16917	26425	6.51	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 9B (mortalin-2) (LOC53184), mRNA
8146	17278	26822	1.83	1.0E-127 BE895415.1	EST_HUMAN		601434784F NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8146	17278	26823	1.83	1.0E-127 BE895415.1	EST_HUMAN		601434784F NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919917 5'
8874	9456	18588	3.11	1.0E-127 AB024597.1	NT		Homo sapiens mRNA for cassein kinase epsilon, complete cds
8874	9456	18589	3.11	1.0E-127 AB024597.1	NT		Homo sapiens mRNA for cassein kinase epsilon, complete cds
8884	17779	23945	1.58	1.0E-127 AB011399.1	NT		Homo sapiens gene for AF-6, complete cds
466	9719	18851	3.7	1.0E-128 BE365817.1	EST_HUMAN		601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2038	11239	20448	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2038	11239	20447	30.04	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2178	11373	20595	153.58	1.0E-128	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2408	11600		6.88	1.0E-128	1143745	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTTP140), mRNA
3371	12599	21735	1.23	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4657	13861	22862	4.92	1.0E-128	11426573	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
6835	16052	24459	1.84	1.0E-128	11420985	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (PDE1C), mRNA
6058	15225	24644	6.7	1.0E-128	BF224345.1	EST_HUMAN	7q88b70.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3'
7120	16297	25779	3.35	1.0E-128	AA639198.1	EST_HUMAN	ns04a11.1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338 CHROMOSOME SEGREGATION GENE HOMOLOG CAS.
7288	16517	26008	5.1	1.0E-128	11425254	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
7308	16524	26015	8.5	1.0E-128	AA926959.1	EST_HUMAN	cmr62h08.51 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gba>X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN); EST387350 MAGE sequences. MAGC Homo sapiens cDNA
8533	17559		5.07	1.0E-128	AW1855280.1	EST_HUMAN	EST387350 MAGE sequences. MAGC Homo sapiens cDNA
4119	9672	18814	0.67	1.0E-129	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, genomic, 1019 nt, segment 2 of 4]
1693	10805	20091	3.35	1.0E-129	AL098860.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1698	10910	20086	1.46	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1698	10910	20097	1.46	1.0E-129	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1813	11021	20214	2.67	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3092	12328	21451	1.51	1.0E-129	Q114585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3092	12328	21452	1.51	1.0E-129	Q114585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3092	12328	21453	1.51	1.0E-129	Q114585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4148	13352	22454	2.08	1.0E-129	AB040892.1	NT	Homo sapiens zinc finger protein, partial cds
4265	13468	22559	2.19	1.0E-129	AW755254.1	EST_HUMAN	CNYA5 Human cardiac muscle expression library Homo sapiens cDNA clones 4151935 similar to CNYA5
4265	13468	22560	2.19	1.0E-129	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
5704	14923	24316	4.43	1.0E-129	AJ006345.1	NT	Homo sapiens KVLTQ1 gene
6130	15314	24748	4.22	1.0E-129	AJ006345.1	NT	Homo sapiens KVLTQ1 gene
6161	15344	24781	9.49	1.0E-129	11420850	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC083694), mRNA
6567	15763		6.3	1.0E-129	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds

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Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7776	16971	26484	3.53	1.0E-129 AA625526.1	EST_HUMAN	BT7207_1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1047589 5'	
7845	15344	24781	10.01	1.0E-129	11420850 NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC33894), mRNA	
8520	17551		4.44	1.0E-128 HB3155.1	EST_HUMAN	YQ480511 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:189112 5' similar to SP:BA8150_B48150 HP-25=HIBERNATION RELATED PROTEIN -TAMIAS ASIATICUS=ASIAN ; DKFZp762K171_1	
8925	17808		1.73	1.0E-128 AL20739.1	EST_HUMAN	SP:BA8150_B48150 HP-25=HIBERNATION RELATED PROTEIN -TAMIAS ASIATICUS=ASIAN ; DKFZp762K171_1	
78	9370	18499	3.47	1.0E-130	7705530 NT	Homo sapiens hypothetical protein (HSP242), mRNA	
1178	10399	18652	0.7	1.0E-130 AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds	
1842	10858	20037	36.78	1.0E-130 BE76182.1	EST_HUMAN	601121985F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:33446368 5'	
1842	10858	20038	36.78	1.0E-130 BE75192.1	EST_HUMAN	601121985F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:33446368 5'	
1852	11168		1.9	1.0E-130 X04092.1	NT	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13	
2728	11905		8.45	1.0E-130 A1010230.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial	
2832	12071	21192	1.28	1.0E-130 BE564219.1	EST_HUMAN	6011343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:33885468 5'	
2832	12071	21193	1.28	1.0E-130 BE564219.1	EST_HUMAN	6011343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:33885468 5'	
3553	12776	21905	1.13	1.0E-130 AF240688.1	NT	Homo sapiens retina dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds	
3750	12071	21192	5.88	1.0E-130 BE564219.1	EST_HUMAN	6011343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:33885468 5'	
3750	12071	21183	5.98	1.0E-130 BE564219.1	EST_HUMAN	6011343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:33885468 5'	
3910	13126	22243	1.57	1.0E-130 AW503580.1	EST_HUMAN	U1-H-BD-akyr-q-06-0-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'	
4049	13299	22381	0.97	1.0E-130 M97710.1	NT	Human T-cell receptor (V alpha 22-1, J alpha RP/M4-265-variant, C alpha 1) mRNA	
4535	13731	22828	8.08	1.0E-130 AW843893.1	EST_HUMAN	CM4-CN0045-180200-51-02 CN0045 Homo sapiens cDNA	
5127	14306	23396	1.18	1.0E-130 AW563289.1	EST_HUMAN	RC0-CT0318-20118931-811 CT0318 Homo sapiens cDNA	
5127	14306	23397	1.18	1.0E-130 AW563289.1	EST_HUMAN	RC0-CT0318-20118931-811 CT0318 Homo sapiens cDNA	
6187	15389	24809	2.09	1.0E-130	11416777 NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA	
6832	16028	25492	2.38	1.0E-130 AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds	
4	8301	18403	2.48	0.0E+00 AA228126.1	EST_HUMAN	ZF58c04_11 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:687580 5' similar to TRG222811	
4	8301	18404	2.48	0.0E+00 AA228126.1	EST_HUMAN	ZF58c04_11 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667580 5' similar to TRG222811	
7	8303	18407	1.29	0.0E+00	4865138 NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA	
15	9311	18413	0.72	0.0E+00	8923349 NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	
15	9311	18414	0.72	0.0E+00	8923349 NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA	
22	9318	18421	3.45	0.0E+00 D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds	
22	9318	18422	3.45	0.0E+00 D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds	
28	9324	18427	23.31	0.0E+00 AF141349.1	NT	Homo sapiens desmosin mRNA, complete cds	

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
38	9332	18437	2.44	0.0E+00	5802997	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
38	9334	18440	0.84	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCFC2) gene, exons 1 through 5
42	9338	18445	5.84	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
59	9355	18472	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
69	9355	18473	2.5	0.0E+00	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
61	9357	18477	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFUjwara) Homo sapiens cDNA clone GEN-516H08.5'
61	9357	18478	1.28	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TFUjwara) Homo sapiens cDNA clone GEN-516H08.5'
62	9358	18479	27.84	0.0E+00	L10558.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
64	9360	18482	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48e07_X1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
64	9360	18483	8.6	0.0E+00	AW069534.1	EST_HUMAN	cr48e07_X1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
75	9369	18497	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN15) mRNA
75	9369	18498	0.73	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN15) mRNA
78	9369	18497	0.62	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN15) mRNA
78	9369	18498	0.62	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPN15) mRNA
81	9374	18504	0.87	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
82	9375	18513	33.19	0.0E+00	4501444	NT	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
91	9384	18513	39.94	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
94	9387	18516	25.33	0.0E+00	U8227.1	NT	Human polynucleic 1 homolog (HPPH1) mRNA, partial cds
101	9394	18523	1.41	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
102	9395	18524	1.65	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
107	9397	18527	0.68	0.0E+00	X91213.1	NT	H. sapiens next gene (exon 2)
118	9404	18533	2.12	0.0E+00	A1623701.1	EST_HUMAN	ts38b05_X1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q989551 Q989551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
117	9404	18533	1.15	0.0E+00	A1623701.1	EST_HUMAN	ts38b05_X1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q989551 Q989551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;
118	9406	18534	2.65	0.0E+00	N35040.1	EST_HUMAN	yy01h08_1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017.5'
118	9406	18535	2.65	0.0E+00	N35040.1	EST_HUMAN	yy01h09_1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270017.5'
128	9411	18545	4.14	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
128	9411	18546	4.14	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
137	9419	18553	1.13	0.0E+00	T56945.1	EST_HUMAN	ya83g04_12 Stratagene fetal spleen #637205 Homo sapiens cDNA clone IMAGE:68310.5'
137	9419	18554	1.13	0.0E+00	T56945.1	EST_HUMAN	ya83g04_12 Stratagene fetal spleen #637205 Homo sapiens cDNA clone IMAGE:68310.5'
158	9438		34.89	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
160	9442	18575	2.05	0.0E+00	BFC036881.1	EST_HUMAN	601460375F1 NIH MGCG_56 Homo sapiens cDNA clone IMAGE:3863803.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
736	9977	19116	4.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
738	9977	19117	4.24	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
738	9979	19120	13.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634) mRNA
744	9985	19128	2.08	0.0E+00	BE241577.1	EST_HUMAN	TCAAAPID0778 Pediatric acute myelogenous leukemia cell (FAB-M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP0779
764	10004	19152	1.52	0.0E+00	AF228990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
764	10004	19153	1.52	0.0E+00	AF228990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
767	10007	19159	1.76	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
767	10007	19157	1.76	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
770	10010	19158	1.02	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
771	10011	19159	2.04	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
773	11977	19161	2.38	0.0E+00	D30812.1	NT	Homo sapiens mRNA for repressor protein, partial cds
774	10013	19162	2.79	0.0E+00	BE268735.1	EST_HUMAN	601445647F1 NIH 3T3 cell IMAGE:3849803 5'
776	10017	19166	3.29	0.0E+00	R48915.1	EST_HUMAN	Y68908.1 Soares br east 2nbHBst Homo sapiens cDNA clone IMAGE:1540465
779	10018	19167	3	0.0E+00	5032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120kD (SF3A1), mRNA
788	10027	19178	1.76	0.0E+00	AB011388.1	NT	Homo sapiens gene for NF-8, complete cds
791	10031	19180	3.24	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
802	10041	19182	0.85	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
802	10041	19183	0.95	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
807	10046	19187	2.72	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
811	10050	19201	3.81	0.0E+00	AB010910	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
811	10050	19202	3.81	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
816	10054	19208	12.64	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
817	10055	19229	10.04	0.0E+00	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIMM1) mRNA
834	10072	19229	1.56	0.0E+00	7857213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
835	10073	19230	2.71	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
837	10075	19232	2.56	0.0E+00	4557686	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
843	10080	19238	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH) mRNA, complete cds
843	10080	19239	1.38	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH) mRNA, complete cds
844	10081	19240	0.85	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH) mRNA, complete cds
849	10085	19245	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
853	10089	19250	2.26	0.0E+00	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIMM1) mRNA
853	10089	19251	2.26	0.0E+00	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIMM1) mRNA
860	10096		1.51	0.0E+00	AF27153.1	NT	Homo sapiens sodium/magnesium cotransporter (SLC5A3) gene, complete cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
864	10100	19262	6.12	0.0E+00	AE0288942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
864	10100	19263	6.12	0.0E+00	AE0288942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
865	10101	19264	8.12	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
866	10102	19265	3.01	0.0E+00	AE0288942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
867	10103	19266	9.08	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
871	10107	19268	1.67	0.0E+00	AE020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
871	10107	19270	1.67	0.0E+00	AE020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
872	10108	19271	2.32	0.0E+00	A533272.1	EST_HUMAN	nr 68d07_s1_NCI_CGAP_Prl0 Homo sapiens cDNA clone IMAGE:997453
872	10108	19272	2.32	0.0E+00	A533272.1	EST_HUMAN	nr 68d07_s1_NCI_CGAP_Prl0 Homo sapiens cDNA clone IMAGE:997453
873	10109		8.85	0.0E+00	Bf577694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:2498155
877	10113	19273	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
877	10113	19274	1.37	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19275	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
878	10114	19276	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	10136	19289	1.84	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C033
908	10143	19304	1.71	0.0E+00	BE089592.1	EST_HUMAN	QY0-BT0703-28040-211-911_BT0703 Homo sapiens cDNA
908	10143	19305	1.71	0.0E+00	BE089592.1	EST_HUMAN	QY0-BT0703-28040-211-911_BT0703 Homo sapiens cDNA
918	10153	19314	2.88	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C033
928	10162		38.57	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67KD, ribosomal protein SA) (LAMR1), mRNA
930	10162		32.73	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67KD, ribosomal protein SA) (LAMR1), mRNA
931	10164	19321	0.76	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor mRNA, partial cds
932	10165	19322	1.87	0.0E+00	Q28101.1	NT	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds
938	10191	19345	1.41	0.0E+00	M37160.1	NT	Human ras inhibitor mRNA, 3' end
939	10192	19346	6.37	0.0E+00	M37160.1	NT	Human ras inhibitor mRNA, 3' end
960	10193	19347	0.83	0.0E+00	M37160.1	NT	Human ras inhibitor mRNA, 3' end
961	10194	19348	1.68	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
961	10194	19349	1.68	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
969	11982	19358	2.74	0.0E+00	A001948.1	EST_HUMAN	cs88e03_s1_NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
969	11982	19357	2.74	0.0E+00	A001948.1	EST_HUMAN	os98e03_s1_NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
971	10203	19359	7.12	0.0E+00	7857298	NT	Homo sapiens KIAA0929 protein Msc2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
982	10213	19369	2.97	0.0E+00	A8030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
980	10221	19375	1.20	0.0E+00	BF366974.1	EST_HUMAN	PN2-GN0014-050980c-001-f02 GN0014 Homo sapiens cDNA
980	10221	19376	1.28	0.0E+00	BF366974.1	EST_HUMAN	PN2-GN0014-050980c-001-f02 GN0014 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HEK Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
990	10221	19377	1.29	0.0E+00	BF368974.1	EST_HUMAN	PM2-GN0014-050900-001-f02 GN0014 Homo sapiens cDNA
991	10222	19378	2.98	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
991	10222	19378	2.98	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1000	10231	19388	2.42	0.0E+00	4757969	NT	Homo sapiens chromosome-like (CDYL) mRNA
1012	10242	19394	2.4	0.0E+00	U83668.1	NT	Human beta-tubulin (TUBA4q) gene, complete cds
1013	10243	19395	37.53	0.0E+00	U83668.1	NT	Human beta-tubulin (TUBA4q) gene, complete cds
1014	10243	19395	9.7	0.0E+00	U83668.1	NT	Human beta-tubulin (TUBA4q) gene, complete cds
1017	10248		13.45	0.0E+00	AF188490.1	NT	Human sapiens 8q22.1 region and MTGB (CBFA2T1) gene, partial cds
1018	10248		12.78	0.0E+00	AF188490.1	NT	Human sapiens 8q22.1 region and MTGB (CBFA2T1) gene, partial cds
1021	10249	19400	2.19	0.0E+00	AF111170.3	NT	Homo sapiens 14q32.2 Jagged2 gene, complete cds; and unknown gene
1022	10249	19400	2.09	0.0E+00	AF111170.3	NT	Homo sapiens 14q32.2 Jagged2 gene, complete cds; and unknown gene
1023	10249	19400	1.72	0.0E+00	AF111170.3	NT	Homo sapiens 14q32.2 Jagged2 gene, complete cds; and unknown gene
1024	10250	19401	2.61	0.0E+00	AF111170.3	NT	Homo sapiens 14q32.2 Jagged2 gene, complete cds; and unknown gene
1027	10253	19404	3.31	0.0E+00	7661685	NT	Homo sapiens DkFZP586M0122 protein (DKFZP586M0122), mRNA
1031	10257	19408	4.14	0.0E+00	580314.14	NT	Homo sapiens inner membrane protein, mitochondrial (mitoflin) (IMMT), mRNA
1033	10259		4.94	0.0E+00	AA458680.1	EST_HUMAN	SW:PRSE_HUMAN P4/210 2S PROTEASE REGULATORY SUBUNIT 8;
1036	10262	18413	0.85	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1036	10262	18414	0.95	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1037	10263	18415	2.06	0.0E+00	475924.9	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
1037	10263	18416	2.06	0.0E+00	475924.9	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
1040	10268		5.28	0.0E+00	8922833	NT	Homo sapiens hypothetical protein FLJ11186 (FLJ11186), mRNA
1054	10280	18431	9.66	0.0E+00	4758569	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPAB6) mRNA
1072	10287	18448	2.84	0.0E+00	4826672	NT	Homo sapiens catenin 6, K-catenin (fetal kidney) (CDH6) mRNA
1072	10287	18447	2.84	0.0E+00	4826672	NT	Homo sapiens catenin 6, K-catenin (fetal kidney) (CDH6) mRNA
1076	10301	18451	7.53	0.0E+00	8923834	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1078	10301	18452	7.53	0.0E+00	8923834	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1077	10302	18453	68.63	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1079	10304		0.78	0.0E+00	8923037	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1081	10306	18457	3.28	0.0E+00	6174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH1), mRNA
1080	10314	19468	10.32	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3), mRNA
1104	10328	19478	2.49	0.0E+00	BE05208.1	EST_HUMAN	MFC-BH0115-200301-003-h08 BN0115 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon seq ID NO:	ORF seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1127	10351	19502		4.27	0.0E+00	7706134	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1127	10351	19503		4.27	0.0E+00	7706134	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1140	10363	19513		1.06	0.0E+00	4B26947	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1140	10363	19514		1.06	0.0E+00	4B26947	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1141	10364	19515		18.48	0.0E+00	4506712	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1143	10366	19517		0.74	0.0E+00	8923280	Homo sapiens hypothetical protein FLJ20308 (FLJ20308) mRNA
1146	10369	19520		8.75	0.0E+00	AB02059.1	Homo sapiens DNA for Human P2XM complete cds
1148	10371	19521		27.94	0.0E+00	AB02059.1	Homo sapiens DNA for Human P2XM complete cds
1149	10372	19522		3.78	0.0E+00	7657468	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1149	10372	19523		3.79	0.0E+00	7657468	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1153	10375	19526		1.82	0.0E+00	7706500	Homo sapiens NpypBP (LOC51729) mRNA
1154	10376	19527		0.63	0.0E+00	X95826.1	H.sapiens ART4 gene
1154	10376	19528		0.63	0.0E+00	X95826.1	H.sapiens ART4 gene
1155	10377	19529		0.79	0.0E+00	A1147650.1	EST_HUMAN
1157	10379	19531		1.09	0.0E+00	AB20270.1	Homo sapiens mRNA for KIAA0903 Protein, partial cds
1164	10386	19537		2.81	0.0E+00	9866844	Homo sapiens chromosome 12 open reading frame 3 (C12orf3), mRNA
1176	10387	19549		2.31	0.0E+00	7305076	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1176	10387	19550		2.31	0.0E+00	7305076	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1179	10400	19553		0.8	0.0E+00	AB037835.1	Homo sapiens mRNA for KIAA1414 Protein, partial cds
1186	10407	19562		34.92	0.0E+00	4557887	Homo sapiens keratin 18 (KRT18) mRNA
1217	10435			1.33	0.0E+00	7657339	Homo sapiens multi (E. coli) homolog 3 (MLH3), mRNA
1230	10448	19604		1.02	0.0E+00	B922593	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
1233	10451	19607		1.44	0.0E+00	AF284750.1	Homo sapiens ALR-like protein mRNA, partial cds
1233	10451	19608		1.44	0.0E+00	AF284750.1	Homo sapiens ALR-like protein mRNA, partial cds
1234	10452	19609		1.02	0.0E+00	AF284750.1	Homo sapiens ALR-like protein mRNA, partial cds
1235	11988	19610		1.63	0.0E+00	AF108718.1	Homo sapiens mRNA for KIAA1507 protein, partial cds
1253	10469	19633		5.36	0.0E+00	4503098	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1254	10470	19634		1.58	0.0E+00	4503098	Homo sapiens prefoldin 4 (PFDN4) mRNA
1264	10479	19640		1.06	0.0E+00	4505740	Homo sapiens NF2 gene
1273	10488			2.95	0.0E+00	Y18000.1	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1281	10496	19655		97.05	0.0E+00	4506718	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1288	10503	19664		3.89	0.0E+00	AF084479.1	Homo sapiens mRNA for KIAA1507 protein, partial cds
1284	10509	19668		3.05	0.0E+00	AB040840.1	Homo sapiens mRNA for KIAA1507 protein, partial cds
1284	10509	19669		3.05	0.0E+00	AB040840.1	Homo sapiens mRNA for KIAA1507 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
162	9444			61.78	0.0E+00	4504444 NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
165	9447	18578		0.97	0.0E+00	AF11168.2 NT	Homo sapiens serine palmitoyl transferase, subunit 1 gene, complete cds; and unknown genes
167	9449	18579		0.84	0.0E+00	BE285973.1 EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
168	9449	18579		0.75	0.0E+00	BE285973.1 EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528864 5'
169	9450	18580		3.95	0.0E+00	W73973.1 EST_HUMAN	zg62b05.1 Soares, fetal heart, NbHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to bbX16282. cds1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
170	9451	18581		0.69	0.0E+00	BE162832.1 EST_HUMAN	CV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
170	9451	18582		0.69	0.0E+00	BE162832.1 EST_HUMAN	CV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
171	9452	18583		2.33	0.0E+00	AF244088.1 NT	Homo sapiens zinc finger protein mRNA, complete cds
174	9455	18586		7.31	0.0E+00	AL163202.2 NT	Homo sapiens chromosome 21 segment HS21C02
174	9455	18587		7.31	0.0E+00	AL163202.2 NT	Homo sapiens chromosome 21 segment HS21C02
185	9464	18594		4.28	0.0E+00	BE018970.1 EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z CE22831;
185	9464	18595		4.28	0.0E+00	BE018970.1 EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863854 5' similar to WP:Y57A10A.Z CE22831;
190	9469	18598		2.81	0.0E+00	AB018327.1 NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
190	9469	18599		2.81	0.0E+00	AB018327.1 NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18600		1.3	0.0E+00	AB018327.1 NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	9470	18601		1.3	0.0E+00	AB018327.1 NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	9479	18612		122.25	0.0E+00	D50659.1 NT	Human gamma-cytoplasmic actin (ACTGFP9) pseudogene
204	9484	18617		4.3	0.0E+00	AF273045.1 NT	Homo sapiens CTC1L tumor antigen set14-3 mRNA, complete cds
204	9484	18618		4.3	0.0E+00	AF273045.1 NT	Homo sapiens CTC1L tumor antigen set14-3 mRNA, complete cds
206	9488	18620		12.98	0.0E+00	AF167174.1 NT	Homo sapiens chromosome X MSL3.2 protein mRNA, complete cds
206	9488	18621		12.98	0.0E+00	AF167174.1 NT	Homo sapiens chromosome X MSL3.2 protein mRNA, complete cds
215	11962	18627		28.1	0.0E+00	A1587308.1 EST_HUMAN	tq04108.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN (HUMAN);
215	11962	18628		28.1	0.0E+00	A1587308.1 EST_HUMAN	tq04108.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN (HUMAN);
217	9496	18630		2	0.0E+00	AF195658.1 NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
219	9498			39.28	0.0E+00	4506832 NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
220	9499			11.09	0.0E+00	AF132000.1 NT	Homo sapiens TADA1 protein mRNA, complete cds
226	9505	18635		1.91	0.0E+00	AB018284.1 NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
227	9505	18635		1.98	0.0E+00	AB018284.1 NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	9506	18636		2.02	0.0E+00	687844 NT	Mus musculus testis-specific protein, Y-linked-like (Tspyl) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
242	9520	18651	6.91	0.0E+00	5453865	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
244	9522		10.25	0.0E+00	AL183201.2	NT	Homo sapiens chromosome 21 segment HS21C001
251	9527	18657	4.08	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
253	9529	18660	1.76	0.0E+00	X89772.1	NT	H.sapiens mRNA for interferon alpha/beta receptor (long form)
261	9537		8.15	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
274	9549	18679	1.3	0.0E+00	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
274	9549	18680	1.3	0.0E+00	450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
276	9551	18682	2.35	0.0E+00	7706028	NT	Homo sapiens hypothetical protein LOC51250, mRNA
287	9561		1.27	0.0E+00	D83227.1	NT	Homo sapiens DCRR1 mRNA, partial cds
288	9562	18695	3.32	0.0E+00	D83227.1	NT	Homo sapiens DCRR1 mRNA, partial cds
288	9562	18696	3.32	0.0E+00	D83227.1	NT	Homo sapiens DCRR1 mRNA, partial cds
289	9563		0.81	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT031-181199-020-B03 CT031 Homo sapiens cDNA
288	9571	18703	8.24	0.0E+00	4567029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
298	9571	18704	8.24	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
309	9582	18714	3.6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA0109 protein, partial cds
310	9583	18715	3.82	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA0109 protein, partial cds
311	11985		14.42	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
312	9584	18716	0.88	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylaminimidazole synthetase, GART mRNA
313	9585		4.5	0.0E+00	AA48002.1	EST_HUMAN	zv18c06_11 Soares_NhMPU_S1 Homo sapiens cDNA clone IMAGE:7535984_5'
314	9586	18717	21.53	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
315	9586	18717	17.61	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
319	9590	18721	1.63	0.0E+00	AF114468.1	NT	Homo sapiens intersector short isoform (ITSN) mRNA, complete cds
332	9602	18730	1.09	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (H42303)
332	9602	18731	1.09	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (H42303)
333	9603	18732	3.8	0.0E+00	76572/13	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
334	9603	18732	2.51	0.0E+00	76572/13	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
349	9617	18744	1.88	0.0E+00	5174674	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (Drosophila) homolog; translocated to 4 (MLLT4) mRNA
350	9618	18745	1.11	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
353	9621	18749	22.13	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
356	9634	18754	1.89	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zf31) mRNA, partial cds
361	9638	18758	2.54	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
361	9628	18759	2.54	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA

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Probe Seq ID NO.	Exon Seq ID NO.	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
362	119866	18760	4.02	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA	
364	9630	18762	0.8	0.0E+00	4607500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA	
366	9633	18766	1.94	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA	
367	9634	18767	1.2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds	
368	9634	18767	1	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds	
370	9636	18768	0.69	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIA1) mRNA	
381	9845	18780	2.68	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000888 5'	
392	9636	18824	7.13	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds	
393	9687	18825	2.49	0.0E+00	A1363014.1	EST_HUMAN	q981n05_x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE2018457 3' similar to gb>X54189	
397	9652	18787	2.84	0.0E+00	AW7764180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN); RC2-CT0320-300100-018-009 C10320 Homo sapiens cDNA	
400	9654	18780	12.1	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
401	9655	18781	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
401	9655	18792	2.32	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
402	9656	18793	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
403	9657	18794	1.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
403	9657	18795	1.8	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
404	9658	18796	0.59	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
405	9659	18797	3.48	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
406	9650	18798	0.61	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA	
407	9681	18789	1.85	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29	
407	9681	18800	1.85	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29	
408	9661	18789	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29	
408	9681	18800	1.89	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29	
412	9685	51.35	0.0E+00	4506808	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA		
428	9291	18393	1.21	0.0E+00	R17795.1	EST_HUMAN	yg09e02.11 Scores infant brain TNB Homo sapiens cDNA clone IMAGE311632 5'	
434	9688	18828	1.24	0.0E+00	4503814	NT	Homo sapiens phosphotriacylglyceride formyltransferase, phosphotriacylglycerinamide synthetase (GART) mRNA	
435	9689	1884	18.84	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPSS5) mRNA	
436	9690	18827	7.31	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds	
437	9691	18828	4.64	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA	
437	9691	18829	4.64	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA	
438	9692	18830	3.52	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds	
450	9703		0.92	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS22(C001	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
452	9705	18843	1.29	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
457	9710		1.48	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
458	9711		2.54	0.0E+00	BE254447.1	EST_HUMAN	601111520 F1 NIH MGCG_16 Homo sapiens cDNA clone IMAGE:3352348 5'
474	9727	18857	8.08	0.0E+00	4504532	NT	Homo sapiens 6-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
474	9727	18858	8.08	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	9732	18868	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
480	9732	18867	15.14	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
490	9743	18873	3.04	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
491	9744	18874	7.23	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
491	9744	18875	7.23	0.0E+00	AL163246.2	NT	Homo sapiens mRNA for KIAA1209 protein. partial cds
500	9752	18880	2.83	0.0E+00	AB033035.1	NT	Homo sapiens cDNA clone NT2RP4. Homo sapiens cDNA clone NT2RP4000837 5'
502	9754	18882	1.88	0.0E+00	AL132898.1	EST_HUMAN	AU132898 NT2RP4. Homo sapiens cDNA clone IMAGE:3615758 5'
510	9762	18888	3.47	0.0E+00	BE85144.1	EST_HUMAN	601274951 F1 NIH MGCG_20 Homo sapiens cDNA
511	11989	18889	1.89	0.0E+00	AW388825.1	EST_HUMAN	PM6-DT0065-130400-002-c6 D10685 Homo sapiens cDNA
514	9765	18891	1.14	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
515	9766	18892	1.09	0.0E+00	892955	NT	Homo sapiens PC328 protein (PC328) mRNA
618	9769		0.75	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-0170800-120-F07 F70159 Homo sapiens cDNA
525	9776	18901	8.28	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
532	11970	18905	1.5	0.0E+00	BE0816227.1	EST_HUMAN	QV2-BT0635-160400-42-h05 BT0635 Homo sapiens cDNA
537	9788	18911	1.08	0.0E+00	BF028005.1	EST_HUMAN	601764853 F1 NIH MGCG_53 Homo sapiens cDNA clone IMAGE:3896998 5'
543	9794	18918	1.13	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein. partial cds
546	9797	18921	8.28	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
547	9798	18922	4.75	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
547	9798	18923	4.75	0.0E+00	4504038	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
549	9800	18925	1.77	0.0E+00	69223831	NT	Homo sapiens anillin (LOC54443) mRNA
550	9801	18926	1.44	0.0E+00	89223831	NT	Homo sapiens anillin (LOC54443) mRNA
550	9801	18927	1.44	0.0E+00	89223831	NT	Homo sapiens X-linked arthridrotic ectodermal dysplasia protein genes (EDA), exon 2 and flanking repeat regions
555	9805		5.12	0.0E+00	AF003528.1	NT	U1-H-B1-acb-h-04-0-U1-s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713957 3'
563	9813	18936	1.42	0.0E+00	AV15324.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
573	9823		7.59	0.0E+00	D10083.1	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCFS1), nuclear gene encoding mitochondrial protein, mRNA
638	9841	18861	3.94	0.0E+00	5174742	NT	Human apolipoprotein A-I (APOA1) gene, exon 1
608	9853		5.9	0.0E+00	J04086.1	NT	Human apolipoprotein A-I (APOA1) gene, exon 1

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T _{op}) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
609	9856	18975	3.34	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH MGCC 75 Homo sapiens cDNA clone IMAGE:4045447 5'
615	9860	18979	1.28	0.0E+00	4501834	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
620	9865	18985	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
620	9865	18986	0.9	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
628	9873	18994	2.58	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
630	9875	18997	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
632	9877	18998	1.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9879	18999	2.11	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
633	9878	19000	2.11	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19001	0.84	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	9879	19002	0.84	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
641	9887	19012	1.32	0.0E+00	AA399486.1	EST_HUMAN	z60c07/r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:726732 5'
645	9891	19016	12.08	0.0E+00	D1078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
649	9895	19019	3.5	0.0E+00	W78811.1	EST_HUMAN	z51b04/r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); z51b04/r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
649	9895	19020	3.5	0.0E+00	W78811.1	EST_HUMAN	z51b04/r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
652	9898		3.55	0.0E+00	4885326	NT	Homo sapiens novel SH2-containing protein 3 (NSP3), mRNA
659	9905	19032	2.48	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
661	9907	19035	1.88	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
664	9910	19039	1.49	0.0E+00	U05255.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
668	9914	19042	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
668	9914	19043	0.87	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
674	9919	19048	4.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
674	9919	19049	4.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
680	11973		1.26	0.0E+00	X57147.1	NT	Human endogenous retrovirus pH-E (ERV9)
689	8832	19063	17.16	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 1 (HMGB1) mRNA
694	8837	19067	4.7	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
704	8848	19082	3.3	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
716	8858	19086	108.97	0.0E+00	AA614537.1	EST_HUMAN	np49d01-s1 NCI CGAP_Brl1 Homo sapiens cDNA clone IMAGE:1129833 3' similar to gb:X57352 INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
720	9982	19100	4.1	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
720	9982	19101	4.1	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
730	8972	19110	1.35	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

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Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1307	10523	19882	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19883	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1307	10523	19884	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1308	10524		3.13	0.0E+00	Af088158.1	NT	Homo sapiens protein phosphatase 2A B R gamma subunit gene, exon 5
1318	11890	19896	1.32	0.0E+00	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1318	11890	19897	1.32	0.0E+00	7657539	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1323	10538	19702	1.51	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1324	10539	19703	2.45	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1326	10541	19704	0.63	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1327	10542	19705	0.68	0.0E+00	5803148	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1328	10543	19706	2.48	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1330	10545	19708	4.21	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1331	10546	19709	5.75	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1332	10547	19710	5.16	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1333	10548	19711	4.94	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1333	10548	19712	4.94	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1345	10559	19725	2.1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1402	10616	19780	1.83	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1402	10616	19781	1.83	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350471 5'
1412	10625	19781	1.3	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cystinosis cylid gene
1421	10634	19803	0.91	0.0E+00	AJ208756.1	EST_HUMAN	q38b0x1 Soares_testis_NIH_Homo sapiens cDNA clone IMAGE:1637427 3' similar to WP:T27A15 CE14213 ;
1422	10635	19804	44.87	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1431	10644	19816	2.73	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1431	10644	19817	2.73	0.0E+00	7705585	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1433	10646	19818	7.39	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1441	10655	19829	3.3	0.0E+00	AF038280.1	NT	Homo sapiens alpha-1-fucosidase (alpha-1-6FucT) gene, exon 7
1459	10672	19844	3.25	0.0E+00	AL132898.1	NT	Novel human gene on chromosome 20
1463	10678	19849	2.08	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1468	10679	19852	9.32	0.0E+00	6812457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1468	10681	19854	2.31	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1468	10681	19855	2.31	0.0E+00	7661985	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1500	10713	19885	1.19	0.0E+00	7708434	NT	Homo sapiens hHDc for homolog of Drosophila headcase (LOC51686), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1512	10728	18898	3.05	0.0E+00	AA_481172.1	EST_HUMAN	aa34a03.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815116-5'
1518	10732	18901	111.36	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1518	10732	18802	111.36	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1520	10734	18905	1.22	0.0E+00	AW_876097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1520	10734	18906	1.22	0.0E+00	AW_876097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1521	10735	18907	1.09	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1523	10737		4.77	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1524	10738	18910	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPMB) mRNA
1524	10738	18911	5.07	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPMB) mRNA
1525	10739	18912	2.82	0.0E+00	7662405	NT	Homo sapiens KIAA09857 protein (KIAA09857) mRNA
1526	10740		6.07	0.0E+00	7855972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1) mRNA
1531	10745	18918	3.68	0.0E+00	MB8-78.1	NT	Human transglutaminase mRNA, complete cds
1533	10747	18919	0.95	0.0E+00	4501770	NT	Homo sapiens titin (TTN) mRNA
1533	10747	18920	0.95	0.0E+00	4501770	NT	Homo sapiens titin (TTN) mRNA
1534	11887		72.34	0.0E+00	4508654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1535	10748	18921	74.58	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1545	10758	18892	13.15	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
1551	10765		2.44	0.0E+00	D00333.1	NT	Human c-yes-2 gene
1559	10773	18948	8.95	0.0E+00	Z83738.1	NT	H sapiens hr-2B gene
1560	10774	18947	2.11	0.0E+00	5921460	NT	Homo sapiens bulbyrophillin, subfamily 2, member A1 (BTN2A1) mRNA
1560	10774	18948	2.11	0.0E+00	5921460	NT	Homo sapiens bulbyrophillin, subfamily 2, member A1 (BTN2A1) mRNA
1561	10775	18949	9.8	0.0E+00	AV_860831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKCB0F02.5'
1561	10776	18950	9.8	0.0E+00	AV_860831.1	EST_HUMAN	AV680831 GKC Homo sapiens cDNA clone GKCB0F02.5'
1564	11988	18953	3.17	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1568	10781	18954	1.39	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1570	10783	18867	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
1570	10783	18958	3.7	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
1572	10785	18959	43.92	0.0E+00	5728876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10) mRNA
1572	10785	18960	43.92	0.0E+00	5728876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10) mRNA
1574	10787	18962	1.25	0.0E+00	MR1803.1	NT	Human sodium channel mRNA
1588	10801	18977	8.91	0.0E+00	H28973.1	EST_HUMAN	y076c05.31 Scores adult brain N2b4H1B55Y Homo sapiens cDNA clone IMAGE:183848.3'
1596	10810	18987	9.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1596	10810	18988	8.46	0.0E+00	AB046828.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1615	10828	20003		1.26	0.0E+00 AW/444637.1	EST_HUMAN	U1-H-B13-8jkw-c-04-0-UJ.s1 NCI_CGA_P_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3
1640	10854	20034		1.25	0.0E+00 BE1443B4.1	EST_HUMAN	MRO-HT0166-19i199-004-b11 HT0166 Homo sapiens cDNA
1640	10854	20035		1.25	0.0E+00 BE1443B4.1	EST_HUMAN	MRO-HT0166-19i199-004-b11 HT0166 Homo sapiens cDNA
1644	10858	20039		13.17	0.0E+00 AI768104.1	EST_HUMAN	wg81607_x1 Scores_NSF_F8_9W_QT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR-Q82788 Q82788 CYS2/HIS2 ZINC_FINGER PROTEIN_1
1645	10859	20040		3.17	0.0E+00 AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1648	10862	20043		2.18	0.0E+00 M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1648	10862	20044		2.18	0.0E+00 M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1650	10864	20046		39.38	0.0E+00 4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1651	10865	20047		1.68	0.0E+00 7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG) mRNA
1655	10869	20050		1	0.0E+00 BE222374.1	EST_HUMAN	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1655	10869	20051		1	0.0E+00 BE222374.1	EST_HUMAN	hui1d05_x1 NCI_CGA_P_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O85147 O85147
1657	10870	20053		1.69	0.0E+00 4557610	NT	MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1660	10873	20056		4.81	0.0E+00 H30132.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1660	10873	20057		4.81	0.0E+00 H30132.1	EST_HUMAN	y659608_r1 Scores breast 3NbHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1662	10875	20059		5.52	0.0E+00 780780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1662	10875	20060		5.52	0.0E+00 280780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1665	10878			17.87	0.0E+00	5031748	H. sapiens H2B/h gene
1674	10883	20072		5.65	0.0E+00	8923584	Hom sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1677	10889	20075		1	0.0E+00	6453855	Hom sapiens per centidler material 1 (PCM1) mRNA
1682	10894	20082		2.52	0.0E+00	4826973	Hom sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1688	10900	20089		5.88	0.0E+00 AB026542.1	NT	Hom sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGB1), mRNA
1690	10902			2.24	0.0E+00 S94400.1	NT	Hom sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1699	10911	20088		1.48	0.0E+00	4557538	Hom sapiens per centidler material 1 (PCM1) mRNA
1718	10930	20115		2.86	0.0E+00 AF273841.1	NT	Hom sapiens sulfat transporter, member 2 (SLC25A2) mRNA
1755	12001			57.99	0.0E+00	4506118	Hom sapiens ribosomal protein S2 (RPS2) mRNA
1758	10970	20155		1.84	0.0E+00	4557556	Hom sapiens E1A binding protein P300 (EP300) mRNA
1759	10970	20153		1.84	0.0E+00	4557556	Hom sapiens E1A binding protein p300 (EP300) mRNA
1761	10972	20159		2.04	0.0E+00 U639853.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1764	12002	20163		5.71	0.0E+00	4505632	Hom sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1765	10975	20164	1.37	0.0E+00	AA113030.1	EST_HUMAN	Zm65cd8.s1 Strategene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:5830563'
1776	10988	20178	18.75	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1778	10988	20181	16.16	0.0E+00	AB0022331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1779	10989	20182	14.48	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1779	10989	20183	14.46	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1779	10989	20184	14.48	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1802	11011	20203	7.84	0.0E+00	6005835	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1802	11011	20204	7.84	0.0E+00	6005836	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1811	11020	20212	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1811	11020	20213	1.4	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1815	11023	20215	3.22	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1815	11023	20216	3.22	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1816	11024	20217	7.42	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1816	11024	20218	7.42	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1819	11027	20221	1.23	0.0E+00	AV207280.1	EST_HUMAN	Ui-H-B1-efn-f-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333'
1819	11027	20222	1.23	0.0E+00	AV207280.1	EST_HUMAN	Ui-H-B1-efn-f-07-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722333'
1841	11049	20239	2.69	0.0E+00	BE277465.1	EST_HUMAN	601179164FI NIH_MGGC_20 Homo sapiens cDNA clone IMAGE:35472395'
1841	11049	20240	2.69	0.0E+00	BE277465.1	EST_HUMAN	601179164FI NIH_MGGC_20 Homo sapiens cDNA clone IMAGE:35472395'
1859	11063	20257	1.73	0.0E+00	BE0062392.1	EST_HUMAN	RC2-BN0128-20030-012-504 BN0126 Homo sapiens cDNA
1888	11085	20285	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1888	11085	20286	1.4	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1891	11098	20288	3.1	0.0E+00	4506384	NT	Homo sapiens RADI (<i>S. pombe</i>) homolog (RAD1) mRNA, and translated products
1891	11098	20289	3.1	0.0E+00	4506384	NT	Homo sapiens RADI (<i>S. pombe</i>) homolog (RAD1) mRNA, and translated products
1898	11103	20295	7.07	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1900	11107	1.45	0.0E+00	AF1517478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	
1901	12005	20289	1.73	0.0E+00	M58478.1	NT	Human transglutaminase mRNA, complete cds
1901	12005	20300	1.73	0.0E+00	M58478.1	NT	Human transglutaminase mRNA, complete cds
1906	11112	20307	1.52	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGF β 3), mRNA
1906	11112	20308	1.52	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGF β 3), mRNA

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Table 4
Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1809 11114	20310		1.16	0.0E+00	7857038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1911 11116			8.63	0.0E+00 AF240786.1		NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1918 11121			3.42	0.0E+00 M56832.1		NT	Human topoisomerase pseudogene 1
1918 12006	20317		1.66	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTNSA2), mRNA
1920 11124	20319		1.35	0.0E+00 BE018098.1	EST_HUMAN	bb73111_Y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045' 5'	
1926 11130	20324		1.24	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1926 11130	20325		1.24	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1936 11140			1.01	0.0E+00 AL163252.2		NT	Homo sapiens chromosome 21 segment HS21C052
1938 11142	20338		1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1938 11142	20339		1.12	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1939 11143	20340		7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1939 11143	20341		7	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1949 11153	20355		1.05	0.0E+00 AB018333.1		NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1949 11153	20356		1.05	0.0E+00 AB018333.1		NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
1955 11159	20360		1.34	0.0E+00 M33782.1		NT	Human TFEB protein mRNA, partial cds
1955 11159	20361		1.34	0.0E+00 M33782.1		NT	Human TFEB protein mRNA, partial cds
1957 11161	20362		1.72	0.0E+00 AW183024.1	EST_HUMAN	x689001_X1 NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2878913' 3'	
1957 11161	20363		1.72	0.0E+00 AW183024.1	EST_HUMAN	x689001_Y1 NCI_CGAP_Pen1 Homo sapiens cDNA clone IMAGE:2878913' 3'	
1958 11162	20364		9.82	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1958 11162	20365		9.82	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1960 11164	20367		12.58	0.0E+00	7862056	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1961 11165	20368		1.95	0.0E+00 AB011149.1		NT	Homo sapiens mRNA for KIAA0377 protein, complete cds
1962 11166	20369		1.04	0.0E+00 Z47538.1		NT	H.sapiens genes for semenogelin I and semenogelin II
1962 11166	20370		1.04	0.0E+00 Z47538.1		NT	H.sapiens genes for semenogelin I and semenogelin II
1969 11173	20379		4.4	0.0E+00 AB040946.1		NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1969 11193	20402		1.15	0.0E+00 AF273841.1		NT	Homo sapiens SMCY (SMCY) gene, complete cds
1969 11193	20403		1.15	0.0E+00 AF273841.1		NT	Homo sapiens SMCY (SMCY) gene, complete cds
2020 11221	20429		1.36	0.0E+00	7708742	NT	Homo sapiens TSPYTG3a (TP53TG3a), mRNA
2024 11225	20433		28.23	0.0E+00 BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198' 5'	
2024 11225	20434		28.23	0.0E+00 BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198' 5'	
2026 11227	20435		0.95	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B)
2027 11228	20436		1.44	0.0E+00 BF207688.1	EST_HUMAN	601881874F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081483' 5'	

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 Table 4
 Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2038	11229	20437	6.57	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2039	11231	20439	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2040	11231	20440	1.7	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2042	11233		4.04	0.0E+00	7657468 NT		Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121), mRNA
2034	11235		2.43	0.0E+00	4585863 NT		Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2035	11236	20443	2.31	0.0E+00	Z42398.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-Qic022
2037	11238		2.23	0.0E+00	A1244247.1	EST_HUMAN	q86f08_x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:19888871 3' similar to contains Alu repetitive element
2042	11243	20452	7.59	0.0E+00	B877226.1	EST_HUMAN	601485_146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2044	11245	20454	4.44	0.0E+00	BF315325.1	EST_HUMAN	601802804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2044	11245	20455	4.44	0.0E+00	BF315325.1	EST_HUMAN	601802804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2050	11251	20463	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2050	11251	20464	4.16	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2056	11257	20471	2.15	0.0E+00	L00520.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2056	11257	20472	2.15	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2061	11262	20476	1.54	0.0E+00	4758489 NT		Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2065	11268	20479	1.28	0.0E+00	BE500985.1	EST_HUMAN	7834c02-x1 NCI_CGAP_GCG Homo sapiens cDNA clone IMAGE:32208610 3' similar to SW:DTD_HUMAN
2084	11284		4.59	0.0E+00	BE787984.1	EST_HUMAN	P50443 SULFATE TRANSPORTER
2085	11285		1.21	0.0E+00	AF018963.1	NT	QV1-GN0065-140800-31B-c10 GN0065 Homo sapiens cDNA
2087	11287	20500	8.37	0.0E+00	BF027562.1	EST_HUMAN	Hom sapiens X-linked juvenile retinoschisis protein (XLRS1) gene, exon 6 and complete cds
2088	11288	20501	1.73	0.0E+00	BE072624.1	EST_HUMAN	601672068F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2090	11289	20502	4.32	0.0E+00	AF240788.1	NT	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2092	11292	20504	4.24	0.0E+00	AV752708.1	EST_HUMAN	Hom sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1), genes, complete cds
2093	11293	20505	4.83	0.0E+00	A1804640.1	EST_HUMAN	IL3-CT019-271099-022-G10 CT0219 Homo sapiens cDNA
2093	11293	20506	4.83	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2146	11344		4.65	0.0E+00	L14787.1	NT	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2152	11350	20568	1.31	0.0E+00	BE274698.1	EST_HUMAN	Human DNA-binding protein mRNA, 3' end
2154	11352	20569	1.28	0.0E+00	D87685.1	NT	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346688 5'
2155	11353	20570	78.41	0.0E+00	AV738288.1	EST_HUMAN	Human mRNA for KIAA0244 gene, partial cds
2155	11353	20571	78.41	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2157	11355	20573	4.48	0.0E+00	AA931691.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2161	11359	20577	47.03	0.0E+00	BF344434.1	EST_HUMAN	cc32e01_s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567886 3'
							602011482F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'

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Table 4
Single Exon Probes Expressed in HEK Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2162	11360	20578	100.43	0.0E+00	BE748898.1	EST_HUMAN	601157218871 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2165	11363	20581	7.55	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-256900-438-b08 TN0141 Homo sapiens cDNA
2165	11363	20582	7.55	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-256900-438-b08 TN0141 Homo sapiens cDNA
2169	12012	20587	5.54	0.0E+00	BF313671.1	EST_HUMAN	6019002817-1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128622 5'
2172	11369	20590	4.03	0.0E+00	BE018750.1	EST_HUMAN	b684602-Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR-Q15170 Q15170 TRANSCRIPTION FACTOR SII-RELATED PROTEIN
2174	11371	20592	33.41	0.0E+00	AA042813.1	EST_HUMAN	2453c07_s1 Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN GMPOTE (HUMAN);
2174	11371	20593	33.41	0.0E+00	AA042813.1	EST_HUMAN	2453c07_s1 Scares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN GMPOTE (HUMAN);
2181	11378	20600	4.19	0.0E+00	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2181	11378	20601	4.19	0.0E+00	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2182	11379	20602	11.03	0.0E+00	766240.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2182	11379	20603	11.03	0.0E+00	766240.1	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2187	11384		2.34	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2188	11385	20608	1.94	0.0E+00	AA282281.1	EST_HUMAN	2412b10.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2195	11392	20614	3.49	0.0E+00	BE897487.1	EST_HUMAN	6014323117F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2205	11402	20627	5.93	0.0E+00	455755.6	NT	Homeo sapiens E1A binding protein p300 (EP300), mRNA
2211	11408	20632	11.03	0.0E+00	766240.1	NT	Homeo sapiens KIAA0952 protein (KIAA0952), mRNA
2217	11414	20639	17.25	0.0E+00	BE895281.1	EST_HUMAN	6014355235F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918807 5'
2221	11418	20643	6.39	0.0E+00	BE905583.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2221	11418	20644	6.39	0.0E+00	BE905583.1	EST_HUMAN	601495208F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3897457 5'
2224	11420	20648	3.52	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2263	11458	20676	2.23	0.0E+00	BF344756.1	EST_HUMAN	60201409F1 NCI CGAP_Bm64_Homo sapiens cDNA clone IMAGE:4149770 5'
2263	11458	20677	2.23	0.0E+00	BF344756.1	EST_HUMAN	60201409F1 NCI CGAP_Bm64_Homo sapiens cDNA clone IMAGE:4149770 5'
2265	11460	20679	4.51	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDGP (mouse homolog) 6 (DEFG), mRNA
2265	11460	20680	4.51	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDGP (mouse homolog) 6 (DEFG), mRNA
2266	11461	20681	3.23	0.0E+00	A1076404.1	EST_HUMAN	od08c07_x1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2269	11464	20684	3.65	0.0E+00	AA428001.1	EST_HUMAN	278a1111 Scares_total_fetus_NB21F8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2269	11464	20685	3.65	0.0E+00	AA428001.1	EST_HUMAN	278a1111 Scares_total_fetus_NB21F8_9w Homo sapiens cDNA clone IMAGE:759740 5'
2271	11466	20687	2.65	0.0E+00	AA690367.1	EST_HUMAN	z11e12_s1 Scares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2272	11467	20688	3.24	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI CGAP_Bm67_Homo sapiens cDNA clone IMAGE:4157339 5'
2277	11472	20694	1.47	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
2277	11472	20695	1.47	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds

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Table 4
Single Exon Probes Expressed in HEIA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No:	Top Hit Database Source	Top Hit Descriptor
2278	11473	20696	1.81	0.0E+00	6325466 NT		Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2285	11480	20702	3.89	0.0E+00	BE676095.1	EST_HUMAN	7F22602_x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:O94939 O94939
2288	11483	20704	8.5	0.0E+00	AF044571.1	NT	Homo sapiens phosphotyrosine kinase alpha subunit (PKA2) gene, exon 32
2289	11484	20705	2.07	0.0E+00	AI625542.1	EST_HUMAN	tY76508_x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2283162 3'
2281	11486	20706	2.04	0.0E+00	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
2284	11489	20708	19.82	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2284	11489	20709	19.92	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2287	11492	20712	7.66	0.0E+00	5803178 NT		Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2287	11492	20713	7.68	0.0E+00	5803178 NT		Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2303	11497	20716	3.58	0.0E+00	7682007 NT		Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2303	11497	20717	3.58	0.0E+00	7682007 NT		Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2307	11501	20722	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2307	11501	20723	2.32	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2317	11511	20731	2.36	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SRP-BETA-1) mRNA
2321	11514	20735	3.85	0.0E+00	AU311142	NT2RP3002064 5'	
2322	11515		85.13	0.0E+00	BE784026.1	EST_HUMAN	601586843F1 NIH_3T3 Homo sapiens cDNA clone IMAGE:3341003 5'
2323	11516	20736	17.68	0.0E+00	7682017 NT		Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2324	11517	20737	1.62	0.0E+00	4758497 NT		Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2324	11517	20738	1.62	0.0E+00	4758497 NT		Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2325	11518						Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP4A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2327	11520	20740	16.29	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	11520	20741	16.29	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2327	11520	20742	16.28	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2328	11521	20743	1.72	0.0E+00	8923088 NT		Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2345	11538				4.01	EST_HUMAN	MFO-B10070-080600-029-d12 BN0070 Homo sapiens cDNA
2347	11570	20790	1.85	0.0E+00	AU118382.1	EST_HUMAN	AU118382 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2379	11572		3.76	0.0E+00	AI042035.1	EST_HUMAN	ox601602_x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1680683 3' similar to TR:O98662
2381	11574	20793	4.62	0.0E+00	8923620 NT		Homo sapiens hypothetical protein FLJ20083 (FLJ20083), mRNA
2383	11576	20794	1.68	0.0E+00	AW303898.1	EST_HUMAN	xv15f07_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2385	11578			1.46	0.0E+00 BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2396	11589			30.25	0.0E+00 AB005622.1	EST_HUMAN	AB005622 Hela cDNA (T.Nova) Homo sapiens cDNA similar to adenylyl kinase isozyme 2A (GRIN2A) mRNA
2399	11592	20810		4.93	0.0E+00	60008002	NT
2403	11595	20814		1.61	0.0E+00 D85806.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2403	11595	20815		1.61	0.0E+00 D85806.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2411	11603	20824		2.27	0.0E+00 AF06275.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2415	11606	20828		2.38	0.0E+00 BF545274.1	EST_HUMAN	602018058F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4153670 5'
2422	11613	20836		4.9	0.0E+00	57287777	NT
2430	11621	20842		1.25	0.0E+00 U13866.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1) mRNA
2430	11621	20843		1.25	0.0E+00 U13868.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2431	11622	20844		131.32	0.0E+00 BF569144.1	EST_HUMAN	602184558F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2440	11631	20852		2.9	0.0E+00 AW1468922.1	EST_HUMAN	he04h04_x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2442	11633	20853		5.83	0.0E+00 AW501010.1	EST_HUMAN	U1-HF-B1P0p-ais-c-07-0-U1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2451	11642			1.22	0.0E+00 A1287878.1	EST_HUMAN	qY23106_x1 NCI CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element MIR repetitive element
2457	11648	20869		1.84	0.0E+00	5453985	NT
2457	11648	20870		1.84	0.0E+00	5453986	NT
2470	11661			2.3	0.0E+00 AW1613853.1	EST_HUMAN	RC3-ST0197-300300-016-c04 ST0197 Homo sapiens cDNA
2475	11668	20885		70.13	0.0E+00 BE795542.1	EST_HUMAN	601582530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2476	11114	20310		3.29	0.0E+00	7657038	NT
2477	11667	20886		2.58	0.0E+00 BF509482.1	EST_HUMAN	U1-HF-B102-b-08-0-U1_x1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086653 3'
2480	11670	20888		2.03	0.0E+00 Z32984.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2482	11672			3.62	0.0E+00	6453871	NT
2485	11675	20892		2.44	0.0E+00 BE910378.1	EST_HUMAN	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2486	11676	20893		6.81	0.0E+00	7657498	NT
2487	11677	20894		2.18	0.0E+00	80223340	NT
2488	11678	20895		8.81	0.0E+00 US3239.1	NT	Human Sae62 (Sae62) mRNA, complete cds
2484	11684	20901		14.6	0.0E+00 BE886480.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
2488	11687	20908		5.8	0.0E+00 BE587551.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2488	11687	20907		5.8	0.0E+00 BE87551.1	EST_HUMAN	601489241F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3891371 5'
2489	11688	20908		2.64	0.0E+00 AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF6
2518	11705	20918		1.89	0.0E+00 BE536821.1	EST_HUMAN	601084173BF1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2522	11710	20926		58.3	0.0E+00 AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2522	11710	20927		58.3	0.0E+00 AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y79AA1001673 5'

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe Seq ID	Exon Seq ID	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
2523	11711	20928	35.33	0.0E+00	BE282896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887855 5'	
2523	11711	20929	35.33	0.0E+00	BE292898.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887855 5'	
2524	11712	20930	1.33	0.0E+00	BF223041.1	EST_HUMAN	7Q2712X1 NCI CGAP_GC6 Homo sapiens cDNA clone IMAGE: 3' similar to TR:000248 000246 HYPOTHETICAL 9.3 KD PROTEIN;	
2527	11715	20932	8.27	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds	
2558	11954	20934	1.76	0.0E+00	AB037638.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds	
2558	11954	20935	1.78	0.0E+00	AB037638.1	EST_HUMAN	U1-H-BW1-amp-f-12-0-U1.51 NCI_OGA_P_Sub7 Homo sapiens cDNA clone IMAGE:30706831 3'	
2559	11745	20935	3.26	0.0E+00	BF533835.1	EST_HUMAN	60215265SF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3231785 5'	
2564	11750	20970	1.78	0.0E+00	BF672818.1	EST_HUMAN	601279873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3621786 5'	
2566	11752	20971	2.67	0.0E+00	BE616685.1	EST_HUMAN	601279873F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'	
2570	11755	20975	0.91	0.0E+00	BF204131.1	EST_HUMAN	601863073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'	
2570	11755	20976	0.91	0.0E+00	BF204131.1	EST_HUMAN	601863073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'	
2574	11759	20979	3.98	0.0E+00	AB037742.1	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28KD (TAF21) mRNA	
2575	11760	20980	2.79	0.0E+00	5032150	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds	
2578	11764	20985	0.29	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds	
2578	11765	20986	2.28	0.0E+00	BE795445.1	EST_HUMAN	601158010BF1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3544304 5'	
2578	11765	20986	2.28	0.0E+00	BE795445.1	EST_HUMAN	601158010BF1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3544304 5'	
2579	11765	20987	2.26	0.0E+00	BE795445.1	EST_HUMAN	601158010BF1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3544304 5'	
2582	11768	20988	1.03	0.0E+00	BE293328.1	EST_HUMAN	601158010BF1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'	
2589	11775	20989	11.83	0.0E+00	BE192472.1	EST_HUMAN	601158010BF1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3539222 5'	
2591	11777	20986	0.91	0.0E+00	AB202070.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds	
2596	11784	21004	3.6	0.0E+00	4504685	NT	MP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA	
2608	11782	21011	4.33	0.0E+00	AF173227.1	NT	Homo sapiens cyclase-activating protein 2 (GUCA1B) gene, exon 1	
2812	11786	21012	1.91	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds	
2813	11787	21013	2.06	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP3 Human sepius cDNA clone NT2RP4001984 5'	
2814	11788	21014	0.92	0.0E+00	M69225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds	
2817	11801	21017	3.04	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Human sepius cDNA clone NT2RP3000779 5'	
2817	11801	21018	3.04	0.0E+00	AU130403.1	EST_HUMAN	RC1-OT0088-220300-01-007 O T0086 Homo sapiens cDNA	
2820	11804	21021	1.65	0.0E+00	AV887015.1	EST_HUMAN	7H15H02X1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'	
2823	11807	21024	1.42	0.0E+00	BF000018.1	EST_HUMAN	7H15H02X1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3628923 5'	
2624	11808	21025	14.04	0.0E+00	BB383165.1	EST_HUMAN	601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3610267 5'	
2625	11809		2.6	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'	
2649	11832	21046	0.9	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA	
2659	11840	21054	1.28	0.0E+00	A8037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2681	11863		33.03	0.0E+00	AA316723.1	EST_HUMAN	EST188-14 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA clone IMAGE:3943591 5'
2682	11864	21076	30.31	0.0E+00	BE784884.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2687	11868	21082	4.57	0.0E+00	U32253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2689	11870	21084	1.69	0.0E+00	AF110763.1	NT	Human sapiens skeletal muscle LM-protein 1 (FLI-1) gene, complete cds
2694	11874	21088	80.93	0.0E+00	BE786376.1	EST_HUMAN	60158178F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2695	11875	21089	1.08	0.0E+00	BF580682.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2698	12925	21093	28.45	0.0E+00	BE563493.1	EST_HUMAN	601335488F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:35889564 5'
2699	11878		3.2	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBB/E09 5'
2701	11880	21096	2.18	0.0E+00	5174486	NT	Human sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2701	11880	21097	2.18	0.0E+00	5174486	NT	Human sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2702	11881	21098	1.13	0.0E+00	8923441	NT	Human sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2702	11881	21099	1.13	0.0E+00	8923441	NT	Human sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA
2703	11882	21100	2.55	0.0E+00	AF280195.1	NT	Human sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2704	11883		83.21	0.0E+00	AV851086.1	EST_HUMAN	AV851086 GLC Homo sapiens cDNA clone GLCC1D07 3'
2705	11884	21101	5.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
2705	11884	21102	5.42	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
2712	11891	21109	14.18	0.0E+00	BE747193.1	EST_HUMAN	60158093F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928472 5'
2724	11803		1.33	0.0E+00	AL163201.2	NT	Human sapiens chromosome 21 segment HS2/C001
2725	11804	21120	4.31	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-8nw->07-0-U1 s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2736	11815	21128	4.15	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2741	11820	21135	1.04	0.0E+00	7427522	NT	Human sapiens protein tyrosine phosphatase, receptor type T (PTPRT) mRNA
2744	11823	21137	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCA03 5'
2744	11823	21138	18.85	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCA03 5'
2746	11825		13.22	0.0E+00	AI879163.1	EST_HUMAN	SW:R13A_HUMAN PA0428 60S RIBOSOMAL PROTEIN L13A;
2749	11828	21143	2.75	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4214679 5'
2750	11829	21144	43.65	0.0E+00	BE872768.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854642 5'
2752	11831	21145	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494_N12RP3 Homo sapiens cDNA clone N12RP3002872 5'
2752	11831	21148	3.13	0.0E+00	AU131494.1	EST_HUMAN	AU131494_N12RP3 Homo sapiens cDNA clone N12RP3002872 5'
2753	11832	21147	94.45	0.0E+00	BE300344.1	EST_HUMAN	6009447194F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2753	11832	21148	94.45	0.0E+00	BE300344.1	EST_HUMAN	6009447194F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2758	9472	18603	2.6	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen (Human, blood, Genomic DNA, 3068 nt)
2761	11838		3.13	0.0E+00	AB053281.1	NT	Human sapiens BTRCP2 mRNA for F-box and WD-repeats protein isoform C, complete cds

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 Table 4
 Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
2767 8982	19125	19125	2.16	0.0E+00 AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds		
2767 8982	19126	19126	2.16	0.0E+00 AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds		
2771 10272	18423		5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA	
2771 10272	18424		5.49	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA	
2789 12020	21158		4.21	0.0E+00 X85680.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene		
2790 12030			1.26	0.0E+00 AF088624.1	NT	Homo sapiens 6-aminoevulinate synthase 2 (ALAS2) gene, complete cds		
2791 12031			1.42	0.0E+00 AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds		
2797 12037			1.15	0.0E+00 AJ238852.1	NT	Homo sapiens partial rp13 gene for ribosomal protein L3, U82 snoRNA, U83a snoRNA and U83b snoRNA genes		
2798 12038	21160		2.34	0.0E+00 AL163201.2	NT	Homo sapiens chrotonosome 21 segment HS21C001		
2802 12042	21163		2.17	0.0E+00 M80802.1	NT	Human ARNIAK nucleoprotein mRNA, 5' end		
2804 12044	21165		1.42	0.0E+00 BE154504.1	EST_HUMAN	PM0-HT0343-281/289-003-e02 HT0343 Homo sapiens cDNA		
2804 12044	21166		1.42	0.0E+00 BE154504.1	EST_HUMAN	PM0-HT0343-281/289-003-e02 HT0343 Homo sapiens cDNA		
2806 12046			1.59	0.0E+00 X73428.1	NT	H. sapiens Id3 gene for HLH type transcription factor		
2808 12048			2.79	0.0E+00 AL163268.2	NT	Homo sapiens chrotonosome 21 segment HS21C008		
2809 12049	21169		1.22	0.0E+00	7019584	NT	Homo sapiens finger protein 22 (ZNF221), mRNA	
2809 12049	21170		1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 22 (ZNF221), mRNA	
2809 12049	21171		1.22	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 22 (ZNF221), mRNA	
2811 12051	21172		1.03	0.0E+00 M88478.1	NT	Human transglutaminase mRNA, complete cds		
2815 12054	21177		25.36	0.0E+00 D50837.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene		
2815 12054	21178		25.36	0.0E+00 D50837.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene		
2818 12057	21181		3.87	0.0E+00 AL088857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes		
2819 12058			10.77	0.0E+00 Y10568.1	NT	H. sapiens mRNA for nuclear DNA helicase II		
2820 12059			1.01	0.0E+00 AF152303.1	NT	Homo sapiens procathepsin alpha C1 (PCDH-alpha-C1) mRNA, complete cds		
2821 12060	21182		125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	
2821 12060	21183		125.82	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	
2833 12072	21184		2.68	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA	
2836 12075	21188		1.36	0.0E+00 AL047599.1	EST_HUMAN	DKF2B886G0621-11 588 (synonym: hulu) Homo sapiens cDNA clone DKF2B886G0621		
2837 12076	21189		1.1	0.0E+00	7861883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA	
2837 12076	21200		1.1	0.0E+00	7861883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA	
2838 12077			1.88	0.0E+00	4503088	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA	
2840 12079	21202		6.06	0.0E+00 BE081898.1	EST_HUMAN	QV2-BT0636-130400-138-n03 BT0636 Homo sapiens cDNA		

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Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	12079	21203	8.08	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0636-130400-138-h03 BT0636 Homo sapiens cDNA
2845	12084	21211	1.41	0.0E+00	68069193 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
2845	12084	21212	1.41	0.0E+00	68069193 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
2848	12087	21216	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2848	12087	21217	2.94	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2849	12088	21218	1.07	0.0E+00	AA215578.1	EST_HUMAN	Z98b11.1.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:883517 3' similar to contains Alu repetitive element;
2849	12084		4.27	0.0E+00	Y19210.1	NT	Homo sapiens Hb5 gene for hair keratin, exons 1 to 9
2859	12097	21227	1.07	0.0E+00	47562279 NT	Homo sapiens Epha4 (EPHA4) mRNA	
2860	12098	21228	47.89	0.0E+00	4503470 NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA	
2861	12099	21229	2.25	0.0E+00	AI561002.1	EST_HUMAN	In1807.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN.;
2861	12099	21230	2.25	0.0E+00	AI561002.1	EST_HUMAN	In1807.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247 O16247 F44E7.2 PROTEIN.;
2863	12101	21232	1.52	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN_132
2864	12102	21233	1.33	0.0E+00	AF1522338.1	NT	Homo sapiens prothrombin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2878	12116	21243	2.8	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2878	12116	21246	2.8	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2879	12117	21247	5.69	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2879	12117	21248	5.69	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2882	12120	21251	6.56	0.0E+00	7681903 NT	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2882	12120	21252	6.56	0.0E+00	7661903 NT	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritox) (Drosophila) homolog; translocated to 4 (MLLT4) mRNA
2883	12121	21253	3.32	0.0E+00	5174574 NT	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritox) (Drosophila) homolog; translocated to 4 (MLLT4) mRNA
2883	12121	21254	3.32	0.0E+00	5174574 NT	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (tritox) (Drosophila) homolog; translocated to 4 (MLLT4) mRNA
2888	12125	21258	1.33	0.0E+00	BF110702.1	EST_HUMAN	7n4dd03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone Q9VLN1 CG17283 PROTEIN.;
2888	12125	21259	1.33	0.0E+00	BF110702.1	EST_HUMAN	7n4dd03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone Q9VLN1 CG17283 PROTEIN.;
2896	12134	21270	2.63	0.0E+00	4505084 NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA	
2896	12134	21271	2.63	0.0E+00	4505084 NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA	
2898	12138	21273	1.31	0.0E+00	4885214 NT	Homo sapiens v-erb-a avian erythroblastic leukemic viral oncogene homolog-like 4 (ERBB4) mRNA	
2898	12138	21274	1.31	0.0E+00	4885214 NT	Homo sapiens v-erb-a avian erythroblastic leukemic viral oncogene homolog-like 4 (ERBB4) mRNA	

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Single Exon Probes Expressed in HELA Cells

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2802	12140	21277	1.23	0.0E+00	AB011083.1	NT	Homo sapiens mRNA for KIAA0511 protein, partial cds
2803	12144	21280	1.94	0.0E+00	4759827	NT	Homo sapiens neuregulin III (NRXN3) mRNA
2807	12145		0.98	0.0E+00	X98494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2810	12148	21283	1.37	0.0E+00	AB033034.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2812	12150	21284	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2812	12150	21285	1.32	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2814	12152	21287	10.32	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2828	12168		1.27	0.0E+00	AI49880.1	EST_HUMAN	q43903.21 Scores: testis_NH1 Homo sapiens cDNA clone MAGE:1752808 3'
2838	12178	21310	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neurofilin 2 (NRP2) gene, complete cds, alternatively spliced
2838	12178	21311	0.91	0.0E+00	AF281074.1	NT	Homo sapiens neurofilin 2 (NRP2) gene, complete cds, alternatively spliced
2839	12177	21312	3.26	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2851	12189	21322	1.83	0.0E+00	7662273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2852	12190	21323	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2852	12190	21324	2.25	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2863	12201	21335	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2863	12201	21336	2.39	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
2891	12228		0.68	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2893	12230	21362	1.2	0.0E+00	M74098.1	NT	Human displacement protein (CCAA1) mRNA
3002	12238	21368	0.65	0.0E+00	450888	NT	Homo sapiens semenogelin I (SEMG1) mRNA
3004	12240	21370	1.08	0.0E+00	AW1976268.1	EST_HUMAN	EST388375. MAGE resequencing, MAGN Homo sapiens cDNA
-3009	12245		4.68	0.0E+00	AF195933.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPPEP2) gene, complete cds
3012	12248	21378	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSP70A) mRNA
3012	12248	21379	10.7	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSP70A) mRNA
3014	12250		7.18	0.0E+00	AL359403.1	NT	Isomeric 2 of a novel human mRNA from chromosome 22
3018	12254	21383	3.07	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3021	12257					NT	Homo sapiens transcription factor IgM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel >>
3042	12279	21407	2.58	0.0E+00	AF196779.1	NT	Human germline gene 16.1 (or Ig lambda L-chain C region (IgL-C16.1))
3047	12283		3.54	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBLS (FBLS) mRNA, complete cds
3051	12287	21413	1.89	0.0E+00	AF188355.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3070	12308	21428	4.81	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3071	12307	21429	10.45	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3076	12312	21433	4.31	0.0E+00	7662139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ("Top") Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3077	12313	21434	1.49	0.0E+00	AF020275.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3106	12341	21469	2.95	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3113	12348	21476	54.11	0.0E+00	L20944.1	NT	Human ferritin heavy chain mRNA, complete cds
3117	12352	21480	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3117	12352	21481	1.3	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3124	12359	21488	38.75	0.0E+00	T94870.1	EST_HUMAN	S29639 BASIC PROTEIN_25K ..
3140	12375	21508	1.17	0.0E+00	BF243336.1	EST_HUMAN	601878507f1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:2516803 3'
3142	12377	21507	1.02	0.0E+00	AI980986.1	EST_HUMAN	wu12h10_x1_NCI_CGAP GC8 Homo sapiens cDNA clone IMAGE:2516803 3'
3147	12382	21514	4.59	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3147	12382	21515	4.69	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3156	12391	21525	1.61	0.0E+00	4758827	NT	Homo sapiens neuregulin III (NRXN3) mRNA
3156	12391	21526	1.81	0.0E+00	4758827	NT	Homo sapiens neuregulin III (NRXN3) mRNA
3164	12399	21534	10.06	0.0E+00	45046581	NT	Homo sapiens nuclear phosphoprotein B23 (NPM) mRNA, complete cds
3183	12418	21552	10.77	0.0E+00	M28899.1	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
3186	12421	21554	7.27	0.0E+00	4502098	NT	Homo sapiens CREBBP mRNA
3192	12427	21562	0.97	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rabinstein-Taybi syndrome) (CREBBP) mRNA
3192	12427	21563	0.97	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rabinstein-Taybi syndrome) (CREBBP) mRNA
3194	12429	21564	7.38	0.0E+00	AA774783.1	EST_HUMAN	aa87511 s1 Strategenes schizo brain S11 Homo sapiens cDNA clone IMAGE:9711133 3'
3202	12431	21572	5.8	0.0E+00	AF288598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3202	12437	21573	5.8	0.0E+00	AF288598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3215	12449	21581	1.45	0.0E+00	4557590	NT	Homo sapiens fibillin 1 (Marfan syndrome) (FBN1) mRNA
3220	12454	21587	0.98	0.0E+00	4507720	NT	Homo sapiens titin (TN) mRNA
3228	12462	21594	1.77	0.0E+00	AF016413.1	NT	Homo sapiens HLA class III region containing tenascin-X gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3231	12465	21597	4.91	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3234	12468	21598	1.25	0.0E+00	7562125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3234	12468	21600	1.25	0.0E+00	7562125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3242	14485	21607	3.5	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3242	14485	21608	3.5	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3259	12492	21623	3.47	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	12483	21624	1.11	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20685 (FLJ20685), mRNA
3274	12507	21639	1.26	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3285	12516	21847	0.74	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3286	12527	21688	8.17	0.0E+00	A1889284.1	EST_HUMAN	tr58fb8_x2_NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW.RL11_RAT P25121 60S RIBOSOMAL PROTEIN L11 . contains Alu repetitive element,
3308	12536	21688	3.01	0.0E+00	AF128883.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3308	12536	21669	3.01	0.0E+00	AF128883.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3307	12537	21670	0.98	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3307	12537	21671	0.98	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3309	12539	21673	1.61	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA
3309	12539	21674	1.61	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA
3312	12542	21676	12.9	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3314	12544	21678	0.93	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3321	12550	21684	0.79	0.0E+00	BET78039.1	EST_HUMAN	6014648857 NIH MGCG_67 Homo sapiens cDNA clone IMAGE:38682465'
3333	12562	21700	0.85	0.0E+00	A1832669.1	EST_HUMAN	wb10f4_x1_NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:23052793' similar to TR_Q91929 Q91929 ZINC FINGER PROTEIN :
3374	12602	21738	2.97	0.0E+00	AU123664.1	EST_HUMAN	AU123664 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3381	12603	21741	0.94	0.0E+00	7363438	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3381	12608	21742	0.94	0.0E+00	7363438	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3384	12811	21744	1.38	0.0E+00	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3385	12612	21745	1.16	0.0E+00	AF211188.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1A) mRNA, complete cds
3389	12616		1.19	0.0E+00	AW887015.1	EST_HUMAN	MR1-SN0033-1004-00-001-c08 SN0033 Homo sapiens cDNA
3403	12629	21759	3.18	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3403	12629	21760	3.18	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3404	12630	21761	0.96	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3406	12632	21762	2.09	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3415	11870	21084	3.07	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FLI1) gene, complete cds
3419	12644	21773	2.84	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3422	12647	21777	6.12	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC
3424	12649	21779	0.95	0.0E+00	7427522	NT	Incompatibility determinants
3427	12652	21782	2.08	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA

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 Table 4
 Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database & Source	Top Hit Descriptor
3432	12657	21787	4.07	0.0E+00	A1835159.1	EST_HUMAN	wp14d10.11 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634
3432	12857	21788	4.07	0.0E+00	A1835159.1	EST_HUMAN	wp14d10.11 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:073634 073634
3432	12861	21793	2.57	0.0E+00	AJ278120.1	NT	NEURAL CELL ADHESION MOLECULE :
3442	12667	21801	2.8	0.0E+00	6552332	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3442	12667	21802	2.8	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3448	12673	21809	1.89	0.0E+00	M14123.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3452	12677	21812	7.14	0.0E+00	U43283.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3460	12685	21820	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3460	12685	21821	2.98	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3468	12693	21830	1.05	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3476	12700	21836	1.23	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRB) domain polypeptide) (ZNF45) mRNA
3479	12703	21838	1.85	0.0E+00	BE304791.1	EST_HUMAN	60114353FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3479	12703	21839	1.85	0.0E+00	BE304791.1	EST_HUMAN	60114353FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3482	12708	21842	1.24	0.0E+00	4826765	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3484	12708	21845	1.98	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG-1) (HAZ203)
3488	12712	21848	0.74	0.0E+00	A1884007.1	EST_HUMAN	Q00498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN :
3508	12730	21887	0.81	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3508	12730	21888	0.61	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3514	12738	21876	0.95	0.0E+00	AB028019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
3516	12740	21877	0.89	0.0E+00	AV701869.1	EST_HUMAN	AV701868 ADB Homo sapiens cDNA clone ADBDAH08 6'
3517	12741	21878	5.33	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3518	12742	21882	2.19	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44-2 protein mRNA, complete cds
3526	12750	21882	1.74	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3529	12752	21885	0.84	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3540	12763	21894	0.9	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080) mRNA
3549	12772	21890	0.98	0.0E+00	6397248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3549	12772	21891	0.98	0.0E+00	6397248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3550	12773		1.1	0.0E+00	AI081807.1	EST_HUMAN	ox77c11_x1 Scores_NhMPU_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP:T19B4.4 CE:13142;
3552	12775	21904	1.13	0.0E+00	6325483	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	12781		5.31	0.0E+00 AW852217.1	EST_HUMAN	Q1V0-CT0225-230300-169-801 CT0225 Homo sapiens cDNA	
3562	12785	21915	1.05	0.0E+00 4504294 NT		Homo sapiens H3 histone family, member K (H3FK), mRNA	
3566	12789		0.8	0.0E+00 AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GCLC) gene, partial cds	
3567	12790	21916	8.28	0.0E+00 BF576393.1	EST_HUMAN	607684553F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'	
3571	12794		1.08	0.0E+00 AA988715.1	EST_HUMAN	0984106_s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1594043 3' similar to contains MER29_b12	
3581	12803	21929	0.72	0.0E+00 AW937977.1	EST_HUMAN	Q1V0-D70047-702000-123-q01 DT0047 Homo sapiens cDNA	
3594	12815		1.18	0.0E+00 4826987 NT		Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA	
3598	12817	21937	0.7	0.0E+00 AW684693.1	EST_HUMAN	hi84q01_X1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'	
3596	12817	21938	0.7	0.0E+00 AW684693.1	EST_HUMAN	hi84q01_X1_Scares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'	
3601	12822	21944	0.82	0.0E+00 7662319 NT		Homo sapiens KIAA0806 gene product (KIAA0806), mRNA	
3608	12829	21949	1.13	0.0E+00 4557752 NT		Homo sapiens midline 1 (Optitz/BBB syndrome) (MID1) mRNA	
3608	12829	21950	1.13	0.0E+00 4557752 NT		Homo sapiens midline 1 (Optitz/BBB syndrome) (MID1) mRNA	
3626	12847	21985	1.9	0.0E+00 DB7327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds	
3630	12851		30.7	0.0E+00 7668491 NT		Homo sapiens glyceraldehyde-3-phosphat dehydrogenase (GAPD), mRNA	
3648	12859	21986	2.32	0.0E+00 AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds	
3650	12871	21988	2.49	0.0E+00 AB007886.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds	
3651	12872	21989	3.61	0.0E+00 AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	
3651	12872	21990	3.61	0.0E+00 AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds	
3659	12880	21989	1.82	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
3659	12880	22000	1.82	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004	
3660	12881	22001	1.03	0.0E+00 AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds	
3660	12881	22002	1.03	0.0E+00 AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds	
3663	12884	22005	1.57	0.0E+00 AW851714.1	EST_HUMAN	MR2-CT0222-281098-006-805 CT0222 Homo sapiens cDNA	
3665	12886	22007	1.6	0.0E+00 5729928 NT		Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA	
3667	12888	22008	1.54	0.0E+00 AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds	
3669	12889	22011	1.67	0.0E+00 O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)	
3680	12891	22021	1.01	0.0E+00 5729733 NT		Homo sapiens activator of S phase kinase (ASK) mRNA	
3680	12891	22022	1.01	0.0E+00 5729733 NT		Homo sapiens activator of S phase kinase (ASK) mRNA	
3684	12895	22024	5.05	0.0E+00 AW288134.1	EST_HUMAN	U-H-BN_O- <i>gag-e-12-0-11_s1</i> NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'	
3684	12895	22025	5.05	0.0E+00 AW288134.1	EST_HUMAN	U-H-BN_O- <i>gag-e-12-0-11_s1</i> NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733022 3'	
3710	12890	22048	1.27	0.0E+00 AB004680.1	NT	Human gene for Type XIX collagen at chain, exon 6	
3711	12891	22049	1.11	0.0E+00 AA463639.1	EST_HUMAN	aa06d101 r1 Scares NlHMPu S1 Homo sapiens cDNA clone IMAGE:8124986 5' similar to SW_KRB4_SHEEP P02445 KERATIN HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];	

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3715	12835	22053	0.9	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0503 protein, partial cds
3718	12838	22055	4.28	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3728	12847	22065	1.04	0.0E+00	AB037835.1	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3742	12862	22077	11.29	0.0E+00	7662168	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3745	12865	22080	33.84	0.0E+00	4508718	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3810	13028		0.68	0.0E+00	AF095658.1	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3811	13029	22138	2.52	0.0E+00	AF179733.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3814	13032	22142	2.35	0.0E+00	7657468	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3814	13032	22143	2.35	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3818	13036	22148	2.12	0.0E+00	4768011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3819	13037	22149	0.98	0.0E+00	10181139	NT	Mus musculus junctophilin 1 (Jip-1-pending), mRNA
3820	13038	22150	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGC071) gene, partial cds
3820	13038	22151	1.18	0.0E+00	AF127851.1	NT	Gorilla gorilla olfactory receptor (GGC071) gene, partial cds
3821	13039	22152	1.3	0.0E+00	A1377689.1	EST_HUMAN	te82110_41 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3822	13040		1.15	0.0E+00	AF152496.1	NT	Homo sapiens proboscadherin beta 3 (PCDH-beta3) mRNA, complete cds
3823	13041	22153	3.87	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DP1) (DSP) mRNA
3825	13043	22154	15.35	0.0E+00	S78885.1	NT	Gorilla gorilla inwardly rectifying K-channel subunit (KCNQ1B1R1) gene, complete cds
3826	13044	22155	2.43	0.0E+00	7710148	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNQ1B1R1) gene, complete cds
3827	13045	22156	1.67	0.0E+00	7662183	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3833	13050	22160	1.06	0.0E+00	6912735	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3837	13054	22167	6.52	0.0E+00	4503178	NT	Homo sapiens transient receptor potential channel 5 (TRPC5) mRNA
3837	13054	22168	6.52	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXorf5) mRNA
3839	13058	22171	3.62	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3840	13057	22172	0.92	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3843	13060	22174	1.29	0.0E+00	48267183	NT	Homo sapiens voltage-gated channel Shab-related subfamily, member 1 (KCNB1) mRNA
3845	13062	22176	2.63	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3847	13064	22178	0.8	0.0E+00	AF086117.1	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3856	13072	22187	2.52	0.0E+00	A1864727.1	EST_HUMAN	Wk0110_1x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR_O43340
3857	13073	22188	1.05	0.0E+00	AL163248.2	NT	O43340_R28830_2; contains element PTR7 repetitive element;
3860	13076	22192	15.3	0.0E+00	4508742	NT	Homo sapiens chromosome 21 segment HS21C048
3862	13078	22194	1.81	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein SB (RPS8), mRNA
							DKFZp43AN0413_11_434 (synonym: hmc3) Homo sapiens cDNA clone DKFZp43AN0413 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3867	13083	22200	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA
3867	13083	22201	0.98	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1) mRNA
3868	13084	22202	2.83	0.0E+00	4504138	NT	Homo sapiens glutamatergic receptor, metabotropic 3 (GRM3) mRNA
3869	13085		1.91	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3873	13089	22205	1.28	0.0E+00	AF149412.1	NT	Homo sapiens heparin-binding and FGF-binding protein gene, complete cds
3882	13088	22215	1.08	0.0E+00	4506758	NT	Homo sapiens tyrosine receptor 3 (TYR3) mRNA
3886	13102	22219	2.28	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3889	13109	22227	4	0.0E+00	Bf355285.1	EST_HUMAN	RC3-HT0850-170850-011-81(2) H10850 Homo sapiens cDNA
3893	13115	22232	2.47	0.0E+00	AF28533.1	NT	Homo sapiens F-box protein FBXb (FBX3B) mRNA, partial cds
3899	13118	22235	1	0.0E+00	UB8281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3902	13118	22238	1	0.0E+00	UB8281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
3902	13122	22240	4.33	0.0E+00	BE378602.1	EST_HUMAN	601256386F1 NIH MGCA_44 Homo sapiens cDNA clone IMAGE:36008900 5'
3906	13130	22247	0.91	0.0E+00	AW580740.1	EST_HUMAN	PW3-LT0031-100100-003-h09 L10031 Homo sapiens cDNA clone IMAGE:3537774 5'
3914	13131	22248	1.01	0.0E+00	BE264898.1	EST_HUMAN	6011989827F1 NIH MGCA_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3915	13131	22249	1.01	0.0E+00	BE264988.1	EST_HUMAN	6011989827F1 NIH MGCA_7 Homo sapiens cDNA clone IMAGE:3537774 5'
3915	13188	22281	5.67	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3953	13189	22282	5.67	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen DPW4-beta2 pseudogene, exon 2
3953	13178		4.8	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPW4-beta2 pseudogene, exon 2
3965	13180		5.59	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
3974	13188	22286	3.74	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3982	13198	22304	1.95	0.0E+00	AL163268.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEFA1) mRNA
3984	13208		82.28	0.0E+00	4503470	NT	Homologous to Human tRNA-Arginine 3' similar to TR_O60309 O60309
4002	13215		1.09	0.0E+00	AL657076.1	EST_HUMAN	KIAA0563 PROTEIN ;
4005	13217	22321	1.87	0.0E+00	U09366.1	NT	Human zinc finger protein ZNF133
4023	13234	22339	15.84	0.0E+00	AB015610.1	NT	Chlorococcus acutus mRNA for ribosomal protein S4X, complete cds
4032	13242		3.9	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA18 gene)
4042	13252	22353	1.68	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4043	13253	22354	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4043	13253	22355	3.29	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4050	13260	22362	11.29	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4050	13260	22363	11.29	0.0E+00	5032026	NT	Homo sapiens phosphoribosylglycaminide formyltransferase, phosphoribosylglycaminide synthetase, phosphoribosylimidazole synthetase (GART) mRNA
4060	13271	22373	1.03	0.0E+00	4503914	NT	phosphoribosylimidazole synthetase (GART) mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4068	13276	22377	5.4	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4087	13277	22378	1.63	0.0E+00	AB0058625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4070	13280	22379	0.59	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4071	13281	22380	9.39	0.0E+00	11419287	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4072	13282	22381	5.92	0.0E+00	AL098857.1	NT	Novel human mRNA from chromosome 1 which has similarities to BAT2 genes
4080	13280	22389	4.73	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4089	10363	19513	1.01	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4089	10363	19514	1.01	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4096	13304	22403	0.99	0.0E+00	5801805	NT	Homo sapiens tubophilin, subunit 3, member A2 (BTNL3A2), mRNA
4097	13305	22404	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4097	13305	22405	1.08	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, beta subunit (60kD) (GABPB), mRNA
4100	12741	21878	0.59	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2), mRNA
4102	13309	22408	0.68	0.0E+00	8822381	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4102	13309	22409	0.68	0.0E+00	8822381	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
4108	13315	22413	0.81	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4115	13322	22422	6.13	0.0E+00	A1882587.1	EST_HUMAN	wu04d04_x1_NCI_CGAP_GC6_Homo_sapiens cDNA clone IMAGE:2515975 3'
4115	13322	22423	6.13	0.0E+00	A1882587.1	EST_HUMAN	wu04d04_x1_NCI_CGAP_GC6_Homo_sapiens cDNA clone IMAGE:2515975 3'
4118	13324	22425	1.2	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4118	13324	22426	1.2	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4122	13329	22429	6.85	0.0E+00	BE274217.1	EST_HUMAN	601120778F1_NIH_MGC_20_Homo_sapiens cDNA clone IMAGE:2867690 5'
4128	13334	22432	0.98	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4128	13334	22433	0.86	0.0E+00	AB032951.1	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4130	13336	22435	2.13	0.0E+00	5729725	NT	ba51704_x1_NIH_MGC_10_Homo_sapiens cDNA clone IMAGE:2800095 3' similar to SW:TH2_BOVIN
4138	13344		6.07	0.0E+00	AW675569.1	EST_HUMAN	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR
4143	13349	22449	1.61	0.0E+00	AW408788.1	EST_HUMAN	U1-HF-BM0-adv-c-02-0-U_1 NIH_MGC_38_Homo_sapiens cDNA clone IMAGE:3083147 5'
4145	13361	22452	1.52	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4145	13351	22453	1.52	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4154	13360		2.25	0.0E+00	5174632	NT	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4165	13369	22468	1.06	0.0E+00	AB037739.1	NT	ZU88707_s1_Soares,_testis_NH1_Homo_sapiens cDNA clone IMAGE:743197 3' similar to contains Aliu repetitive element; contains element MER35 repetitive element;
4174	13378	22477	10.79	0.0E+00	AA401438.1	EST_HUMAN	

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4174	13378	22478	10.79	0.0E+00 AA401438.1	EST_HUMAN	EST_HUMAN	zg68h07_51 Soares_tesitis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Ali repetitive element;contains element MER35 repetitive element;
4177	13381	22482	1.36	0.0E+00 AF157476.1	NT	Hom sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	
4181	13395	22495	1.8	0.0E+00	7662/25 NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA	
4201	8301	18403	6.72	0.0E+00 AA228126.1	EST_HUMAN	G222811 ALPHA_1 CHAIN OF TYPE XII COLLAGEN;	zg58c04_11 Soares_NHMMPu_S1 Homo sapiens cDNA clone IMAGE:687580 5' similar to TR:G222811
4201	8301	18404	6.72	0.0E+00 AA228126.1	EST_HUMAN	G222811 ALPHA_1 CHAIN OF TYPE XII COLLAGEN;	zg58c04_11 Soares_NHMMPu_S1 Homo sapiens cDNA clone IMAGE:687580 5' similar to TR:G222811
4206	13409	22502	4.97	0.0E+00	4758/198 NT	Homo sapiens desmoplakin (DPI) (DP1) (DSP) mRNA	
4206	13409	22503	4.97	0.0E+00	4758/199 NT	Homo sapiens desmoplakin (DPI) (DP1) (DSP) mRNA	
4215	13418		0.92	0.0E+00 AL168303.2	NT	Homo sapiens chromosome 21 segment HS21C103	
4246	13449	22540	0.96	0.0E+00 AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50	
4259	13462	22554	2.79	0.0E+00 J02810.1	NT	Human apolipoprotein B-100 mRNA, complete cds	
4273	13476	22573	0.84	0.0E+00 AW0368589.1	EST_HUMAN	PM2-DT0023-080300-004-608 DT0023 Homo sapiens cDNA	
4281	13484	22582	0.83	0.0E+00	4826827 NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA	
4281	13484	22583	0.83	0.0E+00	4826827 NT	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA	
4283	13486	22585	3.57	0.0E+00 AF174590.1	NT	Homo sapiens F-box protein FB14 (FB14) mRNA, partial cds	
4289	13491	22589	1.36	0.0E+00	6806918 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
4289	13491	22590	1.36	0.0E+00	6806918 NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA	
4289	13492		2.48	0.0E+00 AI189844.1	EST_HUMAN	qd23f06_x1 Soares_placenta_8icqvees_2NbHP8icqW Homo sapiens cDNA clone IMAGE:1724579 3'	
4284	13495		4.58	0.0E+00 U14520.1	NT	similar to contains MER20 b2 MER20 repetitive element;	
4288	13499	22595	0.84	0.0E+00	5174574 NT	Human CBF-FA3 (Cbf3a) gene, partial cds	
4316	13517	22612	1.43	0.0E+00	6563384 NT	Hom sapiens myeloid/sympathetic or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to 4 (MLL T4) mRNA	
4316	13517	22613	1.43	0.0E+00	6563384 NT	Hom sapiens protein kinase C, nu (PRKCN), mRNA	
4323	13524	22619	1.16	0.0E+00 U10981.1	NT	Human G2 protein mRNA, partial cds	
4323	13524	22620	1.16	0.0E+00 U10991.1	NT	Human G2 protein mRNA, partial cds	
4334	13535	22628	8.88	0.0E+00	6912281 NT	Hom sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA	
4354	13558		1.34	0.0E+00 AF153047.2	NT	Homo sapiens gap junction protein connexin-38 (Cx38) gene, complete cds	
4364	13568	22681	4.84	0.0E+00 L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds	
4368	13570	22686	6.52	0.0E+00 Z80780.1	NT	H.sapiens H2Bh gene	
4368	13570	22687	6.52	0.0E+00 Z80780.1	NT	H.sapiens H2Bh gene	

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Table 4
Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4369	13571	22668	1.2	0.0E+00	AW_166933.1	EST_HUMAN	xg68e10_x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2633514 3' similar to TR:R97385 P97385
4375	13577	22674	1.54	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 64; H. sapiens H4/d gene for H4 histone
4375	13577	22875	1.54	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4380	13581	22681	9.12	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4380	13581	22682	9.12	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4388	13589	22691	1.03	0.0E+00	X82338.1	NT	Homo sapiens Mankes disease gene, exon 4
4391	13592	22695	16.08	0.0E+00	4885128	NT	Homo sapiens caudal-type homeobox transcription factor 4 (CDX4), mRNA
4392	13593	22696	1.77	0.0E+00	AJ271736.1	NT	Homo sapiens Xq1 pseudautosomal region: segment 2/2
4393	13594		0.99	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4398	13597	22698	4.76	0.0E+00	AB037781.1	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4424	13624	22719	1.16	0.0E+00	7019456	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4435	13635		8.37	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPFP2) gene, complete cds
4442	13642	22733	28.88	0.0E+00	AJ249785.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4442	13642	22734	26.88	0.0E+00	AJ249785.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4446	13645	22740	0.67	0.0E+00	W28179.1	EST_HUMAN	2467 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4446	13645	22741	0.87	0.0E+00	W28179.1	EST_HUMAN	2467 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4464	13682		2.27	0.0E+00	AF200628.1	NT	Homo sapiens HPS1 gene, intron 5
4487	13685		1.02	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4488	13688	22778	0.72	0.0E+00	AA228126.1	EST_HUMAN	z758c04_r1 Soares_NhHMPU_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4488	13688	22777	0.72	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN
4504	13701	22795	13.33	0.0E+00	AW084964.1	EST_HUMAN	xc68e08_x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2569446 3' similar to SW:AHNK_HUMAN Q08686 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK
4506	14471		2.11	0.0E+00	80516169	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4510	13706		8.66	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4512	13708	22801	3.69	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101189-002-003 HT0305 Homo sapiens cDNA
4517	13713	22806	1.93	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4517	13713	22807	1.93	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4519	13715	22809	1.19	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50), mRNA
4520	13716	22810	1.72	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNIBH), mRNA, complete cds
4524	13720	22815	1.43	0.0E+00	Z86526.1	NT	H. sapiens pancreatic polypeptide receptor PP1 gene
4528	13724	22820	1.14	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4528	13724	22821	1.14	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4538	14472	22820	4.41	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4541	13736	22834	7.2	0.0E+00	AF208161.1	NT	Homo sapiens synctin precursor, mRNA, complete cds
4546	13741	22841	1.23	0.0E+00	AF152337.1	NT	Homo sapiens priococadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4549	13744	22845	1.3	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4561	13755	22853	33.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4568	13762	22858	16.96	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4572	13768	22861	1.1	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4577	13771	22867	1.06	0.0E+00	4502558	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CaMK4) mRNA
4580	13774		1.11	0.0E+00	BE071908.1	EST_HUMAN	601447832F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852127 5'
4583	13777		2.86	0.0E+00	35485.1	NT	Homo sapiens iduronate sulphatase sulphatase (IDS) gene, complete cds
4585	13779	22870	12.86	0.0E+00	7662091	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4585	13779	22871	12.86	0.0E+00	7662091	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4602	13786	22888	2.51	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4605	13789	22889	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4805	13789	22890	11.6	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4807	13801	22891	0.73	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0795 protein, partial cds
4815	13809		0.64	0.0E+00	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4826	13820		1.54	0.0E+00	AA1174072.1	EST_HUMAN	2p18g08.s1 Strategene fetal retina 367202 Homo sapiens cDNA clone IMAGE:6099854 3'
4828	13822		1.75	0.0E+00	7657410	NT	Homo sapiens odd (odd Oz/Gen-m, Drosophila) homolog 1 (ODZ1), mRNA
4830	13824		5.76	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4831	13825	22813	1.18	0.0E+00	HS22741.1	EST_HUMAN	y622001.s1 Seeces, pineal gland, N3HPG Homo sapiens cDNA clone IMAGE:2311721 3'
4831	13825	22814	1.18	0.0E+00	H92741.1	EST_HUMAN	y622001.s1 Seeces, pineal gland, N3HPG Homo sapiens cDNA clone IMAGE:2311721 3'
4832	13826	22815	1.92	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKRTR) gene, complete cds
4833	13827	22816	5.71	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C10
4834	13828		1.76	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4838	13832	22820	1.07	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4843	13837	22826	36.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4843	13837	22827	36.33	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4844	13838	22828	2.55	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4854	13848	22840	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
4654	13848	22841	1.04	0.0E+00	L7810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	
4654	13848	22842	1.04	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds	
4655	13849	22843	1.68	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds	
4655	13849	22844	1.68	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds	
4662	13856	22854	7.83	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K) gag, pol and env genes	
4668	13862	22863	2.3	0.0E+00	BE001627.1	EST_HUMAN	QV2-BT0836-160400-142-h05_BT0635 Homo sapiens cDNA	
4669	13863	22864	1.23	0.0E+00	AA418246.1	EST_HUMAN	QV2-BT0836-160400-142-h05_BT0635 Homo sapiens cDNA clone IMAGE:767605 3'	
4675	13869		2.11	0.0E+00	AF036841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint	
4683	13875	22875	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
4683	13875	22876	1.02	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
4684	13876	22877	2.48	0.0E+00	AB0317820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds	
4684	13876	22878	2.48	0.0E+00	AB0317820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds	
4685	13877	22879	2.47	0.0E+00	M74098.1	NT	Human displacement protein (CCATT) mRNA	
4687	13879	22881	1.63	0.0E+00	AV294800.1	EST_HUMAN	U1-H-B12-ah1-c-05-0-U1.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2126792 3'	
4687	13879	22882	1.63	0.0E+00	AV294800.1	EST_HUMAN	U1-H-B12-ah1-c-05-0-U1.s1 NC1_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2126792 3'	
4689	13881	22883	2.61	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	
4689	13881	22884	2.61	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA	
4690	9419	18553	0.78	0.0E+00	T56945.1	EST_HUMAN	y83304.12 Strategene fetal spleen #93/205 Homo sapiens cDNA clone IMAGE:683310 5'	
4690	9419	18554	0.78	0.0E+00	T56945.1	EST_HUMAN	y83304.12 Strategene fetal spleen #93/205 Homo sapiens cDNA clone IMAGE:683310 5'	
4693	13884		1.01	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH MGIC_21 Homo sapiens cDNA clone IMAGE:3505521 5'	
4724	13915	23016	12.07	0.0E+00	M80902.1	NT	Human AhNAK nucleoprotein mRNA, 5' and Human Haptoglobin and haptoglobin-related protein (HHP and HPR) genes, complete cds	
4727	13918	23019	2.93	0.0E+00	M69197.1	NT	Human Haptoglobin and haptoglobin-related protein (HHP and HPR) genes, complete cds	
4727	13918	23020	2.93	0.0E+00	M69197.1	NT	Human Haptoglobin and haptoglobin-related protein (HHP and HPR) genes, complete cds	
4732	13923	23021	1.32	0.0E+00	AF184110.1	NT	Human sapiens cyclophilin-related protein (NKR) gene, complete cds	
4733	13924	23028	0.61	0.0E+00	7882479	NT	Human sapiens KIAA0184 protein (KIAA1084), mRNA	
4735	13928	23029	1.65	0.0E+00	7882181	NT	Human sapiens KIAA0363 gene product (KIAA0363), mRNA	
4740	13931	23035	1.12	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds	
4745	13936	23040	0.98	0.0E+00	AI098857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes	
4753	13944		0.95	0.0E+00	X58467.1	NT	Human CYP2D6P pseudogene for cytochrome P450 2D6	
4770	13959	23060	1.19	0.0E+00	AF026801.1	NT	Human sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-26	
4772	13961	23062	1.2	0.0E+00	6877700	NT	Human sapiens G-protein coupled receptor (RE2), mRNA	
4772	13961	23063	1.2	0.0E+00	6877700	NT	Human sapiens G-protein coupled receptor (RE2), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4775	13984	23068	0.93	0.0E+00	7018320	NT	Homo sapiens protein AD008 (AD013); mRNA
4775	13984	23087	0.88	0.0E+00	7018320	NT	Homo sapiens protein AD008 (AD013); mRNA
4798	13985	23090	1.98	0.0E+00	AW44637.1	EST_HUMAN	U1-H-B13-ajw-c-04-O-LJ..s1 NCI_CGAP_Sub6_Homo sapiens cDNA clone IMAGE:2733284 3'
4801	13980	23098	1.24	0.0E+00	AF503134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4804	13893		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPCC24-iso mRNA, complete cds
4853	14042	23135	0.67	0.0E+00	J01191.1	NT	Human MHC class I transplantation antigen (hla) gene
4853	14042	23136	0.67	0.0E+00	J01191.1	NT	Human MHC class I transplantation antigen (hla) gene
4860	14048		5.76	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4862	14050	23144	1.87	0.0E+00	X67205.1	NT	M. fasciculatus mRNA for metalloprotease-like, disintegrin-like protein, IVa
4864	14052	23148	2.5	0.0E+00	Af084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9); mRNA, complete cds
4865	14053	23147	1.79	0.0E+00	Af097416.1	NT	Mus musculus zinc finger transcription factor Kelso mRNA, complete cds
4866	14054	23148	5.28	0.0E+00	4503768	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4868	14056	23150	17.49	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC); mRNA
4869	14057	23151	1.01	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4871	14059	23153	1.92	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312); mRNA
4874	14062	23157	5.79	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073); mRNA
4878	14066	23161	1.05	0.0E+00	7681979	NT	Homo sapiens KIAA0187 gene product (KIAA0187); mRNA
4879	14067	23162	1.61	0.0E+00	Ms94081.1	NT	Homo sapiens hypothetical protein J1-1 segments; and Tcr-C-alpha gene, exons 1-4
4879	14067	23163	1.61	0.0E+00	Ms94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-1 segments; and Tcr-C-alpha gene, exons 1-4
4881	14069	23165	1.73	0.0E+00	X824628.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-4
4881	14069	23168	1.73	0.0E+00	X824628.1	NT	H. sapiens MacP-2 gene
4884	14072	23169	3.1	0.0E+00	Al1163280.2	NT	Homo sapiens chromosome 21 segment HS21C030
4895	14083	23176	1.21	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1.28kD (TAF2)
4905	14093	23186	1.59	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2); mRNA
4907	14095	23188	3.26	0.0E+00	X82841.1	NT	H. sapiens MICA gene
4909	14097	23180	2.44	0.0E+00	4585842	NT	Homo sapiens zinc finger protein (KIAA0412); mRNA
4910	14098	23191	0.84	0.0E+00	AB0378984.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4911	14099	23192	1.88	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4912	14100	23193	2.45	0.0E+00	6877848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1); mRNA
4913	14101	23194	1.88	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (called cell prolif-rich) (MGEA6); mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
4915	14103	23198	6.44	0.0E+00	4758189	NT	Homo sapiens desmopletin(DP1, DP11)(DSP) mRNA	
4917	14105	23198	1.31	0.0E+00	5174580	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA	
4917	14105	23198	1.31	0.0E+00	5174580	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA	
4921	14109	23205	3.09	0.0E+00	AF055084.1	NT	Homo sapiens MHC class 1 region	
4923	14111		3.19	0.0E+00	4505508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1) mRNA	
4924	14112	23208	3.02	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds	
4936	14123	23218	3.83	0.0E+00	4503684	NT	Homo sapiens farnesyldiphosphate synthase (farnesylyltransferase) (FDPS) mRNA	
4938	14125	23220	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephroithiasis 2, X-linked, Dent disease) (CLCN5) mRNA	
4938	14125	23221	8.87	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephroithiasis 2, X-linked, Dent disease) (CLCN5) mRNA	
4946	14133		0.62	0.0E+00	AI281128.1	EST_HUMAN	qm1505.x1_NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR:Q61632 Q61632 EN-2/LACZ FUSION PROTEIN;	
4972	14159	23250	1.28	0.0E+00	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
4981	14168	23258	1.19	0.0E+00	AW452278.1	EST_HUMAN	U1-H-B13-aliy-02-Q-U1-s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:3068691 3'	
4989	14176	23287	0.98	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filamin(BFSP1) mRNA	
4992	14178		10.84	0.0E+00	U14987.1	NT	Homo sapiens ribosomal protein L21 mRNA, complete cds	
5003	14190	23290	1.08	0.0E+00	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment	
5005	14192		3.04	0.0E+00	BE408863.1	EST_HUMAN	6013031791 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'	
5009	14198	23295	5.9	0.0E+00	4758199	NT	Homo sapiens desmopletin(DP1, DP11)(DSP) mRNA	
5015	14202	23289	1.97	0.0E+00	7682401	NT	Homo sapiens KIAA0852 protein (KIAA0852) mRNA	
5019	14206	23291	2.07	0.0E+00	AB028968.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds	
5032	14217	23301	2.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA	
5032	14217	23302	2.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477) mRNA	
5046	14229	23311	0.76	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1_NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	
5046	14229	23312	0.76	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1_NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	
5046	14229	23313	0.76	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1_NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140 E239140 SPALT PROTEIN;	
5049	14231	23315	1.88	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds	
5049	14231	23318	1.68	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds	
5051	14233	23318	3.31	0.0E+00	U826712	NT	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Li>	

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5051	14233	23319		3.31	0.0E+00 U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and Li>
5057	9496	18630		0.61	0.0E+00 AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds H. sapiens mRNA similar to D28763 mouse mRNA for seizure-related gene product 6. Shares domains with BMPs, Tolloid, Sushi repeat proteins
5059	14239			1.1	0.0E+00 AL050253.1	NT	
5061	14241			1.06	0.0E+00 4758225	NT	Homo sapiens EZF transcription factor 2 (EZF2) mRNA
5073	14253	23336		1.24	0.0E+00 AF016705.1	NT	Homo sapiens EG-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5076	14256	23339		0.85	0.0E+00 U53588.1	NT	Homo sapiens MHC class 1 region
5087	14267			1.48	0.0E+00 AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5089	14269			33.47	0.0E+00 DS0657.1	NT	Homo sapiens gamma-oyoplasmic actin (ACTG2) pseudogene
5097	14277	23361		1.02	0.0E+00 AF207880.1	NT	Mus musculus tshzif2 (Tsh2) gene, partial cds
5115	14285	23383		2.97	0.0E+00 X52988.1	NT	Bacillus amyloliquefaciens sacB gene for levansucrase (EC 2.4.1.10)
5116	14286	23384		0.66	0.0E+00 X72791.1	NT	Human endogenous retrovirus mRNA for gag protein
5128	14307	23398		0.69	0.0E+00 AF272663.1	NT	Homo sapiens gypsyin mRNA, complete cds
5133	14311	23402		0.89	0.0E+00 AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5133	14311	23403		0.89	0.0E+00 AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5134	14312	23404		1.22	0.0E+00 5454153	NT	Homo sapiens cyclophilin (USA-CYF) mRNA
5138	14316	23407		0.95	0.0E+00 AA683288.1	EST_HUMAN	aa683288.1: Stratagene schizo brain S111 Homo sapiens cDNA clone IMAGE:10203367 3'
5148	14325	23416		2.49	0.0E+00 11421001	NT	Homo sapiens HEF like Protein (HEFL) mRNA
5156	14335	23425		1.75	0.0E+00 Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5156	14335	23426		1.75	0.0E+00 Y12477.1	NT	Homo sapiens putative GPR37 gene, exon 2
5159	14338	23427		1.23	0.0E+00 Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5172	14351	23439		0.85	0.0E+00 5502091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
5174	14352	23440		1.5	0.0E+00 AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
5187	14363	23450		0.63	0.0E+00 7706245	NT	Homo sapiens 4f2 light chain (LOC51597) mRNA
5187	14363	23451		0.63	0.0E+00 7706245	NT	Homo sapiens 4f2 light chain (LOC51597) mRNA
5188	14364	23452		1.06	0.0E+00 7662421	NT	Homo sapiens KIAA0371 protein (KIAA0371), mRNA
5189	14365	23453		0.98	0.0E+00 4826795	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
5198	14374	23461		2.03	0.0E+00 U26555.1	NT	Human vimentin V2 core protein precursor splice-variant mRNA, complete cds
5202	14377	23464		0.94	0.0E+00 U71601.1	NT	Human zinc finger protein Zfp47 (Zfp47) mRNA, partial cds
5210	14385	23470		1.18	0.0E+00 4757898	NT	Homo sapiens chromosome 8 open reading frame 1 (C8ORF1) mRNA
5211	14386	23471		1.16	0.0E+00 AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5216	14473	23476		1.05	0.0E+00 AF167336.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4

Table 4
Single Exon Probes Expressed in HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	14393	23478	0.75	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
5220	14394	23479	1.22	0.0E+00	4828777	NT	Homo sapiens jumonji (mouse) homolog (JMJ) mRNA
5230	14404	23487	1.68	0.0E+00	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
5238	14412		1.31	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA0426 protein, partial cds
5276	14448	23521	1.26	0.0E+00	7662109	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
5280	14451		1.98	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5282	14453	23523	1.82	0.0E+00	4503754	NT	Homo sapiens flavin containing monooxygenase 1 (FMO1) mRNA
5287	14458	23526	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5287	14458	23527	23.87	0.0E+00	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
5288	14485		3.15	0.0E+00	AF083093.1	NT	Homo sapiens acconitase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5302	14534	23537	2.19	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5302	14534	23538	2.19	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
5313	14545	23614	1.76	0.0E+00	9256578	NT	Homo sapiens protoactinin alpha 13 (PCDHA13), mRNA
5321	14553	23623	3.91	0.0E+00	BE931080.1	EST_HUMAN	RC3;GN0076-310800-013-b63; GN0078 Homo sapiens cDNA
5325	14557	23627	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2L1) mRNA, complete cds
5326	14557	23628	3.45	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2L2) mRNA, complete cds
5331	14562	23635	1.86	0.0E+00	X56183.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5331	14562	23638	1.86	0.0E+00	X56183.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5338	14617	23730	6.44	0.0E+00	BE875498.1	EST_HUMAN	7f10c06_x NC1_CGAP_C11 Homo sapiens cDNA clone IMAGE:32842503
5339	14618	23731	1.72	0.0E+00	BE220753.1	EST_HUMAN	h98a02_x NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:31651943 similar to SW:y054_HUMAN
5339	14619	23732	1.68	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN_KIAA054
5339	14619	23733	1.68	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39436045'
5339	14621	23735	5.3	0.0E+00	M28908.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:39436045'
5394	14623	23736	3.48	0.0E+00	AI791363.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4172152 5' similar to gb:M18512 G
5398	18053	23740	4.35	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V-I REGION (HUMAN);
5402	14630		2.86	0.0E+00	BFF65962.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4), mRNA
5410	14638	23768	2.1	0.0E+00	BF526328.1	EST_HUMAN	602118528F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4279254 5'
5410	14638	23787	2.1	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272 5'
5421	15224	24843	2.57	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
5425	14652	23788	4.72	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5425	14652	23789	4.72	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5436	14663	23816	1.92	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA

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Table 4

Single Exon Probes Expressed in HEGLA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
							EST_HUMAN	EST_HUMAN
5447	14873	23832	3.27	0.0E+00	BF528931.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4178888 5'	
5447	14873	23833	3.27	0.0E+00	BF528931.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4178888 5'	
5450	14878	23835	2.69	0.0E+00	BF313139.1	EST_HUMAN	601B97858F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128815 5'	
5457	14683	24033	4.38	0.0E+00	11434392.NT	Hom sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA		
5476	14703		3.14	0.0E+00	AW887316.1	EST_HUMAN	MFO-SN031-030400-001-h07 SN0037 Homo sapiens cDNA	
5485	14711	24087	1.95	0.0E+00	BF292889.1	EST_HUMAN	601105281F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'	
5485	14711	24088	1.95	0.0E+00	BF292889.1	EST_HUMAN	601105281F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887803 5'	
5495	14721	24078	1.64	0.0E+00	11420819.NT	Hom sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA		
5495	14721	24079	1.64	0.0E+00	11420819.NT	Hom sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA		
5499	14725	24084	4.29	0.0E+00	AF064254.1	EST_HUMAN	Hom sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	
5499	14725	24085	4.29	0.0E+00	AF064254.1	EST_HUMAN	Hom sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds	
5502	14728	24088	3.04	0.0E+00	AJ224839.1	NT	Hom sapiens Surf-5 and Surf-6 genes	
5502	14728	24090	3.04	0.0E+00	AJ224838.1	NT	Hom sapiens Surf-5 and Surf-6 genes	
5513	14738	24103	7.42	0.0E+00	MB8719.1	EST_HUMAN	EST02288_Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone IMAGE:3061658 5'	
5518	14743	24110	5.66	0.0E+00	AW405472.1	EST_HUMAN	U1-HFE-BLO-edh-d-02-0-U1r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'	
5530	14754	24121	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA	
5530	14754	24122	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA	
5531	14755	24123	2.09	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA	
5531	14755	24124	2.03	0.0E+00	U36261.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13	
5556	14780	24161	1.72	0.0E+00	AJ008345.1	NT	Homo sapiens KvLQT1 gene	
5565	14780	24162	1.72	0.0E+00	AJ008345.1	NT	Homo sapiens protocadherin beta 2 (PCDHB2), mRNA	
5575	14786	24172	5.12	0.0E+00	11418801.NT	Hom sapiens protocadherin beta 2 (PCDHB2), mRNA		
5580	14804	24177	7.34	0.0E+00	BE586082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'	
5581	14805	24178	3.29	0.0E+00	UB6861.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds	
5581	14805	24179	3.29	0.0E+00	UB6861.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds	
5588	14812	24186	1.99	0.0E+00	BT338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4184321 5'	
5590	14814	24188	3.15	0.0E+00	BE73983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'	
5598	14820	24197	2.21	0.0E+00	BF588905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'	
5815	14838	24216	2.14	0.0E+00	AF217289.1	NT	Hom sapiens cadherin 20 (CDH20), mRNA, complete cds	
5816	14839	24217	2.44	0.0E+00	BE328144.1	EST_HUMAN	RC5-E70027-210800-022-G10 E70027 Homo sapiens cDNA	
5819	14842	24220	2.87	0.0E+00	BE58636.1	EST_HUMAN	601645287F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3930453 5'	
5840	14884		2.25	0.0E+00	AF012618.1	NT	Hom sapiens familial mental retardation protein 2 (FMR2) gene, exon 14	

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Table 4
Single Exon Probes Expressed In HELA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5642	148668	24249	3.34	0.0E+00 BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'	
5645	148688	24253	2.69	0.0E+00 BE889610.1	EST_HUMAN	601512830F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'	
5653	180861	24275	10.36	0.0E+00	9789986 NT	Homo sapiens potassium voltage-gated channel Shal-related subfamily member 2 (KCND2), mRNA	
5679	14899	24292	9.4	0.0E+00 U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds	
5679	14899	24293	9.4	0.0E+00 U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds	
5725	148443	24339	1.66	0.0E+00 BE378007.1	EST_HUMAN	601236276F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808490 5'	
5738	14955	24354	3.41	0.0E+00 U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds	
5748	14867	24368	4.14	0.0E+00 AA204740.1	EST_HUMAN	zq81d03.1 Strategos hNT neuron (#8317233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:GB834195 G854195 LEUKOCYTE SURFACE PROTEIN ;	
5749	14968	24367	3.86	0.0E+00	11545913 NT	Homo sapiens xylosidyltransferase II (XT2), mRNA	
5749	14868	24368	3.86	0.0E+00	11545913 NT	Homo sapiens xylosidyltransferase II (XT2), mRNA	
5763	14982	24381	4.86	0.0E+00 BE257173.1	EST_HUMAN	601108532F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350222 5'	
5779	14897	24399	1.73	0.0E+00	11435630 NT	Homo sapiens peptide transporter 3 (LOC51286), mRNA	
5806	15023		8.8	0.0E+00 AV650020.1	EST_HUMAN	AV650020 GLC Human sapiens cDNA clone GLCCAD09 3'	
5810	15027	24428	3.35	0.0E+00 AW575598.1	EST_HUMAN	U1-HF-B10-sec-g-12-c-U1-s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751 3'	
5812	15029	24430	3.9	0.0E+00 H01255.1	EST_HUMAN	yJ27563_r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:149833 5'	
5817	15034	24435	1.7	0.0E+00 X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase	
5821	15038	24439	4.44	0.0E+00 BE735689.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3839616 5'	
5821	15038	24440	4.44	0.0E+00 BE735689.1	EST_HUMAN	601305368F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3839616 5'	
5823	15040	24442	23.06	0.0E+00 AU118245.1	EST_HUMAN	AU119245 HEMBA1 Human sapiens cDNA clone HEMBA1005390 5'	
5823	15040	24443	23.06	0.0E+00 AU118245.1	EST_HUMAN	AU119245 HEMBA1 Human sapiens cDNA clone HEMBA1005390 5'	
5831	15048	24452	4.25	0.0E+00 BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887863 5'	
5831	15048	24453	4.25	0.0E+00 BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887863 5'	
5887	15104	24515	2.57	0.0E+00 AF1908860.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT1a (CACNA1G) mRNA, complete cds	
5883	15110	24521	3.97	0.0E+00 AW163640.1	EST_HUMAN	eu96h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR:O15390 O15390 G124. [3] TR:O43840 TR:O43205 ;	
5883	15110	24522	3.97	0.0E+00 AW163640.1	EST_HUMAN	TR:O15390 O15390 G124. [3] TR:O43840 TR:O43205 ;	
5906	15123	24532	5.08	0.0E+00 BE789873.1	EST_HUMAN	60158561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3841847 5'	
5908	15125	24533	7.8	0.0E+00 BE889813.1	EST_HUMAN	6015120568F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'	
5908	15125	24534	7.6	0.0E+00 BE889813.1	EST_HUMAN	6015120568F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'	
5914	15131	24540	4.33	0.0E+00 L24483.1	NT	Human antigen CD27 gene, exons 1-2	

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Table 4

Single Exon Probes Expressed in HE LA Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5918 15135	24544	2.29	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004		
5918 15135	24545	2.29	0.0E+00 AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004		
5924 15141	24552	3.32	0.0E+00	6005983 NT	Homo sapiens zona pellucida glycoprotein 3A (spor receptor) (ZP3A), mRNA		
5927 15143	24554	4.12	0.0E+00 A1638412.1	EST_HUMAN	H31f11_x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE		
5928 15144	24555	1.71	0.0E+00 L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds		
5933 15149	24559	4	0.0E+00 AA442584.1	EST_HUMAN	Zw52G03.11 Scores_total_felus_Nb2Hf8_Bw Homo sapiens cDNA clone IMAGE:627292 5'		
5978 15192	24609	7.22	0.0E+00 BE169131.1	EST_HUMAN	PM3-HT0520-2302010-002-c08 HT0520 Homo sapiens cDNA clone IMAGE:627292 5'		
5990 15272	24701	3.28	0.0E+00 AA190755.1	EST_HUMAN	ZP89603.11 Strategene HeLa cell s3 887216 Homo sapiens cDNA		
5997 15279	24710	5.7	0.0E+00 A1940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA		
5997 15279	24711	5.7	0.0E+00 A1B0621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA		
6002 15284	24717	1.76	0.0E+00 11425626 NT	EST_HUMAN	Homologues_CD6_antigen (CD6), mRNA		
6022 14512	23570	13.42	0.0E+00 BE887889.1	EST_HUMAN	601443687F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3847697 5'		
6022 14512	23571	13.42	0.0E+00 BE867889.1	EST_HUMAN	601443687F1 NIH MGIC_65 Homo sapiens cDNA clone IMAGE:3847697 5'		
6023 15231	24630	2.29	0.0E+00 BE550182.1	EST_HUMAN	7B49f03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN		
6023 15231	24651	2.29	0.0E+00 BE550182.1	EST_HUMAN	Q108379 GOLGIN_95 :		
6036 15244	24666	1.69	0.0E+00 BF088376.1	EST_HUMAN	CM1+HT0877-060900-307-911 HT0877 Homo sapiens cDNA		
6039 15247	24669	1.94	0.0E+00 AA185106.1	EST_HUMAN	Z2349f03.11 Scores_NhlMPy_S1 Homo sapiens cDNA clone IMAGE:665332 5'		
6043 15211		11.49	0.0E+00	11034810 NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)		
6051 15219	24639	2.71	0.0E+00 BF568905.1	EST_HUMAN	(CTNNND2), mRNA		
6058 15227		2.04	0.0E+00 J03089.1	NT	Human MYCL2 gene, complete cds		
6061 15251	24673	3.02	0.0E+00 AF217289.1	NT	Homo sapiens cadherin 20 (CDH20), mRNA, complete cds		
6061 15251	24674	3.02	0.0E+00 AF217289.1	NT	Homo sapiens cadherin 20 (CDH20), mRNA, complete cds		
6066 14513	23572	2.97	0.0E+00	11420775 NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA		
6080 14526	23548	6.31	0.0E+00 BE282941.1	EST_HUMAN	601148954F1 NIH MGIC_19 Homo sapiens cDNA clone IMAGE:3501829 5'		
6081 14527	23549	2.22	0.0E+00 Z31976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)		
6081 14527	23550	2.22	0.0E+00 Z31976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)		
6082 14528	23551	2.88	0.0E+00 AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds		
6082 14528	23552	2.98	0.0E+00 AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds		
6083 15288	24720	2.39	0.0E+00 BF569905.1	EST_HUMAN	602185852F1 NIH MGIC_45 Homo sapiens cDNA clone IMAGE:4310076 5'		
6090 15291	24724	3.87	0.0E+00 L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19		

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6098	15298	24730	5.25	0.0E+00	BF506996.1	EST_HUMAN	601888B23F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123648 5'
6101	15301	24733	2.33	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
6137	15321	24756	2.26	0.0E+00	AU133213 NT2RF4 Homo sapiens cDNA clone NT2RF4-201558 5'	EST_HUMAN	AU133213 NT2RF4 Homo sapiens cDNA clone NT2RF4-201558 5'
6150	15334		2.53	0.0E+00	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002385 5'	EST_HUMAN	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002385 5'
6165	14534	23537	2.38	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6165	14534	23538	2.38	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6174	15356	24794	4.35	0.0E+00	11436698	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6174	15356	24795	4.35	0.0E+00	11436698	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6188	15370	24810	34.37	0.0E+00	AJ128344.1	EST_HUMAN	qc67a07.x1 Scares_Placenta_8toweeks_2NbHP8toW Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element;
6188	15370	24811	34.37	0.0E+00	AJ128344.1	EST_HUMAN	qc67a07.x1 Scares_Placenta_8toweeks_2NbHP8toW Homo sapiens cDNA clone IMAGE:1714644 3' similar to SW:ARSD_HUMAN P51689 ARYLSULFATASE D PRECURSOR ;contains element HGR repetitive element;
6189	15372	24813	4.12	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, prenatal (MYH8), mRNA
6190	15372	24814	4.12	0.0E+00	11428392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, prenatal (MYH8), mRNA
6192	15374		14	0.0E+00	BF537375.1	EST_HUMAN	602335098F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4182839 5'
6194	15376	24816	2.36	0.0E+00	AJ128453.1	EST_HUMAN	2760f9.1 Stratagene muscle S37209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:GB06532
6213	15394		2.23	0.0E+00	AU118607.1	EST_HUMAN	GB06562 NEBULIN :
6214	15395	24838	1.95	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6214	15395	24839	1.95	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
6223	15404	24845	7.18	0.0E+00	X07172.1	NT	H.sapiens DNA for ZNGP2 pseudogene, exon 4
6225	15408	24847	9.65	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6225	15408	24848	9.85	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
6231	15412	24853	2.5	0.0E+00	AW650516.1	EST_HUMAN	EST362586 MAGE resequences, MAGA Homo sapiens cDNA
6260	15441	24880	2.71	0.0E+00	AW239326.1	EST_HUMAN	#39e05.1 NCI CGAP Lu31 Homo sapiens cDNA clone IMAGE:2575840 5' similar to TR:Q03050 Q03050 HNF3/F1 TRANSCRIPTION FACTOR GENESIS :
6270	15450	24889	4.1	0.0E+00	11427125	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
6281	15461	24903	2.21	0.0E+00	AW405627.1	EST_HUMAN	UI-HF-BLO-abs-d-07-0-U1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057459 5'
6317	15487	24941	4.45	0.0E+00	AJ1752561.1	EST_HUMAN	cn17d05,x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random

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 Table 4
 Single Exon Probes Expressed

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6317 15497	24942	4.45	0.0E+00	A1752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random	
6374 15564	25011	2.06	0.0E+00	6912735 NT	EST_HUMAN	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA	
6377 15567	25013	5.62	0.0E+00	BF217905.1	EST_HUMAN	601885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'	
6381 15561	25017	3.89	0.0E+00	AU128622.1	EST_HUMAN	AU128622 NT2RPF2 Homo sapiens cDNA clone NT2RPF2005913 5'	
6392 15572	25028	8.75	0.0E+00	4501848 NT	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABCA) member 3 (ABCA3), mRNA	
6395 15575	25030	5.9	0.0E+00	BE739870.1	EST_HUMAN	601583156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'	
6395 15575	25031	5.9	0.0E+00	BE739870.1	EST_HUMAN	601583156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'	
6407 15588	25047	2.02	0.0E+00	BE781610.1	EST_HUMAN	60148171351 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'	
6407 15588	25048	2.02	0.0E+00	BE781610.1	EST_HUMAN	60148171351 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'	
6449 15846	25114	3.8	0.0E+00	BE736046.1	EST_HUMAN	601303858F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3659803 5'	
6457 15854	25123	3.92	0.0E+00	A524872.1	NT	Human amyloid-beta protein (APP) gene, exon 11	
6457 15854	25124	3.92	0.0E+00	A524872.1	NT	Human amyloid-beta protein (APP) gene, exon 11	
6488 15885	25136	2.85	0.0E+00	AA397551.1	EST_HUMAN	ZB1804.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR_G300482	
6488 15885	25137	6.84	0.0E+00	AU142402.1	EST_HUMAN	G300482 POT=REVERSE TRANSCRIPTASE HOMOLOGY (RETROVIRAL ELEMENT); AU142402 YY9AA11 Homo sapiens cDNA clone Y9AA1000277 5'	
6471 158688	25170	7.06	0.0E+00	BF873098.1	EST_HUMAN	AU142402 YY9AA11 Homo sapiens cDNA clone IMAGE:4284128 5'	
6479 15876	25171	3.93	0.0E+00	AW50549.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3077498 5'	
6510 15706						UJ-HF-BN0-akf-f-01-o-U1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:2783798 3 similar to au68b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783798 3 similar to	
6514 15710	25174	12.31	0.0E+00	AW157233.1	EST_HUMAN	TR_O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1];	
6556 15752	25214	2.38	0.0E+00	11427235 NT	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	
6556 15752	25215	2.38	0.0E+00	11427235 NT	EST_HUMAN	2773a608.s1 Stoires testis NIH Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85685	
6574 15770		5.05	0.0E+00	AA398511.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA	
6604 15800		3.33	0.0E+00	BE860737.1	EST_HUMAN	PROHIBITIN (HUMAN);	
6610 15806	25262	3.19	0.0E+00	4758695 NT	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'	
6610 15806	25263	3.19	0.0E+00	4758695 NT	EST_HUMAN	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA	
6626 15822	25282	4.61	0.0E+00	X98922.1	NT	H sapiens mRNA for gamma-glutamyltransferase	
6626 15822	25283	4.61	0.0E+00	X98922.1	NT	H sapiens mRNA for gamma-glutamyltransferase	
6626 15822	25284	4.61	0.0E+00	X98922.1	NT	H sapiens mRNA for gamma-glutamyltransferase	
6650 15845		2.28	0.0E+00	AW513513.1	EST_HUMAN	xp46801.X1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4 RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);	
6652 15847	25306	9.98	0.0E+00	D52690.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-084C02	5

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6661	15856	25315	6.79	0.0E+00 BE378495.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3808709 5'	
6663	15858	25317	2.22	0.0E+00 AA410545.1	EST_HUMAN	232604.11 Socres ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724062 5'	
6891	15886	25345	10.28	0.0E+00 AA892527.1	EST_HUMAN	6892.51 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S	
6894	15889	25349	5.08	0.0E+00 10947037.1	EST_HUMAN	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA	
6894	15889	25350	5.08	0.0E+00 10947037.1	EST_HUMAN	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA	
6708	15903		2.85	0.0E+00 AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone IMAGE:2885098 5'	
6711	15906	25383	2.28	0.0E+00 AU124051.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone IMAGE:2885098 3'	
6739	15934	25393	8.1	0.0E+00 AW5922233.1	EST_HUMAN	h148a09_x1 Socres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2885098 3'	
6739	15934	25394	8.1	0.0E+00 AW5922233.1	EST_HUMAN	h148a09_x1 Socres_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2885098 3'	
6762	15957	25412	6	0.0E+00 11422857	NT	Homo sapiens tumor protein p73 (TP73), mRNA	
6767	15962	25418	7.02	0.0E+00 AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds	
6767	15962	25419	7.02	0.0E+00 AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds	
6769	15964	25422	4.5	0.0E+00 7706638.9	NT	Homo sapiens polycystin-1 (PKD1), mRNA	
6783	15978	25436	3.18	0.0E+00 BE315402.1	EST_HUMAN	60114119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'	
6783	15978	25437	3.18	0.0E+00 BE315402.1	EST_HUMAN	60114119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740 5'	
6790	15985	25445	2.37	0.0E+00 XJ4786.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit	
6799	15994	25462	2.92	0.0E+00 AI954607.1	EST_HUMAN	wg34812_x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW.MGB3_HUMAN	
6802	15997	25485	5.73	0.0E+00 9256595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 : O15480 MELANOMA PROTEIN L23A.	
6807	16002	25492	2.77	0.0E+00 AW958311.1	EST_HUMAN	EST370881 MAGE sequences, MAGE Homo sapiens cDNA	
6822	16016	25481	3.11	0.0E+00 BE794823.1	EST_HUMAN	6011589284F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943463 5'	
6865	16055	25522	2.65	0.0E+00 BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA	
6889	15595	25057	3.59	0.0E+00 11560151	NT	Homologous hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	
6889	15595	25058	3.59	0.0E+00 11560151	NT	Homologous hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA	
6891	15597	25061	12.21	0.0E+00 AI280909.1	EST_HUMAN	qm09a06_x1 NCI_CGAP_L15 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW.RL2B_HUMAN	
6891	15597	25062	12.21	0.0E+00 AI280909.1	EST_HUMAN	P28316 60S RIBOSOMAL PROTEIN L23A.	
6902	16059	25527	4.66	0.0E+00 AF153466.1	NT	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8	
6907	16095		15.37	0.0E+00 BE255829.1	EST_HUMAN	601109842F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'	
6908	16096	25662	24.85	0.0E+00 AW163779.1	EST_HUMAN	BU86C04_Y1 Schneider fetal brain 0004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072	
6925	16118	25584	6.88	0.0E+00 C06158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605	

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Table 4
Single Exon Probes Expressed in HEK Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	16118	25585	6.68	0.0E+00	CG6158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
6927	16120	25588	5.28	0.0E+00	BE745215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
6942	16088	25554	2.48	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
6945	16133	25602	3.1	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
6955	16133	25603	3.1	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2e (KRT2E) gene, complete cds
7001	16179	25650	2.7	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, genomic/mRNA, 498 nt, segment 5 of 5]
7001	16178	25651	2.7	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, genomic/mRNA, 498 nt, segment 5 of 5]
7002	16180	25652	3.47	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
7017	16194	25668	2.39	0.0E+00	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7017	16194	25669	2.39	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7020	16197	25673	16.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7020	16197	25674	16.33	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
7023	16200	25678	2.71	0.0E+00	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
7034	16211	25887	3.28	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7056	16233	25708	3.33	0.0E+00	BE280793.1	EST_HUMAN	601156227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138788 5'
7059	16236	25709	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
7059	16236	25710	9.74	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
7062	16239	25712	6.83	0.0E+00	AV236289.1	EST_HUMAN	xn72b01_x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2898977 3' similar to gb:X02152_cds1 L-
7078	16255	25728	3.3	0.0E+00	AU143873.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN)
7078	16255	25729	3.3	0.0E+00	AU143873.1	EST_HUMAN	AU143873 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
7079	16256	25730	3.59	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
7081	16258	25732	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7081	16258	25733	2.51	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
7081	16268	25745	2.83	0.0E+00	AU136837.1	EST_HUMAN	AU136837 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7091	16268	25746	2.83	0.0E+00	AU136837.1	EST_HUMAN	AU136837 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
7103	16280	25760	2.95	0.0E+00	AU196387.1	EST_HUMAN	z97h11.1 Strategene muscle 837208 Homo sapiens cDNA clone IMAGE:628197 5'
7125	16302	25783	2.32	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
7139	16318	25797	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7139	16318	25798	12.52	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
7167	16344	25822	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_BmB4 Homo sapiens cDNA clone IMAGE:4184939 5'
7167	16344	25823	4.03	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_BmB4 Homo sapiens cDNA clone IMAGE:4184939 5'

Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (T ₀) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7198	16375	25857		2.47	0.0E+00 BF436218.1	EST_HUMAN	nsb45e12x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
7206	16383	25864		5.33	0.0E+00 AW517980.1	EST_HUMAN	xJ74b01_x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:W69066 MOESIN
7208	16385	25868		13.01	0.0E+00 BE549213.1	EST_HUMAN	601078764F NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
7214	163891	25873		2.88	0.0E+00 BE781742.1	EST_HUMAN	601467419F NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3870700 5'
7216	163893	25876		2.52	0.0E+00 BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-003 BT0642 Homo sapiens cDNA
7216	163893	25877		2.52	0.0E+00 BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-003 BT0642 Homo sapiens cDNA
7219	16396	25880		5.18	0.0E+00 BE743215.1	EST_HUMAN	601573895F NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
7219	16398	25881		5.18	0.0E+00 BE743215.1	EST_HUMAN	601573895F NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
7230	16451	25940		2.86	0.0E+00 AW711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
7230	16451	25941		2.86	0.0E+00 AW711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
7232	16453			6.94	0.0E+00 AW813783.1	EST_HUMAN	RC3-ST0197-12020-015-e03 ST0197 Homo sapiens cDNA
7239	16459	25948		7.82	0.0E+00 AW863563.1	EST_HUMAN	EST375636 MAGE sequences, MAGH Homo sapiens cDNA
7252	16472	25963		2.36	0.0E+00 11431124_NT	EST_HUMAN	Home sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7252	16472	25964		2.36	0.0E+00 11431124_NT	EST_HUMAN	Home sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7254	16474	25966		2.16	0.0E+00 AW057621.1	EST_HUMAN	TR-080568 Q80568 VD-X
7262	16481	25973		2.11	0.0E+00 BE243270.1	EST_HUMAN	TCAAAP3D0917-Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homozygous cDNA clone TCAAAP0917
7283	16482	25974		5.64	0.0E+00 AI652239.1	EST_HUMAN	wb28a12_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:25653065 3' similar to contains element
7283	16482	25975		5.64	0.0E+00 AI652239.1	EST_HUMAN	wb28a12_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element
7273	16492	25983		4.32	0.0E+00 11545911_NT	EST_HUMAN	MSR1 MSR1 repetitive element;
7273	16492	25984		4.32	0.0E+00 11545911_NT	EST_HUMAN	Homo sapiens NOD2 protein (NOD2), mRNA
7287	16506	25997		2.37	0.0E+00 AW404795.1	EST_HUMAN	Homo sapiens NOD2 protein (NOD2), mRNA
7289	16509	26000		5.66	0.0E+00 11424829_NT	EST_HUMAN	U1-HF-B10-acm-d-04-0-U1 r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059383 5'
7289	16510	26001		10.37	0.0E+00 4504536_NT	EST_HUMAN	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
7291	16510	26002		10.37	0.0E+00 4504536_NT	EST_HUMAN	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
7292	16511	26003		2.78	0.0E+00 AI691827.1	EST_HUMAN	wb28a12_x1 Soares_Diclofenac_free_cDNA_Homo sapiens cDNA clone IMAGE:2521715 3
7295	16514	26007		2.95	0.0E+00 BE582109.1	EST_HUMAN	601605204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908865 5'
7299	16518	26009		14.1	0.0E+00 BE891630.1	EST_HUMAN	601434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919836 5'
7301	16520	26010		1.83	0.0E+00 89223939_NT	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
7301	16520	26011		1.93	0.0E+00 89223939_NT	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

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Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7315	165333	260222	12.26	0.0E+00	BE803304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
7318	14789	24160	2.45	0.0E+00	A1485905.1	EST_HUMAN	zp95b11_r1 Strategene muscle S37209 Homo sapiens cDNA clone IMAGE:627933 5' similar to gb:X03740
7337	16553	26042	6.57	0.0E+00	BE793498.1	EST_HUMAN	60158828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
7345	16561	26049	26.28	0.0E+00	AV727362_HTC	EST_HUMAN	AV727362_HTC Homo sapiens cDNA clones HTCAQH08 5'
7345	16561	26050	26.28	0.0E+00	AV727362_HTC	EST_HUMAN	AV727362_HTC Homo sapiens cDNA clones HTCAQH06 5'
7358	16572	26064	18.75	0.0E+00	AN516055.1	EST_HUMAN	x04g10_x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852228 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN)
7362	16578	26069	1.96	0.0E+00	AU135741.1	EST_HUMAN	AU135741 PLACE:1 Homo sapiens cDNA clone PLACE:1002794 5'
7367	16583	26072	3.09	0.0E+00	AN563333.1	EST_HUMAN	hg13d02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element
7367	16583	26073	3.09	0.0E+00	AN563333.1	EST_HUMAN	hg13d02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element
7367	16583	26074	3.09	0.0E+00	AN563333.1	EST_HUMAN	hg13d02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element
7369	16585	26075	1.79	0.0E+00	Z34897.1	NT	H.sapiens mRNA for H1 histamine receptor
7370	16586	26076	3.22	0.0E+00	F13089.1	EST_HUMAN	HSC310c031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
7377	16593	26081	1.98	0.0E+00	D10083.1	NT	H.sapiens mRNA for RGH1 gene, retrovirus-like element
7383	16607	26097	2.67	0.0E+00	AN338084.1	EST_HUMAN	xw66f01_x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832885 3' similar to gb:X17115 1G MU CHAIN C REGION (HUMAN)
7384	16608	26098	5.93	0.0E+00	AN451230.1	EST_HUMAN	UJ-H-B13-all-h-e-01-0-U..si NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
7384	16608	26099	5.93	0.0E+00	AN451230.1	EST_HUMAN	UJ-H-B13-all-h-e-01-0-U..si NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
7398	9498		16.35	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
7398	16611	26101	2.2	0.0E+00	AB014587.1	NT	Homo sapiens mRNA for KIAA0587 protein, partial cds
7411	16623	26117	2.76	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
7427	16637	26130	1.88	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
7443	16651	26143	2.9	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
7444	16652		62.57	0.0E+00	BF684061.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'
7447	16655	26146	5.83	0.0E+00	AU168386.1	EST_HUMAN	AU168386 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
7448	16656		11.98	0.0E+00	AN236268.1	EST_HUMAN	xn72b01_x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2696977 3' similar to gb:X02152_cde1
7453	16661	26150	8.59	0.0E+00	AU149809.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN)
7453	16661	26151	8.59	0.0E+00	AU149809.1	EST_HUMAN	qf43c63_x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
7454	16662	26152	4.17	0.0E+00	AN391637.1	EST_HUMAN	qf43c63_x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'

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Table 4

Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7467	16675	26159	21.87	0.0E+00	11424726	NT	Homo sapiens insulin receptor (INSR)_ mRNA	IMAGE:4184979_5'
7474	16682	26165	1.76	0.0E+00	BF340308.1	EST_HUMAN	602037014F1_NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:3163310_5'	
7475	16683	26166	40.58	0.0E+00	BE261209.1	EST_HUMAN	601148357F1_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310_5'	
7485	16692	26175	3.77	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80k-H (PRKCSH) gene, exon 15-17	
7489	16696	26180	2.19	0.0E+00	BE73036.1	EST_HUMAN	RC1-FT0134-170100-012-f07_FT0134_Homo sapiens cDNA	
7489	16696	26181	2.19	0.0E+00	BE73036.1	EST_HUMAN	RC1-FT0134-170100-012-f07_FT0134_Homo sapiens cDNA	
7510	16715	26203	19.32	0.0E+00	AA1740782.1	EST_HUMAN	MSR1 repetitive element;	
7517	16722	26212	3.85	0.0E+00	AFF52303.1	NT	Homo sapiens signalling lymphocytic activation molecule (SLAM) gene, exon 2	
7530	16735	26225	6.93	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (Nakamura) Homo sapiens cDNA clone 3NHC4817	
7537	16742	26233	2.19	0.0E+00	AA748375.1	EST_HUMAN	ce56101111_NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009_5'	
7537	16742	26234	2.19	0.0E+00	AA748375.1	EST_HUMAN	ce56101111_NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009_5'	
7547	16752	26248	2.05	0.0E+00	M78448.1	EST_HUMAN	EST00556_Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HBCC26	
7547	16752	26247	2.05	0.0E+00	N78448.1	EST_HUMAN	EST00556_Fetal brain, Strategene (cat#836206) Homo sapiens cDNA clone HBCC26	
7550	16755	26248	7.75	0.0E+00	AI157608.1	EST_HUMAN	DKFZp761J2116_r1_761 (synonym: hmyz2) Homo sapiens cDNA clone DKFZp761J2116_5	
7550	16755	26258	13.17	0.0E+00	AI116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424_5'	
7560	16765	26258	13.17	0.0E+00	AV693958.1	EST_HUMAN	AV693958 GKC Homo sapiens cDNA clone GKCCNC03_5'	
7572	16777	26270	2.02	0.0E+00	B7368553.1	EST_HUMAN	1L3-NT0104-200501-143-A07_NT0104_Homo sapiens cDNA	
7580	16783	26279	2.07	0.0E+00	BF182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA	
7603	16806	26302	3.42	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA	
7603	16806	26303	3.42	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA	
7605	16808	26316	1.71	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAA0D6_5'	
7618	16821	26316	3.77	0.0E+00	BE898423.1	EST_HUMAN	6011439082F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3048486_5' similar to gb:Y00345_cds1	
							POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);	
7628	16828	26325	3.72	0.0E+00	BE018283.1	EST_HUMAN	601144446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39755403_5'	
7659	16859	26360	5.05	0.0E+00	BE897853.1	EST_HUMAN	601144446F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:1952804_3'	
7660	16860	26361	1.88	0.0E+00	A1459545.1	EST_HUMAN	ae886911_x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804_3'	
7660	16860	26362	1.88	0.0E+00	A1459545.1	EST_HUMAN	ae886911_x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804_3'	
7698	16897	26406	4.25	0.0E+00	4758927	NT	Homo sapiens neuritin III (NP00313) mRNA	
7699	16898	26407	18.73	0.0E+00	BF206561.1	EST_HUMAN	6011870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:2724312_3'	
7704	16903	26412	20.68	0.0E+00	AW207734.1	EST_HUMAN	U1-H5i2-ege-h-01-0-JI s1 NCL_CGAP_Sub4 Homo sapiens cDNA	
7708	16907	26415	6.88	0.0E+00	AB018260.1	NT	U1-H5i2-ege-h-01-0-JI s1 NCL_CGAP_Sub4 Homo sapiens cDNA	
7708	16907	26416	6.88	0.0E+00	AB018260.1	NT	U1-H5i2-ege-h-01-0-JI s1 NCL_CGAP_Sub4 Homo sapiens cDNA	

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7709	16908	26417	3.24	0.0E+00	BE20846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN
7709	16908	26418	3.24	0.0E+00	BE20846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN
7709	16908	26418	3.24	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7731	16462	24904	2.19	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA clone IMAGE:3085026 3'
7734	16931	26438	2.87	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA clone IMAGE:3085026 3'
7734	16931	26439	2.87	0.0E+00	BE507876.1	EST_HUMAN	UI-H-B14-B0k-b-10-o-U1 s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
7767	16953	26475	4.64	0.0E+00	BE507876.1	EST_HUMAN	UI-H-B14-B0k-b-10-o-U1 s1 NCL CGAP_Sub8 Homo sapiens cDNA clone PLACE:1001381 5'
7767	16953	26476	4.64	0.0E+00	BE507876.1	EST_HUMAN	AU135170 PLACE:1 Homo sapiens cDNA clone IMAGE:3889207 5'
7767	16953	26483	2.28	0.0E+00	AU135170.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
7775	16970	26488	10.51	0.0E+00	BE876401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:4099710 5'
7780	16975	26489	10.51	0.0E+00	BE876401.1	NT	Human mRNA for KIAA0241 gene, partial cds
7780	16975	26494	1.86	0.0E+00	DE7882.1	EST_HUMAN	601875830F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
7786	16981	26494	4.77	0.0E+00	BF240536.1	EST_HUMAN	Homo sapiens mRNA for KIAA1316 protein, partial cds
7792	16986	26510	3.35	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
7805	16998	26511	3.35	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
7805	16998	26514	4.11	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
7809	17002	26515	4.11	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
7809	17002	26515	4.11	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
7823	17015	26530	10.15	0.0E+00	BF576267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:2847177 5'
7831	17023	26538	1.78	0.0E+00	AW32873.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:4123948 5'
7833	17025	26541	7.53	0.0E+00	M56083.1	NT	Human gamma actin-like pseudogene, complete cds
7836	17028	26544	41.44	0.0E+00	M56083.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7841	17033	26548	3.52	0.0E+00	BF306996.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7841	17033	26549	3.52	0.0E+00	BF362462.1	EST_HUMAN	QY2-NN0054-2308080-333-604 NN0054 Homo sapiens cDNA clone IMAGE:3924577 5'
7848	17039	26556	28.43	0.0E+00	BF362462.1	EST_HUMAN	6014398605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
7870	17060	26560	4.97	0.0E+00	BE897051.1	EST_HUMAN	Homo sapiens golin-like protein (GLP), mRNA
7880	17068	26594	3.16	0.0E+00	8923698	NT	601889823F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN
7882	17070	26640	4.84	0.0E+00	BE208846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN
7894	17110	26641	4.84	0.0E+00	BE208846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN
7894	17112	26643	5.08	0.0E+00	AW753028.1	EST_HUMAN	QY0-C70225-101289-071-008 C70225 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in HEK293 Cells

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
7901	17117			0.0E+00	AA558707.1	EST_HUMAN	nl42c08.s1 NCI_CGAP_Pt4 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);	
7902	14543	23612		3.33	0.0E+00	AA934954.1	EST_HUMAN	wp08608.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464084 3'
7903	17118	26848		10.87	0.0E+00	AW327895.1	EST_HUMAN	dr02608.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:284619 5'
7921	18080	26867		1.71	0.0E+00	AW292776.1	EST_HUMAN	Ul-H-BW0-aj-d-07-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:27289309 3'
7934	17074	26801		2.83	0.0E+00	BE985909.2	EST_HUMAN	6016592088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895816 3'
7934	17074	26802		2.83	0.0E+00	BE985909.2	EST_HUMAN	6016592088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
7935	17075	26803		4.9	0.0E+00	BE185856.1	EST_HUMAN	IL-6-HT0731-02-20500-077-f05 H10731 Homo sapiens cDNA clone IMAGE:2434178 5'
7949	17088	26817		6.34	0.0E+00	AI046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hiex3) Homo sapiens cDNA clone DKFZp434G178 5'
7949	17088	26818		6.34	0.0E+00	AI046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hiex3) Homo sapiens cDNA clone DKFZp434G178 5'
7958	17097	26827		24.69	0.0E+00	AI923116.1	EST_HUMAN	wn83g83.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
7982	17141	26873		7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q136886 Q13686 ALKB_HOMOLOG PROTEIN_N ;
7982	17141	26874		7.88	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q136886 Q13686 ALKB_HOMOLOG PROTEIN_N ;
7987	17146	26880		2.47	0.0E+00	BE910548.1	EST_HUMAN	601501050F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802928 5'
7975	18410	25888		6.48	0.0E+00	BE876347.1	EST_HUMAN	7f27f12.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3293919 3' similar to TR:Q00409 O00409 CHECKPOINT_SUPPRESSOR_1 ;
7978	18413	25898		1.85	0.0E+00	BE615686.1	EST_HUMAN	601278335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
7978	18413	25890		1.85	0.0E+00	BE615686.1	EST_HUMAN	601278335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
8014	17163	26887		2.83	0.0E+00	L38891.1	NT	Homo sapiens polyysotic kidney disease-associated protein (PKD1) gene, complete cds
8014	17153	26888		2.93	0.0E+00	L38891.1	NT	Homo sapiens polyysotic kidney disease-associated protein (PKD1) gene, complete cds
8027	17164	26701		4.05	0.0E+00	AU138211.1	EST_HUMAN	AU138211 PLACE:11 Homo sapiens cDNA clone PLACE:1008677 5'
8040	17178	26716		3.92	0.0E+00	BE622317.1	EST_HUMAN	601441086F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
8073	17208	26741		26.14	0.0E+00	BE748899.1	EST_HUMAN	w2b1f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:385890123'
8073	17208	26742		26.14	0.0E+00	BE748899.1	EST_HUMAN	60157218671 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:383890123'
8084	17219	26754		3.84	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001388 5'
8084	17219	26755		3.94	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
8087	17222	26758		2.47	0.0E+00	AW008622.1	EST_HUMAN	w2b1f01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2
8091	18081	28762		4.52	0.0E+00	BF002333.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2_TYPE ;
8108	17242	26782		3.67	0.0E+00	AW387776.1	EST_HUMAN	7n22b10.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO ;
								MR4-ST0118-261089-012-b03 ST0118 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8108	17242	26783	3.67	0.0E+00	AW/387776.1	EST_HUMAN	MR4-ST0118-267099-012-b03 ST0118 Homo sapiens cDNA
8128	17282	26805	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8128	17262	26806	4.34	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
8133	17268	26810	7.62	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAW22) gene, exon 5
8135	17268	26812	17.97	0.0E+00	BE378254.1	EST_HUMAN	601237891F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36098623 5'
8135	17268	26813	17.97	0.0E+00	CD378254.1	EST_HUMAN	601237891F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:36098623 5'
8149	17281	26826	2.37	0.0E+00	BE794758.1	EST_HUMAN	6015905388F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
8150	17282	26827	98.17	0.0E+00	BE879633.1	EST_HUMAN	6014981821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:38944220 5'
8160	17292	26833	9.23	0.0E+00	BE409893.1	EST_HUMAN	601289403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628544 5'
8161	17283	26834	1.7	0.0E+00	BE148650.1	EST_HUMAN	MRO-HT0241-150500-011-012 HT0241 Homo sapiens cDNA
8162	17284	26835	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8162	17284	26836	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8162	17284	26837	1.74	0.0E+00	11427345	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8163	17285	26838	2.98	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8163	17295	26839	2.98	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8170	17302	26847	2.12	0.0E+00	AL1132840	EST_HUMAN	AU132940 NT2RP4000928 5'
8173	17305	26849	4.04	0.0E+00	BB903372.1	EST_HUMAN	601678557F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
8182	17314	26856	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
8182	17314	26857	2.31	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4127069 5'
8184	17316	26859	3.09	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8184	17316	26860	3.08	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8191	17323		1.98	0.0E+00	W88984.1	EST_HUMAN	zh73d05 s1 Soares_fetal_liver_spleen_NFLS_S1 Homo sapiens cDNA clone IMAGE:417705 3'
8193	17325		2.05	0.0E+00	BE906402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398 5'
8204	17335	26876	2.78	0.0E+00	98335487	NT	Human endogenous retrovirus, complete genome
8218	18082		15.82	0.0E+00	BF309120.1	EST_HUMAN	60118900534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
8224	17354	26891	75.28	0.0E+00	BE287175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532868 5'
8234	15576	25032	2.25	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; actinin receptor interacting protein 1 (KIAA0705), mRNA
8254	15576	25033	2.25	0.0E+00	6912481	NT	Homo sapiens atrophin-1 interacting protein 1; actinin receptor interacting protein 1 (KIAA0705), mRNA
8265	17392	26922	2.1	0.0E+00	BE140795.1	EST_HUMAN	RC02-HT022-080799-002-D01 HT022 Homo sapiens cDNA
8279	18366	23590	1.91	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8282	18208			1.39	0.0E+00 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21CO46
8284	18215			5.07	0.0E+00 AI190983.1	EST_HUMAN	q617b12.X1 Soares fetal lung NbHL19W Homo sapiens cDNA clone IMAGE:11739231 3'
8304	17411			2.71	0.0E+00 AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
8325	17426			5.01	0.0E+00 AL163246.2	NT	Homo sapiens chromosome 21 segment HS21CO46
8332	17431			3.24	0.0E+00 11417982	NT	Homo sapiens calcineurin binding protein 1(KIAA0330), mRNA
8351	17445			4.53	0.0E+00 5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
8385	18174	23758		1.22	0.0E+00 AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
8397	18184			3.55	0.0E+00 AL041931.1	EST_HUMAN	DKFZp434K0818_11_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434K0819 5'
8423	18334			3.6	0.0E+00 11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTS1), mRNA
8431	17497			4.18	0.0E+00 AL046544.1	EST_HUMAN	DKFZp434G218_71_434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434G218 5'
8444	18219			1.67	0.0E+00 AL063497.1	EST_HUMAN	IL-BT03-27/098-001 BT030 Homo sapiens cDNA
8488	18362			1.73	0.0E+00 N64484.1	EST_HUMAN	y40608_s1 Soares fetal liver spleen INFSL Homo sapiens cDNA clone IMAGE:2452222 3' similar to SW:PCOL_BAEVM P10272 POLYPROTEIN
8504	17543			4.14	0.0E+00 AF106856.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
8507	10089	19250		3.7	0.0E+00 450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8507	10089	19251		3.7	0.0E+00 450750	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
8516	18221			1.76	0.0E+00 10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytosolic, calcineurin-dependent 2 (NFATC2), mRNA
8547	9805			3.58	0.0E+00 AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8584	18031	23855		1.9	0.0E+00 11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8646	18155	23754		3.04	0.0E+00 AW560082.1	EST_HUMAN	hg31e05_X1_NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alt repetitive element; contains element MER22 repetitive element;
8677	18183			1.24	0.0E+00 L20493.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
8707	18217			2.42	0.0E+00 AF068757.1	NT	Homo sapiens somatosatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
8744	17689			5.04	0.0E+00 8635487	NT	Human endogenous retrovirus, complete genome
8765	18209			2.02	0.0E+00 AI204914.1	EST_HUMAN	an05h04_X1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:11684759 3'
8817	17735			1.78	0.0E+00 AI904646.1	EST_HUMAN	QV-BT065-020398-103 BT065 Homo sapiens cDNA
8828	18207			1.58	0.0E+00 BE249782.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
8839	11162	20364		1.69	0.0E+00 6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8839	11162	20365		1.69	0.0E+00 6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
8858	17761	23934		1.41	0.0E+00 AF036365.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds

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Table 4
Single Exon Probes Expressed in HEla Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	10873	20058	2.95	0.0E+00	H30132.1	EST_HUMAN	y59e08_r1 Scores breast 3NBHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
8872	10873	20057	2.95	0.0E+00	H30132.1	EST_HUMAN	y59e08_r1 Scores breast 3NBHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
8898	17781		28.04	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
8898	17783	23916	5.39	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
8898	17783	23917	5.39	0.0E+00	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
8891	17788		1.74	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
8909	112622	20376	1.55	0.0E+00	47584893	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
8945	17822		1.37	0.0E+00	AW_684989.1	EST_HUMAN	hi86e06_x1 Scores cDNA clone IMAGE:2879154 3'
8953	17827	23906	1.34	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8957	17830	23908	1.31	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8990	10448	18804	1.62	0.0E+00	89225582	NT	Homo sapiens hypothetical protein FLJ10697 (FLJ10697), mRNA
8997	17858		2.87	0.0E+00	11526281	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9021	12516	21647	3.3	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
9032	14093	23188	2.05	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9038	17881		1.79	0.0E+00	AB026900.1	NT	Homo sapiens CST gene for cerebroside sulfatase, exon 1, 2, 3, 4, 5
9078	17903	23902	2.37	0.0E+00	9958724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
9103	18377		6.14	0.0E+00	AL163244.2	NT	Homo sapiens chromosome 21 segment HS21CO46
9110	9877	18988	2.2	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9157	10879	19852	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9190	17978	23859	1.41	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
9198	17983		3.67	0.0E+00	7697020	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
9217	17898		1.3	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
9231	18007	23848	1.35	0.0E+00	8567337	NT	Homo sapiens peroxisome proliferator (Drosophila) homolog 3 (PER3), mRNA
9257	18025	23853	2.2	0.0E+00	AW025032.1	EST_HUMAN	wu83c07_x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2527596 3' similar to TR:Q12844 BREAKPOINT CLUSTER REGION PROTEIN contains TAR13 TAR1 repetitive element;
9260	18028		1.77	0.0E+00	AV656287.1	EST_HUMAN	AV656287 GLC Homo sapiens cDNA clone GLCEPG06 3'
9276	10386	19537	3.04	0.0E+00	9868844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

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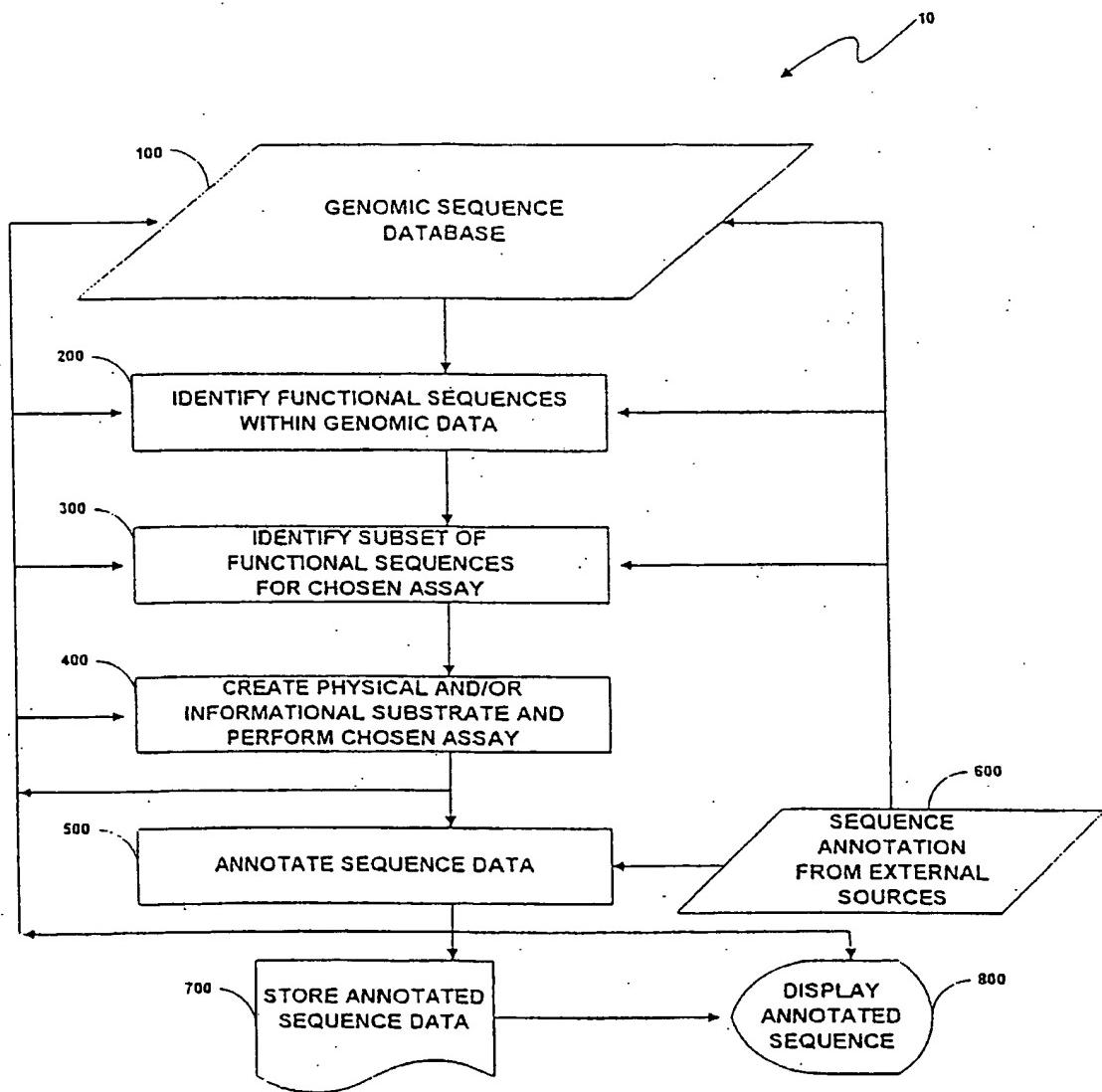


Fig. 1

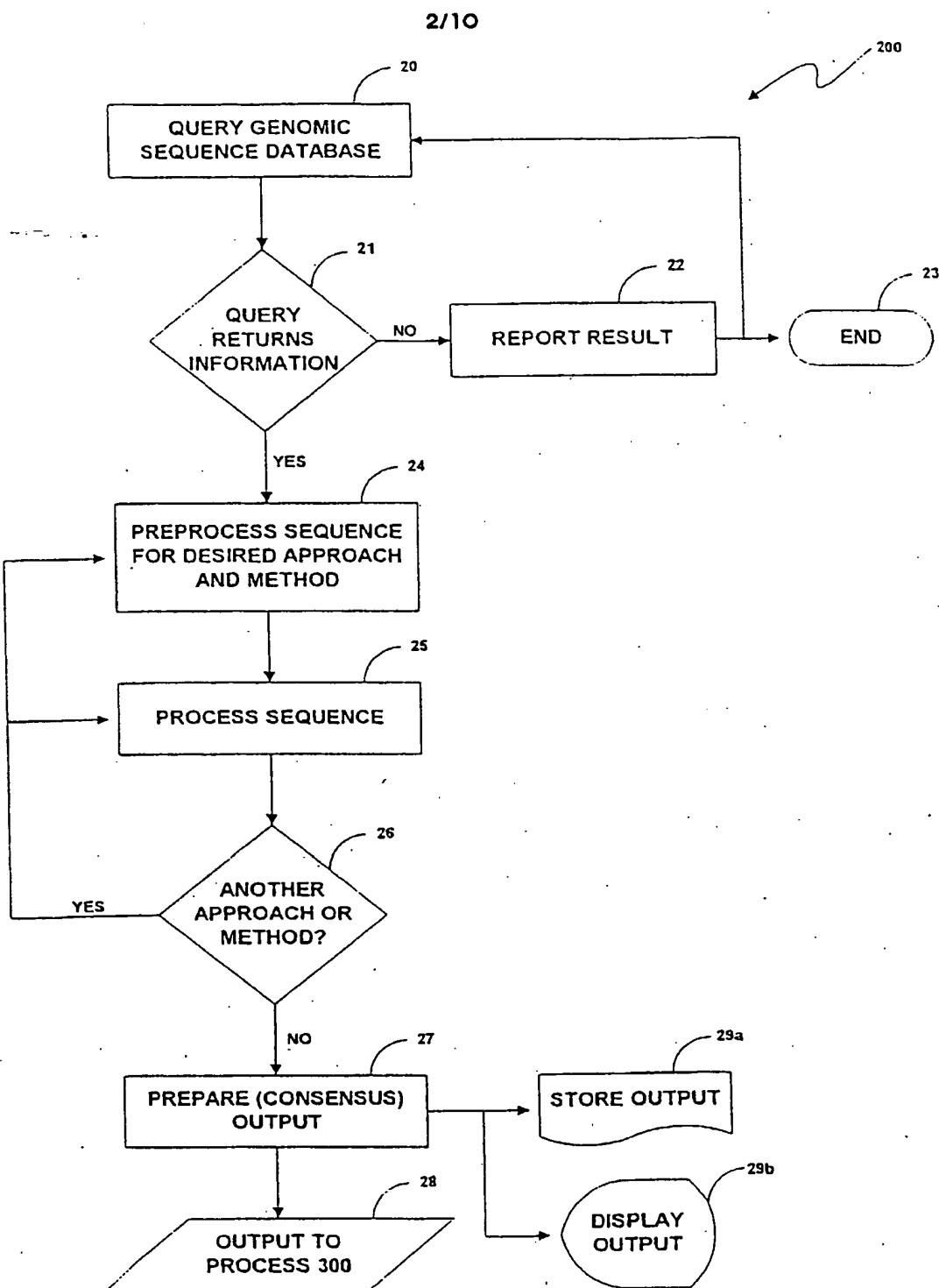


Fig. 2

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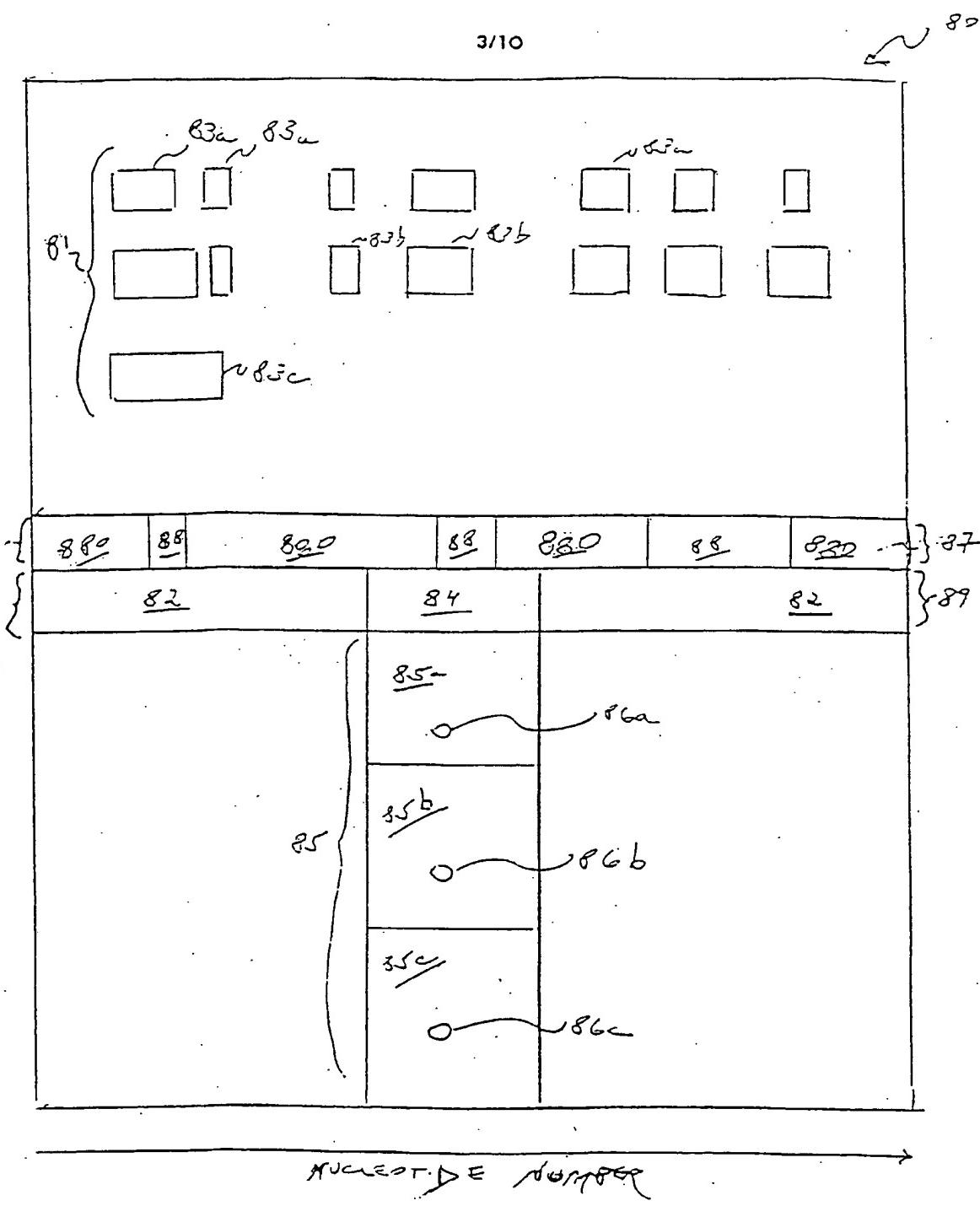


Fig. 3

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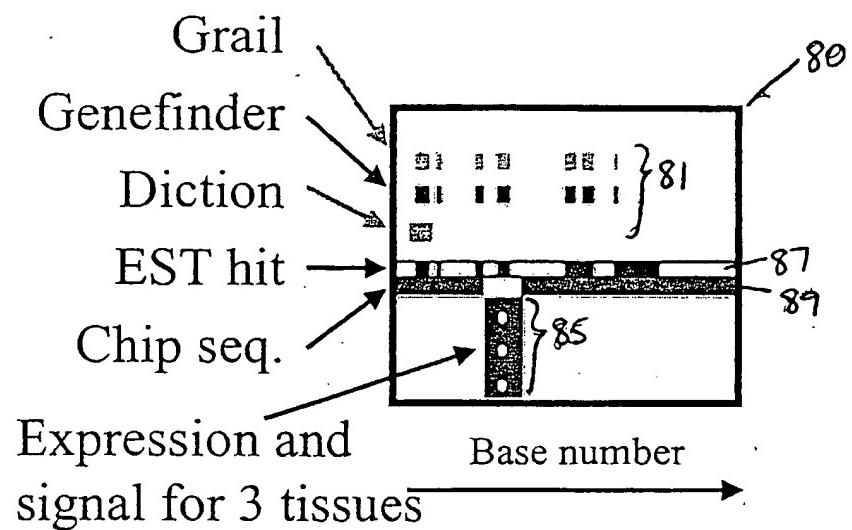


Fig. 4

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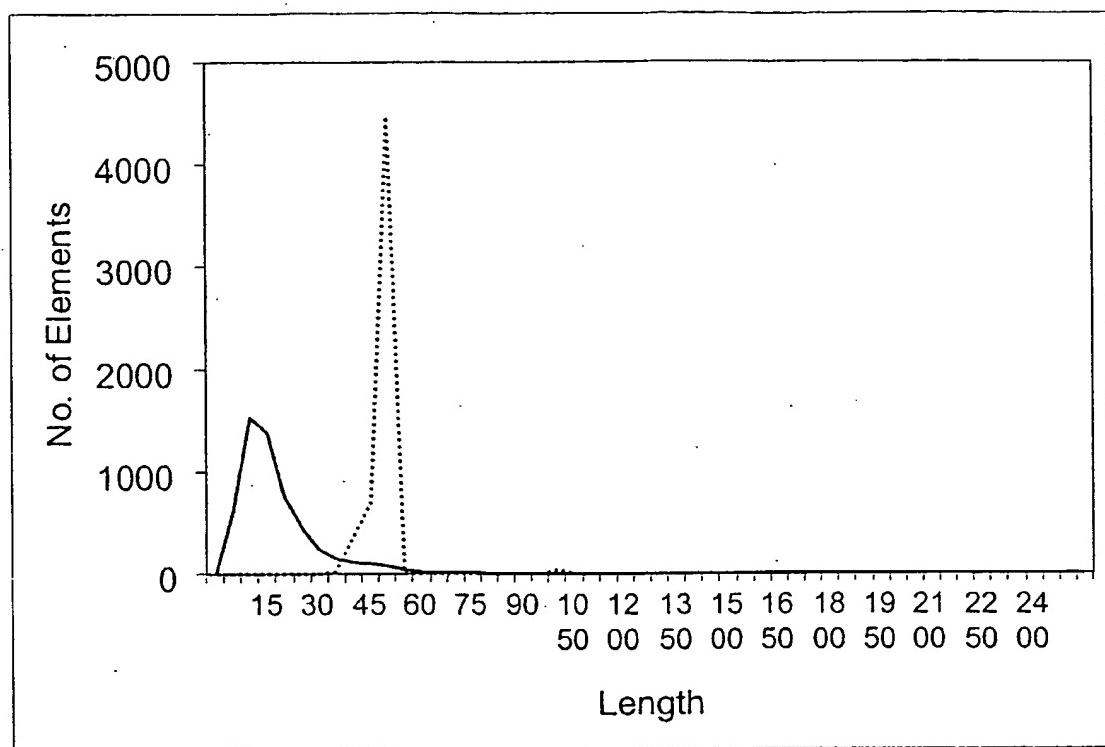


Fig. 5

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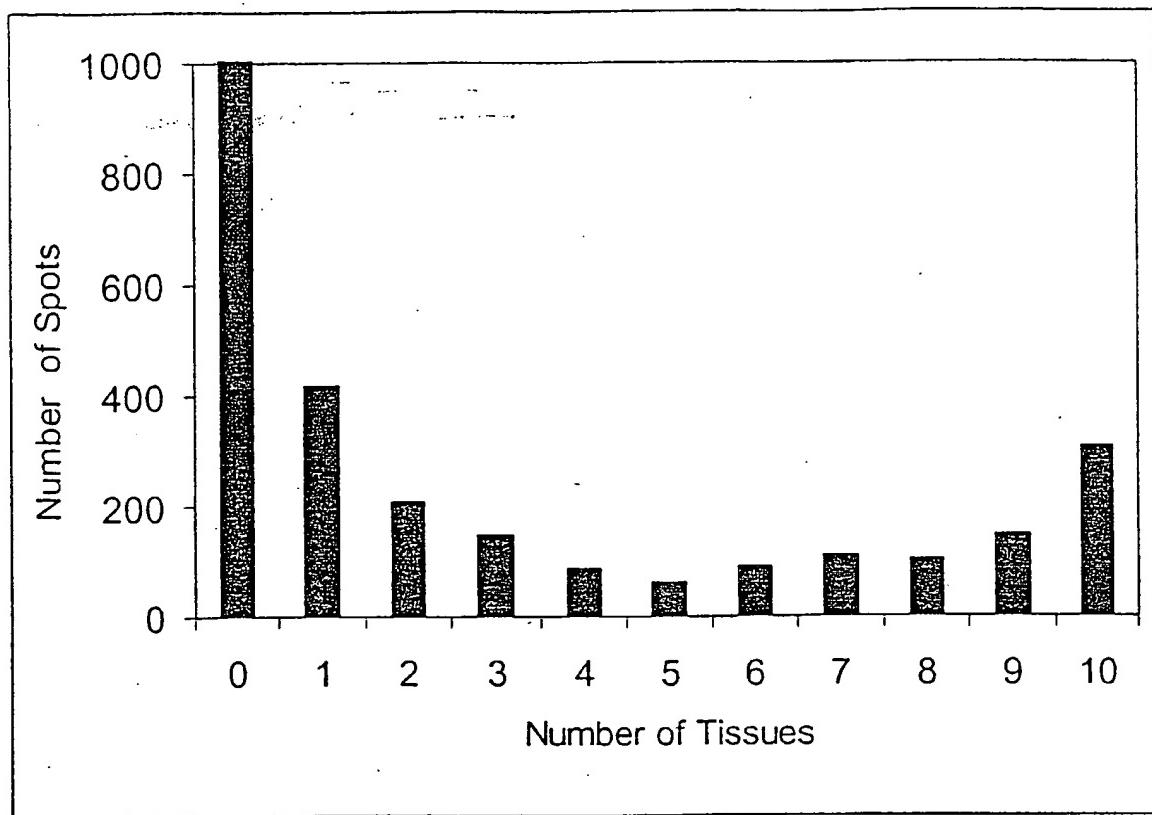


Fig. 6

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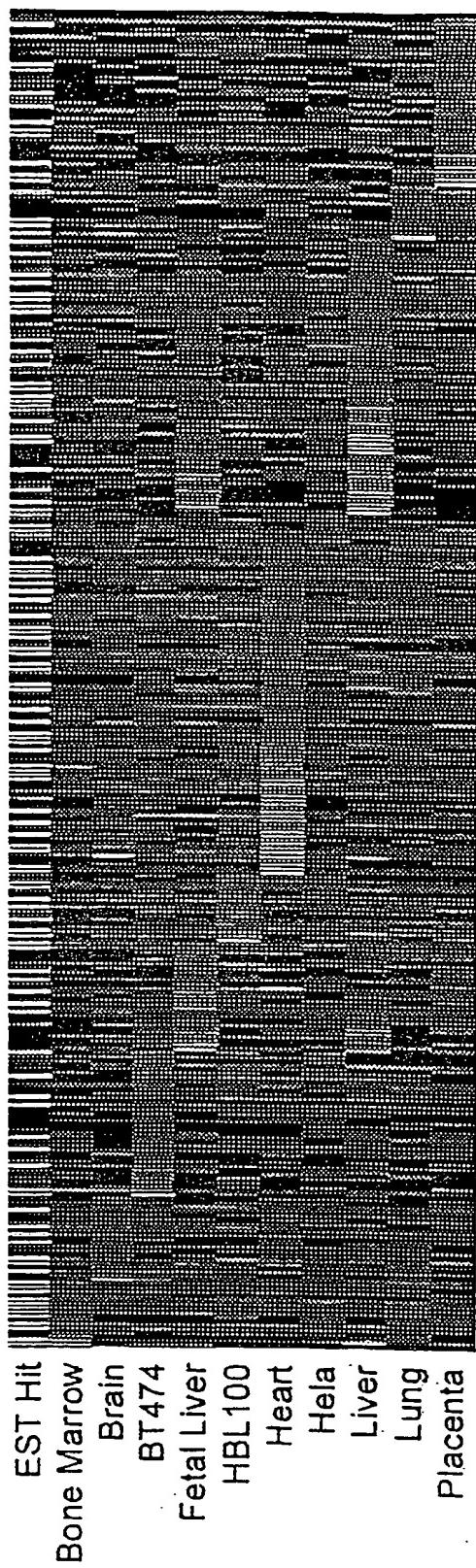


Fig. 7a



Fig. 7b

Fig. 7c

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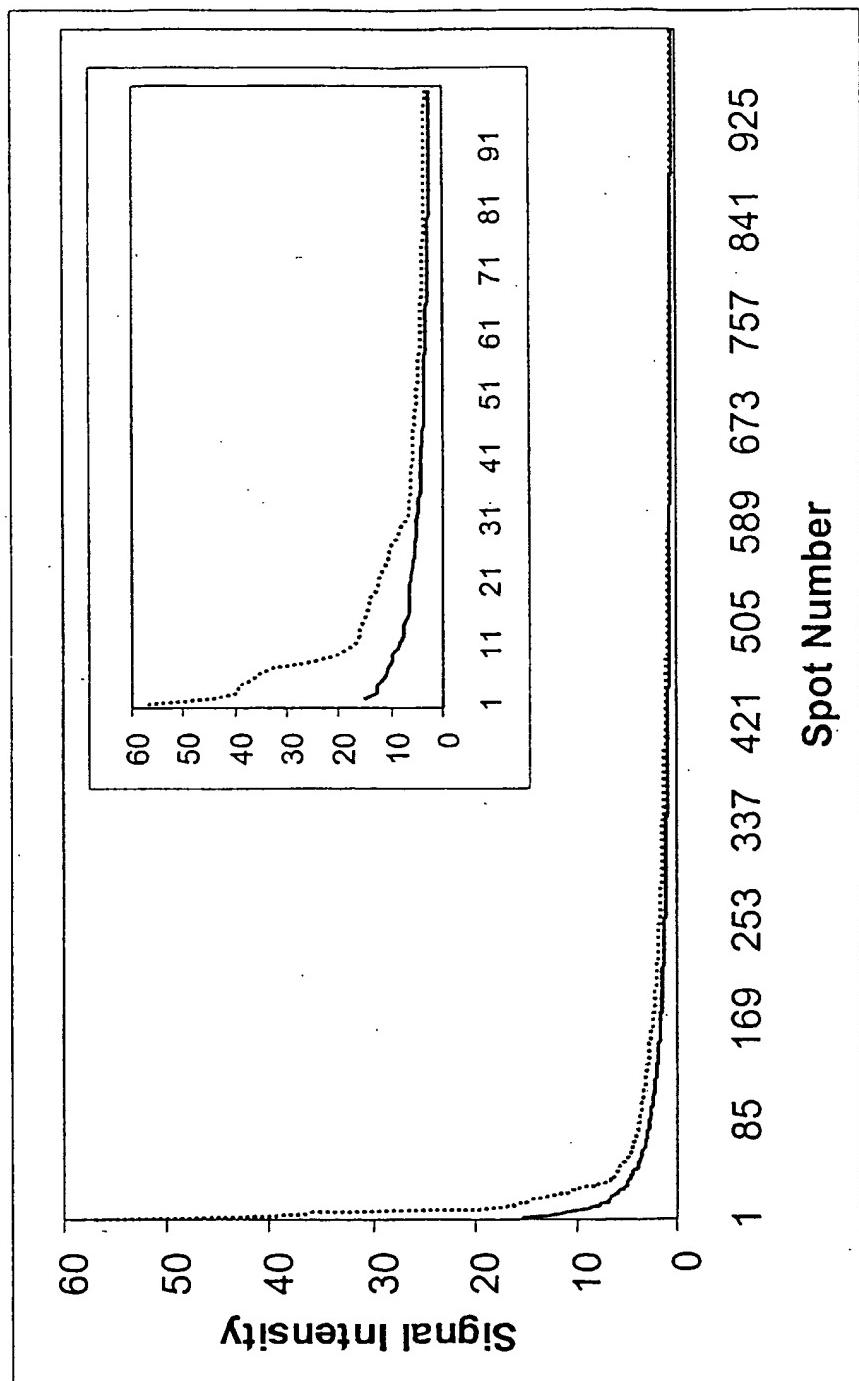


Fig. 8

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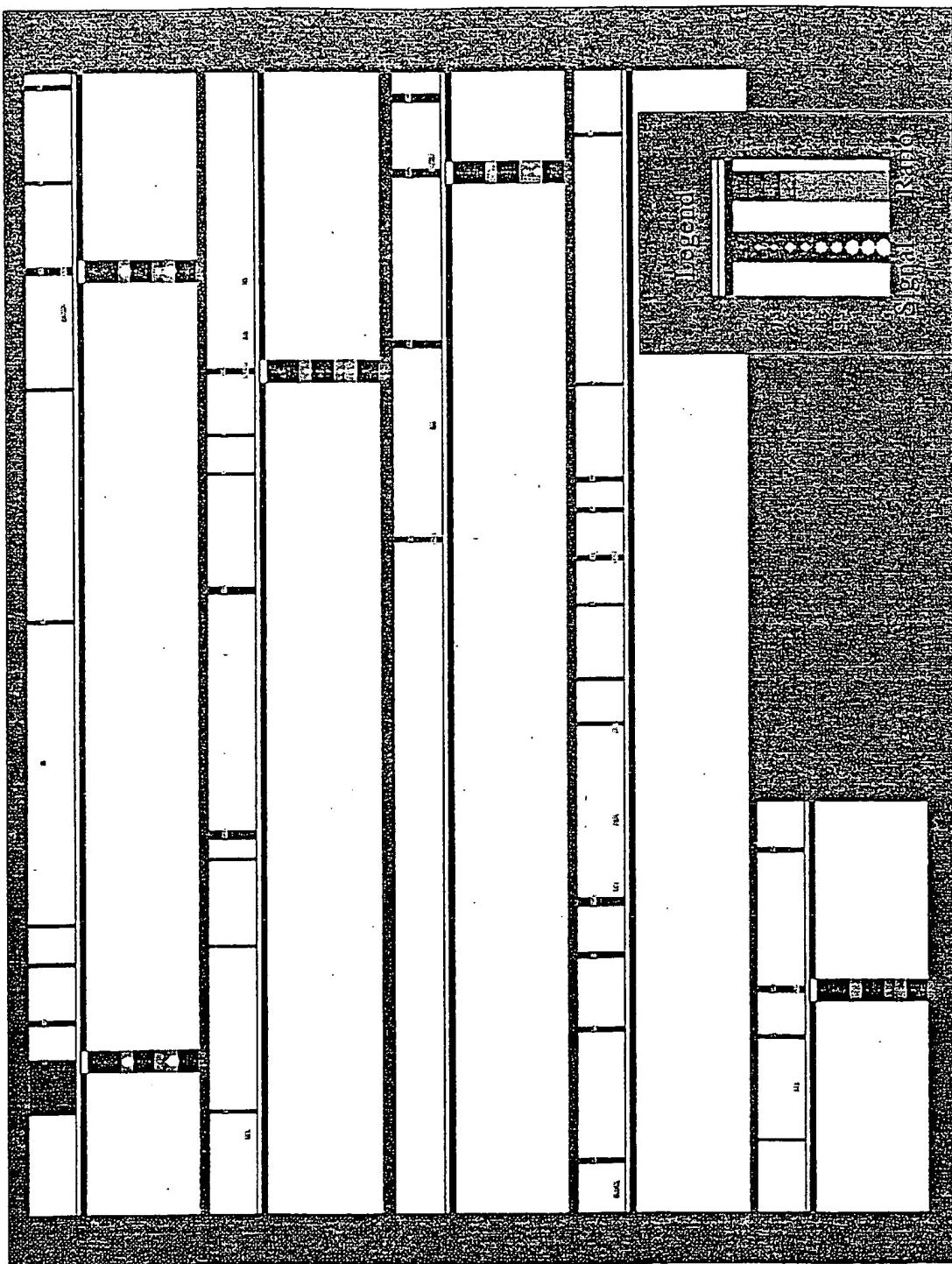
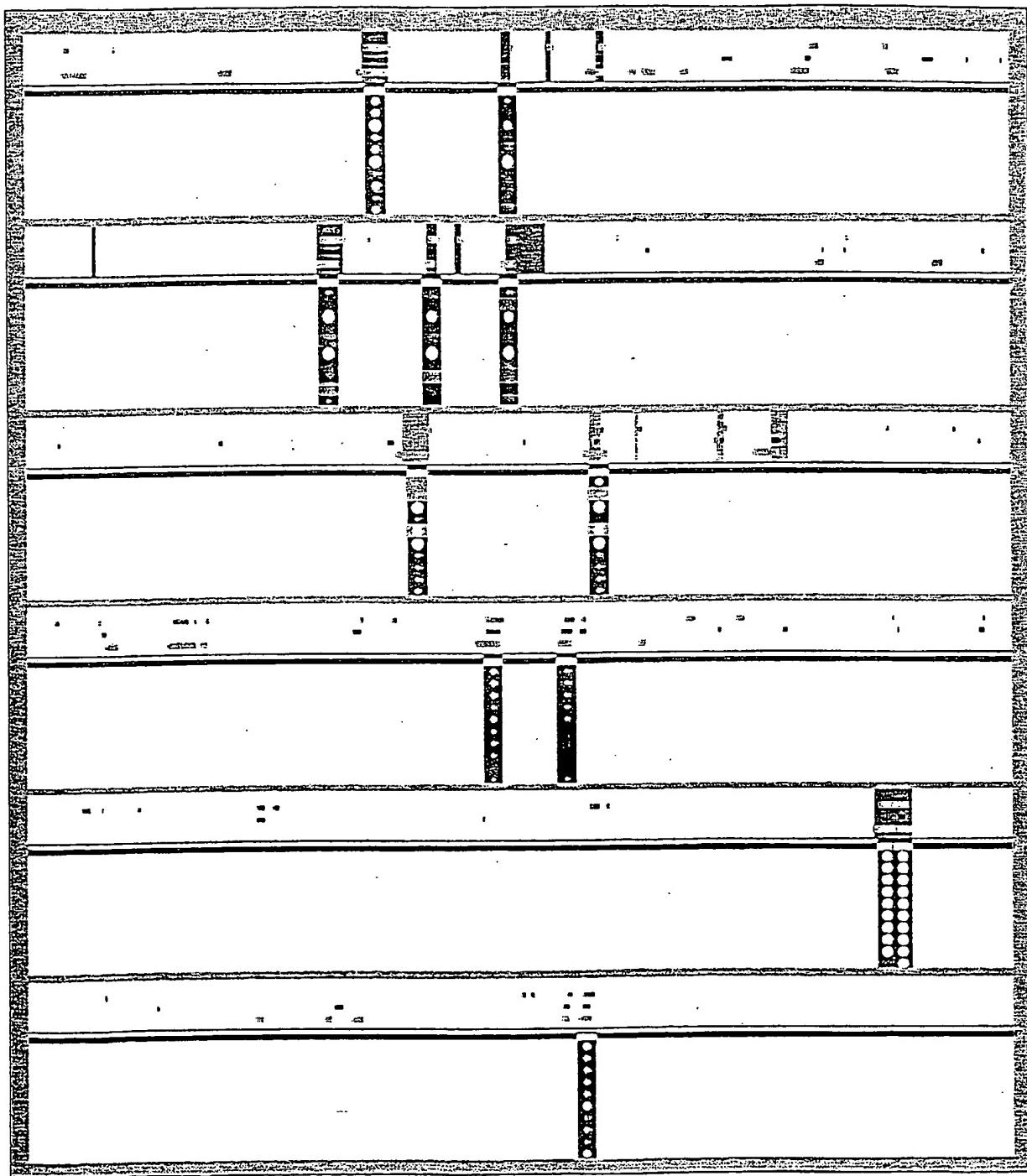


Fig. 6

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Fig. 10



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(71) Applicant (*for all designated States except US*): AEOM-ICA, INC. [US/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).

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A3
WO 01/057278

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEЛА CELLS OR OTHER HUMAN CERVICAL EPITHELIAL CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human HeLa cells is described. Also described are single exon nucleic acid probes expressed in the HeLa cells and their use in methods for detecting gene expression.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00670

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12Q1/68 G06F19/00 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 C12Q C07K G06F

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EBI 'Online! EMBL, Heidelberg; Accession Number T05900, 2 September 1993 (1993-09-02) ADAMS MD ET AL.: "3,400 expressed sequence tags identify diversity of transcripts from human brain" XP002184364 abstract --- WO 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) page 58, line 34 -page 63, line 15; claims; figure 5 ---	13
X	---	1-27

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00670

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE BIOSIS 'Online' BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 1992 ZIEGLER BENEDIKT L ET AL: "Single-cell cDNA-PCR: Removal of contaminating genomic DNA from total RNA using immobilized DNase I." Database accession no. PREV199395027417 XP002184283 abstract & BIOTECHNIQUES, vol. 13, no. 5, 1992, pages 726, 728-729, ISSN: 0736-6205	1,12,13
A	WO 98 01148 A (HARVARD COLLEGE) 15 January 1998 (1998-01-15) page 43, line 15 - line 27	1-27
A	SCREATOR G R ET AL: "GENOMIC STRUCTURE OF DNA ENCODING THE LYMPHOCYTE HOMING RECEPTOR CD44 REVEALS AT LEAST 12 ALTERNATIVELY SPLICED EXONS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 89, no. 24, 15 December 1992 (1989-12-15), pages 12160-12164, XP000470187 ISSN: 0027-8424 abstract; table 1	13
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims	1-27
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document	1,12
A	WO 99 39004 A (COLLINS FRANCIS S ;CHEE MARK (US); EDGEMON KEITH (US); US HEALTH () 5 August 1999 (1999-08-05) page 20, line 20 -page 25, line 20	1-21
		-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00670

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	GUAN ET AL: "GRAIL: an integrated artificial intelligence system for gene recognition and interpretation" PROCEEDINGS OF THE CONFERENCE ON ARTIFICIAL INTELLIGENCE APPLICATIONS. MONTEREY, MAR. 2 - 6, 1992, LOS ALAMITOS, IEEE COMP. SOC. PRESS, US, vol. CONF. 8, 2 March 1992 (1992-03-02), pages 9-13, XP010027422 ISBN: 0-8186-2690-9 the whole document ---	1,12,13, 21-24
A	SOLOVYEV V V ET AL: "PREDICTING INTERNAL EXONS BY OLIGONUCLEOTIDE COMPOSITION AND DISCRIMINANT ANALYSIS OF SPLICABLE OPEN READING FRAMES" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 22, no. 24, 1994, pages 5156-5163, XP002915964 ISSN: 0305-1048 the whole document ---	1,12,13, 21-24
A	WO 98 02576 A (UNIV MASSACHUSETTS) 22 January 1998 (1998-01-22) the whole document ---	1-27
A	DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 24 June 1999 (1999-06-24) MASUYA YOSHIRO ET AL: "MAP kinase-independent induction of proto-oncogene c-fos mRNA by hemin in human cells." Database accession no. PREV199900356381 XP002184284 abstract & BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 260, no. 1, 24 June 1999 (1999-06-24), pages 289-295, ISSN: 0006-291X ---	1-27
A	DATABASE EBI 'Online! EMBL, Heidelberg; Accession Number AL049837, 11 May 1999 (1999-05-11) HEILIG R. ET AL.: "Sequencing of the human chromosome 14" XP002184365 abstract --	13 -/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00670

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NOBLE LUIS S ET AL: "Prostaglandin E-2 stimulates aromatase expression in endometriosis-derived stromal cells." JOURNAL OF CLINICAL ENDOCRINOLOGY & METABOLISM, vol. 82, no. 2, 1997, pages 600-606, XP001037435 ISSN: 0021-972X the whole document ---	
P,X	PENN SHARRON G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, vol. 26, no. 3, November 2000 (2000-11), pages 315-318, XP001037413 ISSN: 1061-4036 the whole document ---	1-27
X	DATABASE EBI 'Online!' 9 May 1997 (1997-05-09) MARRA M. ET AL.: "The WashU-HHMI mouse EST project; vc72c02.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:780098" Database accession no. AA414703 XP002208274 abstract ---	13,14, 18,20,21
X	DATABASE 'Online!' 16 October 1997 (1997-10-16) MARRA M. ET AL.: "The WashU-HHMI mouse EST project; v160c06.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 976618" Database accession no. AA619735 XP002208275 abstract ---	13,14, 16,18, 20,21
A	DATABASE EBI 'Online!' 27 April 1999 (1999-04-27) DICKHOFF R. ET AL.: "Sequencing of human chromosome 14q31 region" Database accession no. AC007372 XP002208276 abstract -----	13,14,18

INTERNATIONAL SEARCH REPORT

I nternational application No.
PCT/US 01/00670

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27(partially)

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 9291 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, the peptide encoded by SEQ ID 1 or 9291 (claims 26-27) having the sequence SEQ ID 18393 (see ISA form 206), which is the translation from SEQ ID 9291 (see p. 66 of the description).

2. Claims: 1-27(partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 9292 (see p. 92 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 9292 having the sequence SEQ ID 18394, which is the translation from SEQ ID 9292(see p. 66 of the description).

...Inventions 3-9290: similar subject-matter as above related to SEQ IDs 3-9290.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1 and 2.

- 1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, 1. 6-11).
- 2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 and 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.
- 3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. SEQ ID 18393 and 18394 (Art. 6 PCT).
- 4) Claims 15-21 relate to nucleic probes, solely defined in that they code for a polypeptide having the sequence SEQ ID 18393 and 18394. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 9291 and 9292.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

INTERNATIONAL SEARCH REPORT
Information on patent family members

International Application No
PCT/US 01/00670

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